

606

AACACGGTTC	CTGTGAAATT	TTTCAAAGAA	CAGGCTAGGA	TGATGTCTAT	GTCGGACCGA	9240
CGTGAGCAAT	TTCAATACGC	ATTTTGGAT	TCAGGTATAG	GAGGATTGCC	CTACGCACAC	9300
GCCTTACGCG	TGCGTGTGCC	TGAGGCCTCA	CTGGTGTACG	TGGCGGACCG	TGTATACTTT	9360
CCTTATGGGA	ATAAAAGTTC	TGCACAGATT	ATTGCGCGTG	CGTCTGCAGT	TTTGCAGAAA	9420
GTGCAGACGA	ATTTTTCACC	ACACATAGTG	GTACTCGCGT	GTAACAGCAT	GTCTGTCAAT	9480
GCACTTGAGT	TTTTGCGTGC	GCAGGTTTCG	GTTCCAGTGG	TGGGGGTGGT	GCCTGCAATT	9540
AAGCAGGCGG	TGGCGTGCAG	TCATAAAAAG	CACATTGGTG	TCTTAGCTAC	ACAATGCACG	9600
ATTACGCATC	CGTACACAGC	GTGTTTGAGA	GCACAGTTTG	GTGCaGGGTG	TGTGTTTCAG	9660
AATgCtGCGG	ATGCACGCCT	TATTGAGTGT	CTTGAGCGCG	GGTTAATTTT	TGAAGTCgAA	9720
GACATGCaGC	GGGAGGCAGT	GGCGCGCTCA	GTTATGCCCT	TCCAGGAAGC	GGGGTGGAT	9780
GTGCTCGTGC	TCGCGTGCAC	CCATTTTGTG	CACGTGCGTC	ATCTTTTTCa	GGACTGTGTT	9840
GGTACCTCGT	GTACGGTGGT	AGATTCGCTA	GAAGGTGTGG	TACGCAGGAC	GTTACGTCTG	9900
TGTCCACCGC	AATCTCAATT	GCGTGGGAAC	GCCGCCTGTT	ACGTAACGG	TGCGCGCGAT	9960
GCAGTGTGCG	CGGCACGATA	CGCACGGTAT	GCGCAGCACT	TTGGATTGCG	CTGGGCGGGT	10020
TTTTTGGaCk	TATGAACACG	GCACTGGATA	TCGGGTGCGT	GCACTGTGTG	TGTTTGTGTG	10080
GAGGCGGTAG	ATAAgAgAgG	CTGATAgACA	GCGCGGTGCT	GCGTGCCTAC	AATGGGCCAT	10140
GGGGAAGCCG	AGgTtTCGTG	CAGTGGCCTT	TGACATtGAT	GGGACAcTGT	ACCcTGGATG	10200
GCGCCTTGaT	GCGTGTtATg	CCCTTtATGA	TTCGCAATGC	GCGCTTGATG	CGTGCCTTCC	10260
GTGCGGTGCG	TCAGGAGCTA	CGTCGTGAGC	AACGTACGGC	ACTTATTCCT	TTGAAGACT	10320
TTTTTTTTGc	GcAAStACgC	GCATCGCGCC	GcGCGTGGGT	TTATCTGCAG	AAGAAGTGCG	10380
AGCCTTCCTC	GACACAGCGC	TGTATCGGGG	GTGGAGGCGT	CACTTTTTTAC	ATATAAAGCC	10440
ATTTCTCTCAC	GTGCTTTTCT	CGGTGTTGGA	GCTGAGGCGG	CATGGGCTGA	AGATAGCGCT	10500
TTTGTCGGAT	TTTCTCCGA	GTCAGAAAGG	CTGTCtATGG	GGGGTGC GCG	CGTTGTGCGA	10560
TGTAACGTTG	GGCACAGAGG	AGATTGGGTC	CCTCAAGCCT	TCTCCCCGGG	CCTTTTACGC	10620
GcTGGCGCAG	AGACTGAATC	TGcGCTGTGA	AGAAATTCCT	TACGTGGGGA	ACAGTGTTCa	10680
TGACGTGGAA	GGCGCGCACG	CAGCAGGTAT	GAGGATTGCC	TGTGTGCGCA	GgCCCTTTAC	10740
GAGTCTTCGC	GTTCGGCGCA	cGCGGaCTGG	CTCTTTTCCG	ACTATCGCAC	ATTGTGcGCA	10800
TATGTGATAG	CATGAGCGCC	GGCGCAGGGT	AGTCTGCCGA	ACCCACACG	TCCAGCGTGG	10860
CGCCCGCGGG	TACCCGCTGT	GCGTCGCGTG	AAGACGAAGt	GAGTGGAGCA	TGGAGTACTT	10920

607

TCTGACGGTT GTCATTGCCT GCGCGATTTC CCTCGTGATG GTTGC GTTCT CCCGCCAGCT 10980
 GGACAAAGGT AACCGTTCTC TTGAAAAGGT CAAGCGCTAC GCGKACTACA TAAAGGAAGA 11040
 TCTTGAGTCA TcAGCGCAGA GAAGATTGCG ATGCTCAAGG ATGCGGCCAT CGAGTTAAAT 11100
 GTAAAGCAAG AGCAGGCGAT TGCCTCAGTG AAAAAATGG ATCACCTCTA CGACCAGTTT 11160
 ATGAagaAGT CTACTGCGCT TGCGGTGCAA A 11191

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

GGAAAAAACC TTAAATTCC CGGTACAATT GTGCAGAGAG CGTTTATTA TGA CTGATGA 60
 CAAGnGTCGG TTTTTCAnG CGTGCAATAA CGTTTGCAAC TGTAACGTT TTCCCCGAAC 120
 nGGTAACACC CTTGAGCGTT TGAAAACGCG CCCCCGCATG CAAGCCACGC ACGAGTGCGT 180
 CGATTGCGGC AATCTGATCG CCTGCAGGTT GGAAAGAAGC GTGTAATTTA AATTCTTTCA 240
 TGTGCTTCGC AGTATCGGTT ATTACCATAG GATTTAAAAA ATCTGTAGTA CATGCTGTGC 300
 CTTTCCCTTT GATTTTGCTC TCTTAGAACC TCTGGTTGAC AAACCACACC CATGGTGAAT 360
 AGAGTGGACC CCGCTTAAGA GGAGGCACGT TATGGTCAAG TTGCTTAGCA TTGGTGGATC 420
 GGATGCTTCA GGTGGTGCGG GCATCGAGGC GGATCTGAAA ACTTTCCAAG AGTATGGAGC 480
 GTTCGGTGTG GcTACGCTCA CCGCATCGT TACTATGGAC CCATCCCGGA ACTGGTCGCA 540
 TCGGTACAT TCACTTGAGG AAGACTGTGT GCGCGATCAG CTTGAAACCG CATTTGCAGG 600
 CGTGGGGGTC AGCGCGGTGA AAAGCGGTAT GCTTGCTCT GTCCATGCAA TCGAATGTGT 660
 CGCGGAGTAT CTCGAACGTT TTGCAGTTGC TGCATACGTC TTTGATCCTG TCATGGTATG 720
 CAAAGGATCG GGAGATGCAT TGCACCGTGA GTTGAACGAA TTGATGATCC AGAAACTTTT 780
 GCCACGCGCG ACAGTTGTTA CTCCCAATCT TTTTGAAACC GCCCAGATTG CCGGTATCAG 840
 CGTACCACGG ACAGTGGACG AAATGAAGGA GGTGTCACGT TTGATTCACG AGCGCGGCGC 900
 GTCGCACGTG TTCGTCAAAG GCGGCGGAAG ACTCCCCGGT TGCAAGCACG CTCTGGATGT 960
 TTTCTACGAC GGCAAGACGT TTCACCTCGT TGAAGATGAA CTTGTGCAGA GTGGATGGAA 1020
 TCACGGCGCG GGCTGCACCG TATCTGCGGC TATTACTGCA GGACTGGGCC GAGGACTCAC 1080

608

CGCCTACGAC GCGATACTGA GTGCTAAGAG ATTCTGTGACT ACAGGCCTCC GCCACGGATT 1140
 CCAAGTCAAC CAGTGGGTTG GAACAGGAAA CCTCAGCAA TGGCGCGACC GCTTCCACTG 1200
 ACTCAGGCGG TACATACGTG GGCGATCAGT GCTGGTATAG GTGCTTGAAG TATTCCAAGT 1260
 CGGTTGAGAG GATCTTCTCC GTGTCGGGGA GCGATTTCTT GTACACCTCC AAGCTTTTCC 1320
 AGAAGCCGTA GAACTCAGGA GATTTCCCGT ACGACTGCGC GTACACGGCC GCGGCGCGGG 1380
 CGTcTGCTTC ACCcTTGATA CGCTCTGCCT CCTCGTACGC TTTTGAAAGT AAAcTGC GTT 1440
 TTTCTGTGTC GAGCTTTCCA aGCCACTCTG CCTTCTTTCC TTCGCCTGTG GAGCGGAACA 1500
 TTTGCGCGAT CTGGTTGCGC TCTTTTACCA TCCGATTGAA CACAGATGCT TGCAGCTCAT 1560
 CTGAGTACTT AATCCCCTTG AAGATCACAT CGACAACGAC AATACCGAAA TCTTTTAACT 1620
 GATCATTCGC CGCCTGTGAG ATCTCCCGCG CAAGAGACTC TCGCCCCTTT TCTATCGTCA 1680
 TATGCGCAGT TTTCTCCGCA CCCCTATCAA AGGCAAGCTG CGACACCGGG ACGTCAAAC 1740
 GCTCGGAGTG ATTGGACTCG TTGATAGCGn TTn 1773

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

CAGCACATGC ACATGCATAT TCTTCCTTTT CGTTCATGAG CGGTATCCGT TTCAGGTCAT 60
 TCAAATATGC CGTGAGAGTA TTCTCATCGT GCGGGAAGT CATTGTCTC ACAGAGTACT 120
 CCTTTTGTTT GAAAGGTACG TACCATATAC TCAGCAAATA TCATGCCATT TACGATAAAC 180
 CAGAGGAGAT CTGTTCCGTG TCCCTATCAC GCCACTGGAC CCTCTGTGCA TACCTCCCTT 240
 TCCCACGGCG CGCTACAGTT CTCTTGATTC TTCAAAAGGA AATGTATAGA ATGCGCCCCG 300
 CGcGGTGCGT GTAGGCATAC GCGGCAAACG TGAAGATATG ACTCGTTATG AGGAGGAACG 360
 CATGAAAATT ATACCGCTCG CGGACCGTGT CCTGGTAAAA ACTGATAAAT CGGAAACTAA 420
 GACTGCTTCT GGAATCATCA TCCCGGACAC TGCGCAGGAG AAGATGCAAA GCGGTACCGT 480
 CATTGCTGTT GGTTCCTGACT CGGAAAAGAT AAAAGTTTCG GTGGGTCAGC GTGTCTATGCA 540
 CGATAAATAT GCCGGAAC CAGTAAAGAT TGATGGAGAG GAGCACCTGC TGCTCAAGGG 600
 TGCTGATATC CTAGCTGTCA TCGAGTAGTT TCATCTCTTT AACGGGcTGC GCGCGCTGGA 660

GCAGTGCACG CGCGGCCACC GTCTTTCCCT GTTGCTGCAA AAGTTGTCCT GCACGCTGGT	720
ACCATTCTCT CCAGCGCTGT GCTTTCCCCG CCGCCGGGcG CkCTCGAGGA TGTTCCTCGG	780
CCTCCCCCTC TCCCCGnTCC TTTTGAAGTT GTCGTA CTGA TTCgCGCGTT GCTTCGTCTG	840
CCGCAAGCAC AAAGTGTTCCT GCAGCCGCGG TTTTCTTGCC CATCCGCTCA AGCACTATCG	900
CTATGTTTTG GgArCGnCTG tGCGCGCTTC CACAGCGCGT GTCGCTTCCA CCAAGCCCCC	960
GAGGATACTC TCCACCCTCC CCGTACGAGA AGCTGcAGCA AGTGCCCGAT AGAAAGCATC	1020
CTCAGGACCA CCTCCTGCAT CACTGAGACC AAACGCTGAC TCATATTCCC CAATTGAAA	1080
AAAGAACCAA CGTGCATACC GACGCACtGT GTGTCCACAG GgAAGACTTC AAGCAACTGC	1140
CACAGCGCGC CCCGACTGCC CTGTAGTCTC TTTTGTGCAG GATAACAAAA ACGAAAGTAT	1200
TCCAATGCAA AACGCACATC TGCCCGCCCA TGcATCGCCT CTGTGCTAA TTCCGCCAGC	1260
AATGACCGAG CCTCCACAGG AAAATGGGGA GACAAAAAGT GTCCTGTTC CATCTGCACA	1320
GAATACACCC CCCTTTCAGA GAGCAATTCC GTAACAGAAT CGCGCTGTCT GTGTGCTGCA	1380
CGAAAGGCAA TGCTCTCTCG CGCATAGCAC GCAACGGCAG GATAGTACGT TTTATCCCCC	1440
TCAACACACT GCGCGAGCAT CCGAACACGC TCCTGTGCAT GAGGAGCAGT GAGTGCTAGA	1500
TTGTAGAGTG CATGTGTGGA TGTTCAGGA AAACGGTCAA CGTACGCGTA CAAAAAGCA	1560
CGTGCACGCG CTCTATCCCC TCCATCGAAA GCGGCATCTG CCGcTAACAG CAAGTGAGTA	1620
CGGGCGTGCG TCGAGGCGGC AGAGTACGTA CCGAACAAAT CTGCACGTGC AAGACTTATG	1680
GGGAGCAACT CAAAGACCAA AGAAAACTGT CCTGCGTCAT AGGCGACTGT GGCCCAGAAT	1740
GCCGTATTCT CCGGTGCCTC AGTACCCAGT ATACGGGAGT ACAGACGGAA CGCAGCATGC	1800
AACTCCCCCA CGCGGGCGTA CGCACACGCG GCATTCTGGA GAAAGGCATG CATACCACTG	1860
ACACCAAAGG CTGCAAGCaA AGCGCAGGAG CAATGCGGGC AAGTGCGATG CCAGTTGTAT	1920
GCCGTATTGG CGGCGACGGT TCTACACGAA ACTGCTCTTC TCCCCGGTCA AGAGGGAACG	1980
CCGTCACGTG CGCTTGATCT CTACCCCCCT GAACCTGAGA AACTCAACA GGCTCCTCTG	2040
GCACGTGCTC GGCTCTCTCA CTGTGAAAAG AGCCCCGAGA TGGAGAGTCA CCTCCTGTGC	2100
GCGAACCTAT GAGAGCAGCC TTTATCAGTG CCTCTGCGCC AATACTCTCA TATCCCTTGT	2160
GCACCACCCG GGGGACATAG GAGATTGCTT CCTCGAAACG AGCCTCCCGC AGGAGAAGAT	2220
GTATACCAA TGCAGCAAGC CTGCCATCAT CTGCACTTCT TCGTATGCCA CGCTGGAGTG	2280
TACGCAtGCC GCAGCGGAGG CTGAGAGTTC CATCTGACGC TTGGCAATAC TCAGATACTG	2340
CGACGACTCT CGCGCGTGTC CCACCATACG CGCAAGACCG CGCAAGGCTG CGCCTTTGCG	2400

CtTCCTGAGC AATCAGACTA TCTGCACGCG CAAGTCTCTC CAAAAAGGGC CGACTCCCCC	2460
AAACGGAGCG ATAGATGCAT AGCCCAGCAA TACCCACCCC AACTACTCCA AGGTAAGAGA	2520
GGAGGTGGCG CTTACTACGC ACTTTTAGCA ATGTTATCGA GCACACCATT TACAAAGCGG	2580
AAGGAGTCGT CcGTACCGAA ATCCCGAGCG ATACTGACCG CCTCGTGTAT AACGACGACG	2640
GGGGGAATGT CTTTTTGAAA GAGTAGCGAA TACGCACTTA GGCGCAGGAT GGCCTTGTC	2700
ACCTTGTTCA AACGCACAAA ATCCAGTGT TCCAACCGTG AACTCACACA ACCGTCAATT	2760
TCCCGCAGGT GCTCGAGCGT ACCGAGAAAG AGGAGTCGGG AAAACCCCAA ATCCTGGGTA	2820
GAAGGAGGCG GGTTCCTCCG CAACCAAGTA AACTGAGTTA ACGTCTCCGG CGTGATGCCC	2880
GCCGCGTCCC AGGCAAAGAG AGCCTGAAAA GCCAGAATCC GAGCGCGCCT CCTCCCTATC	2940
TTTGGGAATA CTTCACTCAC CAGTCGAGCA CCTTGCCGAG CTCTGCGTCA GCCAAGAATA	3000
CCTTATAGGT ACCAGACTTC CTCAGcTCCG CCGACACTTC CCGGATAGCG TCCTCGAGCG	3060
CTTTTGTGTTG GATTGGGAA GTAAGAAGAT TCTTGATAAA CTCGTAAAGC GAGACGGTCT	3120
TGTCAGGCTC CACCAAATCG CTGAGCGTTA GGATCTTCGC TTCCTCTTTC TTCAAACTA	3180
TGAAGCACTG ATAGTCATTA GCCGTTTCAT TCACGTCCGA AACAGCACCA ACTCCCATGC	3240
CAAAAATTTT AAGCAACGCC TCCATCGTCA GACCAAGCTG CGTGGCAGTA ACCGCAGTCT	3300
TCCCCAGGTA TATTTCCCCG GCAGAGTAAC CCGCCTGTGC ACCATTTGCC TTACTCTTAA	3360
TGTCAGCCGT GGCTTTGACA CCGGAACCTT TAAGTTTCTT AACAACTCT TGCGCTTTCG	3420
CCTTTCAGC AGCAGGACCT GAAAcTCGG GACAGAAATA AGAAACAACT TAACCGTGTC	3480
AGGGCGGAAA AAGGCCTGTT TATTAAGCTC GTAGTAGGAA CGGATTTGAG AGTCCTCAGG	3540
TCCCTTCAAA TTCCGAACT CGTCTGCCTT CTTTGTGTC ACGTAGCGCT GCGTGCTCAC	3600
CTGCGTCTTT AGAACTTTT TGTATTCTGC CATAGTCATG CCGTTTGTCT GCTTCATGAA	3660
CTGATCGAGC GAGATATTCT GCTTCTCCTT GACGTAATTG GCGAACTCAG CCTCCGTTAC	3720
CGCACGTCCA ATCTGTTGAG AAAGCATTCC ATTAAAATAC TGATTCACTT CAGCATCCGT	3780
TACCTGGATA CCCGCCTTTT CTGCCGCTTG AGCAAAAAGC TTTTCGTCAA TAAGACTGTC	3840
CATGAATTGT CTACGCTCAG CAGTGCTGAG CTTCTTTCCC ATCTCTTTCT CAATCGCAGA	3900
AATTCTTGCC TTAATCTGTC CGAGCGTCAc CGGCTCACGC CGGAATAAAT TCACTTCGGC	3960
GATAGGCTGC AGCGCCGACT GCGCGTGCGC AAACCCATA CCCGCCACGC ACAACAGAGC	4020
GGGAACTATG TATCTGCCCA TGAGAACTCC CCGTAACAAC CGCGACTcAG TCACCAGCAC	4080
ACACGCCGGA GAACTATAC GCAGCAGGGC AAGTTACGAC TTTTCCCCGC TTTTCTCAAG	4140

611

AATCGCGCGA	ATACGCCGCA	CCCCCGCCGC	ACTCGACTGT	TCCTTTTGAA	TAGAAAACCG	4200
CCCGAGCTGC	CCGGTACGTG	CTACATGTGG	ACCGCCACAC	ACTTCCCGAG	AAAAAGTTCC	4260
TATGGAGTAC	ACCTTTACAG	TTGATTGTA	TTTCTCACCA	AACAACGCCA	CGGCACCAGA	4320
ATTTCATCGCA	TCTTCGAGCG	ACATCACTTC	ACAGCACACC	GGCAAGTCTG	CCCGGATCTG	4380
CTCATTCACC	AACTGTTCCA	CCTGCACCTT	CTCCTGCGCA	CTCATCGGTC	TTGGGTGAGA	4440
AAAGTCGAAA	CGCAGGCGTT	CTGCCGTAAT	ATTTGAGCCT	TTTTGCTGCA	CGTGCGTACC	4500
AAGAACCACT	CGCAATGCCT	GGTGCAGCAG	ATGCGTCGCC	GTGTGGTACG	CTGTGCTTTC	4560
CGCTGAATGA	TCAGCCAACC	CACCCTTAAA	TACTCGCTGT	GCACCGATCC	GAGAGCACGC	4620
CTGGTGCGCC	TGAAACGCGG	TGTCAAACCC	TGCACGGTCC	ACCCGTAAAC	CCGATTCACG	4680
CGCAAGTTCC	TCGGTCAGCT	CAAGGGGGAA	TCCATACGTA	TCGTATAGCC	GAAAGGCAAC	4740
TGACCCAGGT	ATTTCTCGCT	CTGTCCCTTG	TAAAACTTG	GGTATCATCC	TCTCGTACTC	4800
TGCCTCACC	TTCTGAGGG	CGTCGAGGAA	CTTACGTTC	TCGTTTGCAA	GCTCCTGCGC	4860
AATACACGTA	GCTTTCTCTT	CCAGTTCCGG	GTATACCGCA	GCGTATTGCC	CAATCACCAC	4920
GCGCGCGAGG	GAGGACAGGA	ACTCCCCATC	GATACCGAGC	TTCTTCCGT	GGCGGACTGA	4980
ACGGCGAATG	ATTCTGCGCA	GTACGTAGCC	TGCACCCACG	TTAGATGGGC	GTACAGGGAC	5040
AGGATCGCCG	AGGATAAAAG	TGGCCGCACG	GATATGATCG	CATACAATCC	GCATGGATAC	5100
GTCGTGCGCT	CCCTGACACC	CATACCTCTT	CCCACATAAC	TGACCTATCC	GCTCCAGGAG	5160
CGGGGTAAAG	ATCTCCGTAT	CATACACTGA	CCGCTTGCCC	TGCAAAACCG	CGACGGTGCG	5220
TTCAATACCC	ATACCGGTGT	CCACACAATA	ACGTTCAGC	GGCCGGTACC	TGCCGTCTGC	5280
GTCTTACGA	TACTGCATGA	ACACGTCATT	CCAAATCTCT	ACGTACTTGC	CGCAAGAACA	5340
TCCCGGACGA	CAGCTCACAC	TGCAAGGAGG	AACTCCAGTA	TCAAAGAATA	TCTCGGTATC	5400
CGGACCACAT	GGCCCTGTTT	CCCCCGTAGG	TCCCCACCAG	TTATCCGCAC	GTGGTAAAAA	5460
ATGAATATGG	GTGCGCGCGA	TACCAAGTCG	TTCCCAGATA	GCGGCAGATT	CCTCATCACG	5520
CGCAACAGCC	TCATCCCTTG	CAAAAACAGT	CACCGAAAGC	CGGTCAGGGG	ATATGCCGAG	5580
CCATGGAGCA	CCAGTAAGAA	ATTCAAAGCT	GAACGCGATT	GCCTCCTCCT	TGAAGTAATC	5640
GCCCAACGAC	CAGTTACCCA	ACATCTCGAA	AAAGGTCAGA	TGCGAGTTAT	CGCCCACCGC	5700
ATCGATGTCA	CCGGTGCGCA	GACACTTTTG	CGCATTGACC	AAGCGGGTAC	CAGCCGGATG	5760
TGGCTCACC	ATAAGATAGG	GAACCAACGG	ATGCATGCCA	GCAGTAGTAA	AAAGCACGGT	5820
AGGATCGTGC	TCGGGCACAA	GGGACTTACC	CGAGATAACC	ACATGAGCCT	TCTGGCTAAA	5880

GAAGGCGAGA TAACGCGAGC GTAgCTGATC GCGCGAATA GGAATGCTCA TGGAGGGTAT	5940
TATCGCCTTT TCCCTGCTGC GGTCAACATC TGACCCATAA CGGGAAAAAG AAACGGGGAC	6000
TCTCTGAGCA ACCTTGCGAC AAGATCCTTG ACAGAATTCTG CACACACCTC TAGCCTCTCG	6060
CAAGACAGTT TCGCACCCCTT AAAAAATATA AGGAGCACAC ACATGACCAC GTCATTTGTG	6120
ATCGGTGTTG TCCTTGTTAC TGTCGGTTTA AcCTTCGGAT GGACCATTCTG CTGGCTCTAC	6180
GCCAGATTTC ACTTATCCGC CTGTGAGCAA CGTGCAGAAC GTATCCTCCA GGAGGCACAA	6240
AAAGAAGCTG AATCCAAAAA GAAAAGCATT CTCTTGAAG CAAAAGAATA TGTCTTCTGC	6300
GAAAGAAATC AGCAGGAACG AGACGACAGA GACCGAAGAG CTGAGCTGCA GCGTGCAGAG	6360
CGACGCCTTC TTCAAAAAGA GGAAGCCCTC TCTACGCGCG CGGGGGAGCT TGATTCTCGA	6420
GAACGATCGC TAAAACAGCG GGATCAGTCC CTCTGTCAAG AAGAGGCCCG CTATCGCCAG	6480
GAGCTCGAGC GTGTCTCTGG CCTCACTCAG AATCAGGCAC GGGATCTCAT CATCAAAAAC	6540
CTTGAGAACG AGGCGAaCA CGACGCACAG GCTCTCATCA ACAAGATAGA GGAGGACGCG	6600
GCTTTGAACG CTGAGCGTCG CGCGCGCGAC ATCCTCGTTA CTACCATGCA GCGTATTACT	6660
GCTGATGTCA CCGGTGATGT GACCGTCTCT ACGGTGAATC TACCCAGTGA AGAAATGAAA	6720
GGACGCATCA TTGGGCGCGA GGGACGTAAT ATCCGCGCGT TAGAGACACT CACTGGTGCT	6780
GACGTTGTCTG TAGATGACAC ACCTGAAGCT GTCGTCATTT CCTGTTTCGA CCCGGTACGC	6840
AAAGAGATTG CGCGCATCTC TCTTGAGCGT CTGTACTTTG ACGGTCGAAT CCATCCGGCG	6900
CGCATTGAGG AAATTGTGCA GAAGGTGACG CAGGAAGTTT CTCAAAAAAT CTATGAGGAA	6960
GGGGAGAAAG TGCTGTTTGA CCTCGGTATT CACGATATGT GTCCCGAGGG GGTACGGGCA	7020
CTGGGGCGCC TGTATTTCCG TACAAGCTAC GGACAGAATG TACTCTACCA CTCAAAGGAG	7080
GTGGCTCTGC TCGCTTCCAT GCTCGCCTCG GAAATCGGCG CAGATGTTGC CATTGCCAAA	7140
AGGGGCGCGT TGCTGCACGA TATTGGCAAG GGAGTGAAA CTGATTTCAGA CCGCAACCAC	7200
GCAGAAATTG GTATGGAGAT GGCTCGCAA ATGAATGAGG ACCCGCGAGT GGTAACGCC	7260
GTGGTTCTC ACCACAACGA CATAGAGCCG TGTGTGTTG AGTCTTGGCT CGTTCAGGTA	7320
GCTGATGCTA TCTCTGctGC GCGTCCTGGT GCTCGGCGTG AAATGGTGGA TCacTACGTC	7380
AAGCGTCTAG AAAACCTCGA GCGATTGCT GAGGGGTTCT CGGGTGTAGA GAAAGCCTAC	7440
GCTATTCAGG CCGGGCGCGA GTTGCCTGTT TTAGTGAACA ACGATAAAAT CCCCACAGG	7500
GACGTGAAGG CACTTGACG TGACATCGCA AAGAAAATAG AGAGCGACTT GAAGTATCCT	7560
GGCGTATCC GGGTCACTCT TATTCGAGAA ACGCGCGTCG TGGAGTATGC CCGCTGAGCC	7620

TCAGGGAGAG GGGAGAGAGT GCACGGGCGT CCGTGCAGGT TTGCATCGGC TGCAGTGACT	7680
CTCCTACCTC CCTATTCTAG TCCGGCGATA TTGGTCAACA AGGCACATGG GAGTATCATG	7740
GCACAACAGC GTATTACGTC TGATATCTTT GCTCAGCTGC TCACCCTTTC TCACCTCGAA	7800
AGCAGCGAGT GTGCAGTAGG ACTTGCAACA CAGATCGAGG ACATTATCCA GTATTTTTC	7860
GTTGTAGAAC AGTTCGACCC CGGTCCACGC GACGATCCTG ACACGGATAA CGCACAAGGC	7920
CGTTGCTCCC AGGGGAATAA AATTGACGTG GACTGCTGCC CGGACTGGGT ACGCAAGGAT	7980
GTGCGATTAC CTGGTCTTTC CGTTCACGAT CTCAAGCGGT TGTCCACAGA GTTTGCTGAC	8040
GGTTAcTtTy kCGCAcCGCG CGCGCTCGAT GGTAGCGCAT AAATGGACGC GCATGCTATT	8100
ACCTGTGCAA GCTGGAATAT GTTAAAGGCT CAGCTTGAAG CCGGTGCAAT CAGCTCTTTG	8160
CAGATTGTGC GTGCGTTTCG CAACGTATAC GAGGAAGACA CACGCAGCGC GTCCCCGCTT	8220
GGGGCTTTGG TCGAGTTTTC CTCTGATGCG GAGGAGCAGC CGCGTACGGC AGACAATCTC	8280
CGTGCCTCGT GTGCCCAGAG TACTAAAACA GCTGGAGCAA ACGGGGGGAG TGTCTCAGGT	8340
AAGCCTTTGT TAGGTCTACC CTTTGCTGTC AAGGACAATA TTTCAGTGAA AGGAAAGCAC	8400
TGCACGTGTG GCAGTAAACT CCTTGACAGC TATAGGGCTC CGTACGATGC CACCGTTGhT	8460
TGCcGnCTGC GCGcCGcAGG TGCTaTCCCG CTCGGGAGAA CGAACATGGA TGAGTTTGCT	8520
ATGGGCTCTT CCACCGAGTA TTCTGTTTAT GGGCCGACGC GTAATCctCG GGATCGGAGC	8580
CGCACCAGCG GGGAAAGTTCC GCGGTTTCGG CTGCCGCCGT nCGCAGGCGG TnCAGGCACC	8640
GTTTGCACTC GGTACCGAAA CGGGAGGCTC GGTACGCCCTG cCAGCTGsTT aCTGCGGCCT	8700
cTATGGCtGA AgCCGACcTA TGGTCTCTTG AGTCGATATG GGGTGGTTGC CTTTGCGCTCC	8760
TCTCTAGACC AAATCGGCTT TTTTGCTACC TGCATTGACG ATATTGCCCT CGCCCTCTCC	8820
GTCACCTCAG GGAAAGACCT GTACGACAGC ACGAGCACTT GCCCCCTCC TGCACGGGG	8880
CGACACGCTG TGCTCACCA TCTTGCCCCCT TTTTCTGCCC ACGAGTGCTC TATCCTGCGT	8940
GCTGCTGTTT CCCGCGAATT AGTAGATGCT CCTGGCGTGC ATCCTGACGT GTCTGCGCAA	9000
TTTCAACGCT TCCTCACCTG GCTGCGTGCC CAAAACGTAC AGGTAGAAGA AGTGACGCTT	9060
CCTGCACTAC AGGCGGCAGT GCCTGTATAT TATCTTGTCG CGACAsctGA AGCCGCCAGC	9120
AATCTTGCGC GTTTTGACGG TATTCGCTAC GGGCAGAGGG GAGACACTGA TGCTCTTTTG	9180
GAAAATTACT ACCGCGCCGT CCGTACCTCA GGCTTTGGAC CCGAAGTACA GCGAAGGATC	9240
ATTGTGGGGA ATTATGTTCT TTCACGCCAT TTCTCCGGTG ATTATTACCG AACGAGTGTG	9300
CGCGTACGTT CGCGTATAGA ACAAGAATGT ACGCAGCTCC TCTGTTCCCTA CCACTTTATT	9360

GTTTGTCTTA	CTGCCGCTAC	CGGTGCCTTC	CCGCTTGGAG	AACGCATACA	TGACCCGCTG	9420
GCCATGTATT	GCTCGGATTT	ATTCACCACC	TTCGTTAACC	TTGCCCCGCT	ACCGGCGCTA	9480
TCAGTACCAG	TGGGAACATC	AGGCACTGGC	CTACCCATCG	GAATACAGAT	TATCGGTTCT	9540
CAGTGGCAGG	AGTGTGCCGT	TCTCCGGCTA	GCAAAACGTT	GGGAGGAGGC	ACCTCATGTC	9600
TGACCTCCAA	ACAGGCACAG	TTCCCTCCAT	TGCAGGCGCC	ACAGATGACA	CACATGCCGC	9660
ACCCTTTTTT	TACGAGGTAA	TTATTGGCTG	TGAAATTCAT	TGTCAGCTTC	TAACAAAGAC	9720
CAAAGCTTTC	TGTGCTGTGC	AAATCGCTCA	GGAGGAATGC	CGAATAGCCG	TGTGTGTCCT	9780
GTGTGTCTTG	GGTTGCCAGG	AGCGTTGCCC	GTTGTGAGTG	AAGAGTACGT	GCGGCTCGGG	9840
GTGCGCGCCG	GACTTGCGTT	GGGGTGCACT	ATCCAGCTTT	GGTCCGCTTT	TGATCGCAAG	9900
CACTATTTTT	ATCCAGATCT	CCCAAAGGGT	TATCAAATTA	CCCAGTACGA	CGCTCCCTTG	9960
TGTACGGATG	GTGCAGTGGA	TGTACAGGGA	GTTGACATGC	CCGTGCAGCG	cGTGTCCGTA	10020
TTGAACGGAT	ACATTTGGAG	GAGGACGCAG	GCAAAAGCCT	GCATGCTGCA	GACGCTTACA	10080
GCTATATTGA	TTTCAATCGT	TGTGGGGTGC	CGCTCATTGA	AATTGTATCT	AGGCCGGATC	10140
TGCGCTCTGC	AGAGGAGGCC	GCATGTTTTA	TGCAGACGAT	CCGCGAGATT	CTCACCTTTA	10200
TCGAGGTAAC	GGATGGTAAT	TTAGAAGAAG	GCGCACTGCG	ATGCGACGCG	AATGTTAATG	10260
TGAGGATTCT	GTACAAAGGG	CAAGAACACC	ACACTCCCAT	TTCTGAAATC	AAAAATATGA	10320
ACTCGTATCG	TATGGTGCGG	GACGCGTGTA	CGTATGAGGT	ACAGCGTCAA	TTGCAGGAGT	10380
TTTGCCAAAA	GGTCTCTGCG	AGCAAAGAAG	AGATGCAGAG	AAAACGCACG	ATGGGCTGGG	10440
ATCCGGTCTGA	AGGGGTTACG	CTTTTACAGC	GTACAAAGCA	CTCACTGCGC	GATTATCGTT	10500
TCATGCGCGA	TCCAGACTTA	CCTGACCTGC	ACTTGACCCC	TGCATATGTC	CAGCATCTCT	10560
CTTACACAGT	CGGGGAACCT	CCGGCAGCGC	GGCGTGACG	TTTCAAACCT	GACCTTGGCT	10620
TGTCGGCGTT	TGCAGCCCCA	ACGCTTACCG	GCAGCCGCAT	GCTCGCAGAC	TGGTTTGAGA	10680
AGGCAGCGCA	TGCGTCTAAG	AATGCGCGAC	GAGTGGCAAA	CTGGATTCTG	TCGGAGGTTT	10740
TTGCGGTAGT	AAACGAGAAG	AATATCTGCA	TTGCAGAGCT	CAATCTGAGT	CCTGAAGCAA	10800
TTGCCGAAC	AATGGATGCA	GTTGAAGATC	AGCGCATTAC	CGGAAAACAA	GCAAAGGATA	10860
TATTTGCACA	AATGCTTGCC	ACCGGTGCGC	GAGCGCAGGA	CATTATCTCC	GCACAGGGTC	10920
TGGCACAACT	TTCAGATGAG	GAAGAAATCG	CAACGTTAGT	GCAGACGGTG	TTTCAAGAAC	10980
ATCCAAAGGc	nCTGCGTGAT	TGGCAACACG	GTAAGACAAA	CGTGGCTGCC	TGGCTCATGG	11040
GGCAAGTAAT	GAAGCGTTCC	CGCGGGCGCG	CACACCCTGC	GCGAGTGGCG	ACGCTCGTCC	11100

ACCAAGCACT	CTCTCAGCTG	TAACAGCTGG	AAAAACTCCA	CGGAAGAGCG	GCGGTCTCTC	11160
TTTCAGCATA	CGCCCGGyCC	CGcTCACGCC	AGGAGAAGAA	AGACGCACCA	AAGGGCTACT	11220
ACGCCTTCGC	CTTGCTAAAT	ATCTCCGCAA	TTGTCTGTGC	GAGCGTACCC	ACCACCCGTA	11280
GGGTATAAGG	AGGCGGTGTG	TCGTGTTCAA	CCCCATATAGG	TACATATATC	GTTGAAAAATC	11340
CCAGACCATA	CGCCGTCTTT	AGCCGCGTCT	TTAGCCGACG	CACAGGTCTGA	ATTTCTCCTG	11400
ATAAACTTAC	CTCACCATA	AACGCGGCAT	TTGTTTTTCAC	TGGGGTGTTC	TGCCGCGCTG	11460
AATACAAGGC	CATTGCCAAC	GCCACATCCA	CCGCAGGCTC	ATATAACCGG	ATACCCCTG	11520
CCACATTAC	GATGATATCC	TGATCTGAGA	ATTTCAAACC	CACACGTTTC	TCAATTACCG	11580
CTGCAACACG	ACTGACGCGG	GCCGAGTCGA	TACGATCAGA	AAAAACGCGC	GTAACACTAC	11640
TTTTTGCAGG	AACGGTCAAT	GCCTGTATTT	CTACCATAAA	AACACGGCTC	CCCTCACACA	11700
CGGGCACAGT	TGCAGACCCA	ACAGGAAACA	TTCCCTGCCT	GGTACTAATA	AAAAATCCTG	11760
CAGTGTCTCTG	CACAGCGGAA	AGTCCATTTT	CACCCATGGT	AAAAATACCC	AGCTCATCAA	11820
CAGAACCAAA	TCGATTTTTT	AATGCACGTA	AAAAACGAAT	ATCCTCTTCA	TTCCGTTCAA	11880
AAGAAATCAC	AGTGTCCACC	ATATGTTCCA	CTACTTTTGG	CCCGGCAATA	TTCCCATCTT	11940
TCGTTACATG	CGCAGTAAAA	AAGAGAACAG	AGTCCCGTTC	CTTTACCCAC	GcTATCAACT	12000
CATTTGCGCA	ATATTTTACG	TGATTGATAG	TCATAGGAAT	GGCACCTGCT	TCGGGGGAAA	12060
AAACTGTCTG	AATCGAATCA	ACAATAACGA	AGGTAGGGCA	TCGTGTATTT	AAAACACGCT	12120
CGACATCCTC	GACCCGCGTC	GCACAAAGCA	ACTCGATGTT	CTGAATTGGA	ATATTCAGCC	12180
GATCCGCACG	CCCACGAATT	TGCCCCGGAG	ATTCTTCACC	CGAAACATAG	AGAACCGATT	12240
TCCCGCAGgC	TGCAGCGATT	TGTAACAGTA	ATGTAGATTT	ACCAATGCCC	GGTTCCCCGC	12300
CAATCATGAT	CGCGGAGyGT	CTTACGGCGC	CTCCGCCGAG	GACACGATCG	AACTCTGCGA	12360
TACCACAAC	AATACgCTGc	gCATCCTGCG	CGCGCACAGC	ACACAGCGGG	AACGCCTGTA	12420
CAGGAGAAGA	AGATGCCTTT	TTTACAGCAC	GAACATCGCC	GGAGGACAAC	GAGGGTGTCT	12480
CTTCGAAGGA	ATTCCACTCC	CCGCACTCAG	GGCAACGCCC	AAGCCACTTA	GGATGAACGT	12540
AACCACACCC	CACGCAGGAA	AAGGCACGTT	CCGTCTTTTT	AGCCACTCCA	TTTCTCTTAC	12600
GTCAGAAAGA	AAAAGCACTG	CACGGCGGGC	CGcTACGCAC	CCTCCGTTTC	TACCGCAAGA	12660
CAGCGACGAA	CGAGCGAAGG	AGAAAATTGC	CTCCGCTGCA	ATGCACGCTG	CAACGTATGC	12720
GGCCCATATC	CCCGCcTTCG	CAGCTTCTCC	AGCAACCTCA	AGCAGAGCGT	TTCTTCATCT	12780
TGCTCTTGAA	ACAAGAGATC	TAACGCGCCT	TCTGCATCTG	CATGAGAAAC	CCCTCGCCTT	12840

TTTAACTCAC CTAATAGCTG AGCACGGGAC GCAGGACGGG AATCGACGCG GTTTCGCAAC 12900
CACGCCCCGCG CGAATCGcGT ATCATCAAGC CAAGAATATC TTTTAAGAAC CGGGAACACG 12960
CTCTCAACGA CCCTCTTCTC AAAGCCTCTT TTCAAAAGCT TAAAACCCAG CTGCTGAGCA 13020
CTCGTCTCAC TCCGAGCGAG CAACCGCACT GCGACGCACT CAGCCTCATA ACACCTACAT 13080
GCAAAGCACA CCGCCCCGTa CTGCTCATCA GTGGGACGAG TACCCACCAA CTCCTCTATC 13140
GGGAGGAAA GCGCGCCAAG GTAACCTCAAG CGAGTCTGCA GAACAGCACC CACCTCATCC 13200
GTAAGTTTAA GCACATCCTC CTGGAGGCTC TGGATAGCAC AGAGACAAA GCGCCTATCG 13260
CTTACTGAAT TGAAATCTAC GCCGTGCACC GCGCTGGCCA TACTTCTTGC GCTCTACCAT 13320
GCGAGAATCA CGCGTGAGCA ACCCACCTGC ACGCAGCGAA GCCTGATTTG AAGCGTCAGC 13380
ACGCACGAGA GCGCGCGCAA TACCATGcGC ACACGCACCA GCCTGCCCCGT CAAGTCCGCC 13440
GCCATACACA TTGACAATCA CATCGTAACG CCGCTCGTTC GCGGTAgCGA AGaGGGGTTC 13500
GCGCACCCGA CGCAATTGct CCGCCGTAGG AAAATACGCG CCGACATCCC GTCTGTTGAC 13560
GGTAACATTC CCGTTCCCCA TACGGATACA CACGCGAGCG ACAGCCGTTT TCCTTCTCCC 13620
TGTTCGGATC CCAAGATTCT TCACGCTCTT TACCACTCCT TAACACGACA GCGGCACGGG 13680
ATTCTGCGAC TCGTGCGGAT GCACAGATCC CGCGTATATC TTCACATTCT TGATAAGCTT 13740
GCGTCCCAA GGCCCCTTGG GTAGCATACC CTTAACC GCG TGACGCAACG GTTCGACAGG 13800
CCGGCGCTTG ACCAACGCGC TAAACGACAC GCTCTTGAGC CCCCAGGAT AGCCTGAGTG 13860
GCGGTAGTAC ATCTTGTCCT TCGGTTTAGT CCCACTCAGG AACACCTTCT CAGCGTTGAT 13920
TACCACAACG TAATCACCCA TTTCTTGGTT TGGCGTGAT GATGCTTTAT GCTTACCACG 13980
CAGGAGACAC GCAACGCGCG cGGCAACAG CCCCAGGGG CGCCCCGCTG CGTCAATCAG 14040
GTGCCAAGCG CGAACAGCCT CGCGCTCATT AACAAAGATT GTCTCAGGCT CTCTGCTCCT 14100
TTATCCACAC GCTCCGGTAG CTTGCGCGTG GCGCGACGAT CACGCATGTT TGCCACCCCT 14160
ACAAGGAGAG ATATAAAACC AGCAAAAATA CCGCCGACTG GCGCAGCACC ACGCAAGAAC 14220
CGCAGTGCAT CCGTGCAGG CCGGAGACCA CAACCGTACT CCATAGGGGA AAGAAGAGCG 14280
AAAACCGCG CTCCCATCAG CAGCACACCA ACCAAAACCG CGCCCACCAC CGCctCCCCG 14340
GCAAAATCTC CCGATCGTCT CATAAAAATC ATTCTGTGTC AAGnTGCGCT AGcACAAAGA 14400
CAGTTAGAAT GCGTATACTC TCCAGATAGT TGCGGAAAAC TTCTTGAAGA AACCTTCTGC 14460
TGAAAGAAAT cAGCTAACTT GAACAAACGC TCAGTCCGCC TGATGATGGG CGCATAACGC 14520
ATGCAAAGAT TTGAAGACAT TCCGTACACG CGGCCACACA TGGACATACT CGAGCATGCC 14580

GTCGACGCGG	CTCATGGGGA	GTTCGCGCAG	GCCCCGTTGTG	CACGCGATGC	GTATGCGTCT	14640
ATACTCGCCA	TAGAGGATCT	CCAGCGCCAA	TATCTTACCG	CACAGGCACT	AGCGAACATG	14700
CGCTGTTCCT	TTGATACACG	CAACACCTTT	TACCGCAGAG	AACAGGATTT	CTTCGATGCT	14760
GTACATCCTC	GCTTTGCCCG	CTTAGATCAT	GCCTTCAACC	AGCTGcTGCT	TGCATCACCA	14820
CAGCGCGACG	GTCTTGAAAA	ACTTATTGGC	ACTCACCGCT	TTACCCCTTGC	ACGCCTTCAG	14880
AGCAAAACCT	TCTGcTCGGA	GATTATGGAA	GACCTCGCAG	AAGAAAATCG	TCTCACCAGC	14940
GCCTATGAAA	CACTCCTCGC	TTCCGCACAC	ATTCTCTTCC	GAGGCCACCA	CTACACTCTC	15000
GCCCAGCTGT	CCCCCTTTAT	GGAACACACC	GACCGCAACA	CGCGGcGCGA	CGCGCATGaG	15060
GCATACTATC	ACTTCTTTGC	TCAACATGAA	TCGGAGCTCG	ATACCCTCTA	TGACACGCTG	15120
GTACGAGTGC	GCACACGCAT	CGCACGCACG	CTCGGCTATG	ACAATTACAT	CCAACTCGGc	15180
TATGACCGCC	TGTTACGCAG	CGACTACGAT	ATGCAAGATA	TTGCGcgTTA	CCGCACCTAC	15240
ATCCTGCGct	ACGCCGTACC	CCTCGCTGCG	GAACTACATG	AACAACAGCG	ATCTCGACTT	15300
GGACTCAGTG	AACTTCTCTT	TTATGACGAG	CCGTTGTACT	TCCCTTCTGG	AAATCCAGTT	15360
CCCCAGGGAG	ATGCACCCTG	GATATTGAAT	CAGGCCGCTT	GTATGTACCG	CGAACTGTCC	15420
CCAGAAACAG	ACCAGTTCTT	TACCTTTATG	CGCGAGTACC	ACCTATTTGA	TGTCTGTGCA	15480
CGTATTGCAA	AAGCGAGCGG	TGGATACTGC	ACAACCTTGA	GCACATATCG	TGCGCCTTTT	15540
ATTTTTGCAA	ACTTTAATCG	CACTGCACAT	GACGTGGAGG	TTATGACGCA	CGAGGTGGGC	15600
CACGCCTTCC	AAGCCTACCA	ACGCTATCGA	GCGCGTCTTG	ATCCCTGTTT	GGAAGCGTAT	15660
GTGTGGCCCA	CGTACGAAGC	GTGCGAGATC	CCCTCAATGA	GTATGGAATT	TCTCACCTGG	15720
CCGTGGATGG	GGCTCTTTTT	TGGTGAACAG	AAAGAACGCT	TCTACCTGCG	CCATTTAACA	15780
CAGGCAGTGG	AGCTTTTACC	GTACGGGGCA	GCTGTGGACG	AATTCCAACA	CTGGGTGTAC	15840
GCACATGCGG	ACGCTTCTGC	CACTGAACGC	AAGAAGGCGT	GGCGCGCATT	AGAAACTCAG	15900
TATTTACCTC	GCCGTCGGTA	CGGAGGGCAG	CACTACTTGT	CCTGCGGGGG	ACTGTGGATG	15960
CGTCAAAGTC	ACATTTTCTG	TATACCTTTT	TACTACATAG	ACTACACGyT	CGCGCAGATA	16020
TGTGCGTTGC	AATTTTGGA	TCGCAGCCGC	GTTGCATACA	CTCACCTTTC	TACTCTCACC	16080
GGCGCGGCAC	CGTACGCCAG	CATAACTCCT	ACTGCCTATG	CGGAAGCCTG	GCATGACTAT	16140
TGCGTACTGT	GCAGCCGAGG	CGGCAGCGAA	CCGTTTCATG	GTCTGCTTGC	CACAGCGAAT	16200
CTGCACAACC	CCTTTGAGGA	AGACACGTTT	GTTTCAACAC	TCGCTTCCTG	CCGTGCGTAT	16260
TTTCGCACGg	TTGGTGACCG	CCTTTCCTAG	GTCTATGAAA	AAAGGGTAAA	AGATGCCTCG	16320

CCAAAAAGAG	AACTACCTGT	CACCGTCCCC	CGTGGTCGGG	ATTCTTCGTG	ACTGGGGAGT	16380
GCTGTGCACC	TTACGCTTAA	AGGGGAAACA	CATGAAGCTT	GTCTACAGTA	CGGATTGCGA	16440
ATACCACATT	GGACTGAAAG	CGTCAGACAT	CGGACACTAT	GTTATCTTAC	CGGGGGATCC	16500
TGCACGAAGC	GAAAAGATTG	CCCAACATTT	TTCTCATCCT	CACAAAGTTG	GCCACAACCG	16560
CGAGTACGTC	ACGTACACGG	GCACCCTCTG	CGAAACACCA	GTCAGCGTCA	TGTCCACCGG	16620
TATTGGGGGG	CCGTCAACTG	CAATTGGTGT	TGAGGAGCTC	ATCCATTTGG	GCGCACACAC	16680
CTTTATCCGC	GTAGGGACCT	CAGGGGGCAT	GCAGCCTGAT	ATTCTTGCCG	GGACGgTAGT	16740
TATTGCAACC	GGTGCGATTG	GCTTTGAAGG	CACCAGTAAA	GAATATGCCC	CCGTGGAGTT	16800
TCCTGCGGTG	CCGGACTTTA	CGGTCACTGC	TGCACTCAAA	CACGCTGCAG	AAGACGTGCA	16860
GGTGCGCCAC	GCGCTcGGTG	TGTTTCAGTG	TAAAGACAAC	TTCTACGGTC	AACACTCCCC	16920
CCATACCATG	CCCGTCCATG	CAGAACTCAC	GCAAAAATGG	cACGCATGGA	TTGCATGCAA	16980
CACACTCGCA	TCCGAAATGG	AGTCTGCAGC	GCTCTTTGTG	CTCGGGAGCG	TACGGCGCGT	17040
GCGCACCGGC	GCAGTGcTCT	TAGTCATTGG	AAACCAAACC	CGCAGAGCAC	AGGGATTGGA	17100
AGACATTCAA	GTTACAGACA	CCGAAAACGC	CATACGGGTT	GCAGTCGAAG	CGGTCAAATT	17160
ACTCATCACC	CAAGACTCCC	CGCGCTAGGC	GCACTGCAGT	GCTTTAGGCA	AAGTGTCGCG	17220
GATCGGTTAT	TTCTAACAGC	GCGGAGTCAA	GCTCGGTCAA	AAAGCGGCTG	GGCTTCATCG	17280
CCGTGTGTG	TCCCCACATT	CTGCGGTACG	CACACGCGGT	AAGGTATAAG	CTATCCATAG	17340
CCCGCGTGCA	GGCAACGTAC	ATCAAACGCC	GCTCTTCTCTG	TATATCTGCT	TCGTCAACAC	17400
GCGGAAACAC	CCCGTTCTCT	AGTCCGGTCA	GAATCACCCG	TCGAAACTCC	AGCCCTTTTG	17460
TATTGTGAAT	GGTGATCAAG	TGCaTGCGTC	AGCCGcTCCT	CCCTCGTCGG	CCATATTTTG	17520
GTCCAATTGG	ATGTGTTCTA	GGAAACTCAC	TAACCCCTCA	TGCGAACATG	CATACAGTGA	17580
CGCTGCGTTC	ATTAACTCCT	GCACGTTGAC	CGCGCaTGCG	TCCCTTCTTC	CTCATCCTTC	17640
TGTCGATACC	ATTCTTCCAG	CCCCGTGTGT	TCCATTACCA	CAGAAACAAA	GCGCGCAAGT	17700
CCtTCTGCaT	CGTGGGTGCG	CTCctCTACC	GGCTCCTCAG	GCGGCGCACT	GGTGCGAGCT	17760
TCTTCTCCCG	CTGCGGGGGC	CTGTGGCATG	CGTGACGCA	GCGCACGTAA	CAGCGACAGA	17820
AAGCTACTGA	CCTTTTGCCg	CGCACGCGTG	CCAAGCGCGG	TCAGGTGGGT	GGACTGGAGT	17880
GTGGTAAAAT	CAGTTATGGC	TGCCTGCTGT	GCACAGACAA	ACAATGCGTC	TTGTGTCTTT	17940
TCTCCAATGC	CCCGAGGCGG	CTTATTTCAGC	ACCCGCCGGA	GGGCCAGTTC	ATCTGAGCCA	18000
TTGACTATGA	GCTGGAGAAA	CGCCAGCACG	TCTTTTACCT	CTGCGGCACT	GTAGAATTTG	18060

619

AGCGTGCCGA CAATGCGATA CGGAATGCGA TTCCGCAAAA AACACTGTTC AAAACTCAGC	18120
GACTGTGCAT TTACCCGATA TAAAATCGCC CAATCCGCGT ATGGGATGCC gCGCGCACGC	18180
kCTTCTTGAA TGAGGTGCAC GCACAGCGCA gCTTCTTCAT CTTGATTATT CAGCAAGAAC	18240
AGGCGCGGCT TAGTACCTCC CGTGCCTGG GCAATCAGCG CCTTTCCTAA GCGGTCTTGG	18300
TTTTTTTTCA CTACCGAATC AGCAACACGC AGAATTGCGT CTGTGGACCG GTAGTTGTAC	18360
TCCAGGCGGA TAATCTGGGT ATTTTGAAAG AACTCAGGGA AGGTCAAGAT ATTTTTTACC	18420
TCTGCTCCGC GAAAGcGATA GATGGACTGA TCGTCGTCCC CTACCACACA AAGATAGGTG	18480
TGCGcACCGG TGAGCACCTG CAAGAAATGA AACTGCGCCA CGTTTGAGTC TTGATACTCA	18540
TCTACCATGA CCACCTGCCA CCGTGCATGC AGCTGTTCCG CGACGTCCTG GTgcTCACGC	18600
AAGAGCTGCA CCGGAAGCAT AATCAGATCC CCAAAGTCTA CCGTTCCCAT TTCGCGCATA	18660
CGCCGATGGT wTCACGCATA TGCGTGCGCA AACTGCCTGT CACCCAGAAC GGCTCTGGCA	18720
GCGCATGCAG GAGCGGAGAC ACGCGCGTGC ACTGACTCAA ACGAGGCGCA GTCGAGCCCA	18780
TAGTCCTTTG CCTGAGAAAT TCCACGCGCG AGCATGCCTG CCCGACTGTG ATCGCAATGA	18840
GGCAGGATTT TTGGCAAGAG TGCACGGACG TCATGGTCGT CATAAATACT AAAATGGGGG	18900
TTCAATCCCA GACGGACTGC ATAGCGACGC AGGATCCACA CCCCCAGTGC GTGGAAGGTA	18960
CAGATAGTTG CCCCTGCGCG GCAGACTCAA GCGCGCAGGC ACGCGTGCGC ATCTCAgCGC	19020
CGCTTTATTG GTAAAGGTTA CTGCCAGAAT CTGCTCGGGG CGAACCTGCC GGGAACGGAT	19080
AAGATGGGCG ATTTTGGTGG TGATAACGCG CGTCTTTCCT GAGCCTGCGC CGGCAAGGAT	19140
AA	19142

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

TATCTATTTC AGTTGGATTT TGGCGCCTGG AACTGGGGAT TTTTCGTGTG CCACTTTCTG	60
ACACGCTAGC TCTGTGGCGC ACATTGAAGG AGCGCCTcTC AgGGTTGTGCTTCTCCACGC	120
TTGCGgTGGA CTTGCCAGGG GGTGGAGGAA AGTTTCCGCT TGTGGCATTG GCCTTGACGC	180
AAGATGTCAC GTGGCATCAG GAACGCGAgG CGTTCCTCCGC ACGCGGcATC GATGGCGCGT	240

620

GGTACACGTA	cCCGTTCTGA	CCGTCAAAAC	ACCCCGCGCC	TCATCGAGTG	GAGAGTGCGC	300
CGCGTGGTAC	AsGGGGCAGC	GCGAAACACC	CCTGCGTGAA	GGTAGGCGGA	GGAGGGGGTA	360
CGGTGGTATG	CACCGAACCC	AGTGATGCAC	CGCCGCCCCC	CCCCGAGGGG	TCCTCTTCTG	420
CCCCGCGCGC	CCACGCAGCG	CCGCAGAACG	GTGAGAAAAG	AGGACGCGCT	CTCTACCGGC	480
TAACACATAT	CACGCGTGCA	CGCAGCCCCC	TCGCTGCCGT	TGATGCGAGC	TTCCAAAACC	540
TCGAGTGCAT	CGCGAAGCTG	CTGTGGCAGC	CGCGCGCCAA	ACTTTGGGTA	GTGATTCTCT	600
CGGATGTCTT	TAATTTCTCT	TTTCCATCCG	GCTATGTCCA	CCGACAAAAG	CTCTTTCACT	660
GCCTGCGTGC	TTACGTTTAA	CCCCTCTGTG	TTCAAGGCTC	CCTCTTTGGG	CATCCAACCG	720
ATCGCTGTTT	CCACCGCGTT	GTCCACACCA	TCACAGCGGT	CAAAGATCCA	CGCGAGTACT	780
CGGcTGTTAT	CGCCATATCC	GGGCCACAGG	aAGTTGCCct	CTGCATCTTT	ACGAAACCAG	840
TTAACGCAGA	AAATCTTTGG	CAGGTTTTCG	GCACGTGCCT	GCGATCCGAG	CTTAATCCAG	900
TGCGAAAAGT	AGTCTGCCAT	ATGGTAGCCG	CAGAAGGGGA	GCATCGCGAA	cGGGTCTCGG	960
CGAATCTGAC	CTACCTGGTC	AGAGATAACT	GCTGCAGTTA	CCTCCGAGCC	GATGATGGAA	1020
CCTAGAAACA	CCCCGTGATT	CCAGTCCCGG	GCCTGATGCA	CCAGGGGAAC	CGTACTGGGG	1080
CGACGGCCGC	CAAACAGAAA	AGCGTCGATA	GGGACCctTC	GGGATCTTCC	CAGTTACTTG	1140
CAATTGCAGG	GCACTGTCGC	GCAGgAGCGG	TAAAACGCGC	ATTCCGATGC	GCAATTTCTT	1200
CTCCTTTTGG	ACTTTTATCG	CGTGTAGGTG	CGGGGCGCGA	CACGCCGTGC	CAATCAATGA	1260
TTGTTCCCTT	AGCGGGATAG	CCGATACCCT	CCCACCACAC	GTGCGCGTCT	TCGGTCAGAC	1320
CACAGTTGGT	GAAAATGGCG	TTTTCTTGA	TAGAGTCCAT	GGCATTCTTG	TTGAGAAAT	1380
CAGATGTCCC	TGGTGCTACG	CCGAAGAACC	CCGCTTCAGG	ATTGATAGCG	TACAGGCGGC	1440
CGTCCTTTCC	GAATTTTCATC	CACGCGATGT	CATCGCCTAC	GGTCTCGACC	TTCCATCCAG	1500
GAAGGGTAGG	GATCATCATA	GCCAGATTCG	TTTTTGCCACA	TGCAGAGGGA	AACGCCGCAC	1560
CAATGTACTT	GGTCTTTCCA	GCAGGGTTGG	TGATTTTAAG	GATGAGCATG	TGCTCTGCAA	1620
GCCACCCTTC	GTCTCGTGCG	AGTACTGAAG	CGATGCGTAA	TGCGAAACAC	TTTTTCCCCA	1680
ACAGGGCATT	CCCTCCGTAT	CCTGAACCGA	AAGACCAAAC	CAAGCGCTCT	TCAGGAAAGT	1740
GAGAGATGTA	TTTGCGCTCC	ATATCCGCGC	AGGGCCACTG	GCCTGCGTCA	GTTACGCCCG	1800
GTCCTAACGG	CTTCCCCACA	GAGTGCAAAC	AGGGGACGAA	CTCACCATCA	GTACCCAACG	1860
CCTCAAGCAC	GCGGGTACCC	ACGCGTGTCA	TGATGTGCAT	GTTGCAAACG	ACGTACTCAG	1920
AATCGGTGAT	TTGATGCCA	TTTTTAGAGA	TGGGTGAGCC	GACCGGTCCC	ATGGAAAAGG	1980

621

GAATGACGTA CATGGTACGG CCCTTCATGC ACTGGGAATA GAGACCGGTC ATAGTCTTTT	2040
TTAATTCTGC aGGATCGGTC CAATGGTTAG TGGGTCCTGC ATCATCCTCC CTTTTTGAGG	2100
CGATGAnAGT GTTCGCTTCG ACGCGCGCAA CGTCGGAGGG CTGTGAGCGA AAGAGGAAGC	2160
AGTTCTTACG TTTTTTTA	2178

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

TAAATATCTT GTAAGCTACG AGGAGCGAGA ATGTCTGCAT TGTTCCTT GGTGCGGTG	60
TACGTGCTTG TGTGCGGCT GCACAAACAG ATTAAAAAGT ACGCGTCTGT CTGCTACCTC	120
GGCAGTGCGT GTGTCACTGT TCGGTTGTC TGTGCTGTGT GGAGCGGCGC AACCAAGGGG	180
AATTTGGCG TCGTGTGCT TCTGCATCCG CTGACGAGTG CGAGTTTTTC CACCGCGATC	240
TTTACATTTG TGATGTGCGC GAGTGTGCTG AAGAACGGTT TGCTCAAGCA GCGTGTGATG	300
GGGTGCGTG CGGAACGGC CATCACCGCG GCGATTCTCA CTCTCGGGCA TAACATCGCG	360
CATGGAAGGG ACTACCTGGT GCGTCTGTGC GGGAGTACCG GGGATTGTC TACAGGGTTT	420
CTGTGCGCG GTGCTGTCAG CATGGTCTC GTTCTTTTGA TGAGCATTTT GCGGTAACG	480
TCTTTCAAG TAGTGCGCAG GCGCATGGG GCAAAGACAT GGAAGCGTGT GCAACGCCTT	540
GCATATCTCT TTACGGGCT TACGTATGTG CACCTTTCCT TTATCCTCCT ACCGACCGCT	600
TTGAGGGGGT ATATCCCGAG TGTCGTCTCC TACGTGTTGT ATACCGTCAT TTTTGCCACG	660
TACGCGTTGC TCGTGTCCG CAAGGCGTTG GGAAAGCGGA AGGGTGCTTG CGCGTTGTGC	720
TCCGCGGCGG TTGCTGTGTC CTCGTTGCG TTCGTCTTGG GCGCGTCTCA CATGGTCAGG	780
CACACGAGGC GTGCGCACAC GGAGAGGACT ACGCGTGCAA AGGCGCGGAA GTGTTCTCCT	840
GCAGAGATGA AGGACGGCGT CTATGAGGCT AGCGCGCAGG TCACAACGGA AAGCTAAGTT	900
TGAGGGTGAC AATCTCGCAG GGTAGGATTG AAGCTGTAC CGTCGTGGGG CACAGCGACG	960
ATGATCCTTA TGCTCCTGG GCGGTAGAGG GTGTCTCGGC GGCAATTGTA GGGGCTCAGT	1020
CTACCGATGT CGATGTGGTG AGTGAGGCAA CTCCACTAG CGAGGCAATA ATTGGGCGG	1080
TGGAGAAAAT TCTCCAGCAA CCGCAACCGT AGATCTAAGA AGAGCGGCGG TGGGATGTGC	1140

622

TTGTTTGTCT TCGTTTGTCT GGGCGCGTGC GGGGGTCGGT GTGTCTGTGA GTAAAGGTTT	1200
AAGGGGTACG CTCATTGGTG TGGGCGTCTC ATTGGCTTTC CTGTTGGTGG TATATCGCCT	1260
CTTCGCGGGG AGCTATAACC GTATGATCTC GCTTGATGAG GCTGTCAAAA GTGCCTGGAG	1320
TCAGGTAGAG GCGGTCTGTC AGAGGCGCTT AGATCTGATC CCCAACTTGG TCTCGACGGT	1380
CAAGGGTTAT GCAGAACATG AGTCGGATAC gCTGAAGCGT GTTGCAGAAh GCcGTTGCGg	1440
TGCCGGTGGC GTTATGCAGG TGGGTGAAAG CGCACTCTCT GATCCGAAA AGTTTGCTCG	1500
GTTCACGCGT GTCCAAGCAG AAATAGGCGG TGCACTCGGG CGTTTGTTCG TTGTCAGCGA	1560
GCAGTATCCT GCCTTGCGCG CAAACGAGAG TTTTCTTTCG TTGCAAAGTC AGCTGAAGG	1620
AACTGAAAAT CGTATCTCTG TGGAGCGGAC GCGCTACAAT CGCGCCGTCC AGGAATACAA	1680
CGCCTATATC CGTCTTTC CACGCAGTGC GGTGGCGCGT TGGGGTAATT TCAGCTCCCG	1740
CCCGTACTTT ACGGCACATG AGGGGGCTGT TGcTGCGCCT CGCGTTCGGT TTTGAGTGTG	1800
TGCGTTGCCG CGCCAAGAGC GGTGTGGTTT TCTTTGCGTA GGATCGGTGA TCTTCTCTCA	1860
TGGCTCGTGG GGAGTAAGGG GGTTCGTGGG TCTTTTGTG CCGATCCTGT CCCTCGTGTG	1920
GATGGCGCGC ACGGTGGCGA TGACCCGAGG CGGGAGGAGG AC CGGTTCGGG CGCTTTTCAT	1980
ATTCCCCGTT TTGCTGCTCG GTTAGGACTG GACTCTGCAG GACTGCTGCG TATCCAACGT	2040
ACGGTGGCTC GTGTCAAGG ACACACTGAC GGAGAGGTGG CGCTCGCTCT TATCAAGGAA	2100
AGTGATTTCG ACTCGGTCTA TGAGCTGTTT TTCGCACTCG TACTTGCTGG CGCTGTTTT	2160
TGCGTTCAGC TGAGCATGGT GTCGGTGCTT GAACAAGCGT TTGCgCGTTT CTTTGGGCG	2220
CCGCCATCGT GGTATATGCC gCGGTTTATG GTAGCGTCGA GTGTGGCAGC GTGTGTACTT	2280
TTTTTCTTTA TCGCAAACAT TCCGTGGGTG GATCGCGCGC TGGTACCGGG ACCTCTCAAG	2340
CAGCAAAAGA GCTATGCgCg cCGGGTGC GCaCTTTGTGG AAAGTGGTGT GTGCAATACG	2400
CGCAATCGCA CGGGGATTCT CATCTTTATT TCTGTGTTGG AGCGGCGTGT GCTGGTGCTC	2460
GCAGACGTGG GGGTGAGCGC GTACGTGCCT GCCGgTGAAT GGA CTGAACT GTGTCAAATA	2520
ATTACTGCGG GGTTCGCTC GCGTCGTGCA GCGGACGCCT TATGTGAGGC ACTTACCCGT	2580
GTGGAACAGG TGCTCgctAC GCgGATGCCA CCTCAGaAAA AAAGTTCCAA CGAGTTACCG	2640
GATGGGTAG TGATTTTGAG TCACTAGAAT TGAATCGGTG TTCTGCGTAt GTGATTCCAC	2700
TAGGTAAGCG GCATGGGCAT TCTGCTGTGG CCGTGTGTTT GCGGGGTGTT TCTGTGTTCA	2760
GAGGAGAGAA GCGATGGAT GGGGTGCGGG GCGCCCTGAG TGCCCTGCGT TCGCTGATGC	2820
GTGCGCAAGG GGTAGATATT TGTTATATCT CCGGTGAGAA CGCGCATGGG CAGATAGATG	2880

GTGCGCGTGA ATATTTTCTT GGTATTACAG GCTCTGCAGG AATAGTGGTG GTGACcACA	2940
ACGTGyGTTT TgTGGACAGA TGGACGGTAT TTTATCCAGG CTGAGCGTGA gcTGTCCGCA	3000
TGTGAAGTGT GCCTTTTTCG TACAGGGCAG GCGGGCGTAC CTCGGGTAAC TGAGCTTTTG	3060
CGTACAGAAC TCCGTGCTTT TTCATCCGGG CCTGGGCACG GAGGGGGAAC GCTCGCAGTG	3120
GATGGCCGTA CGATTTCTGC GGCTGTATGG GAGCAGTTTC AGCAGGAGCT TGTGGATGTA	3180
TCGctTCGCC TAGACTTTGA TGGGgCsCTC CTGCTACCGC AGaGCATCGC tTCCGTAtT	3240
CCTTCCctGC GTTTTTGTG TATGAGCGCT ACACGGGgTT GAgtGCGGCG CAAAAGCTCA	3300
CCCAACTGCG CGCAGCGCTC AgTGCACGCA GCTGTGATGC AACGGTGTG TCCACATTGG	3360
ATGATGTGTG CTGGCTCACC AATGTGCGCG CACACGATGT GCCGTGTACA CCGCTGTTGG	3420
TGGCATACAT GGTGCTCAG CACACCCGTG CCTTCTTTA TGTGGATATG CGCAAAATTT	3480
CTTCTGCATT GCATCAAGCT TTGTATGCGC AGGCGTTGAG TGTATGCCGT ACGATACTTT	3540
TTTTGATCAG GTGTGTGCGC GCTGTGGGAT CAGGAACCGA CGGTACATGC TGTGGGGAAA	3600
GGAAGAGCAG GAGTGCAGGA AGTGGCAGGC AGAACGCCAG TGcGTGTTGT TGGACTTTGA	3660
GCGTTTCGTGT GCTGCACTGG TGGATCTCTT TCGTGATCG CCGCAGtGTG TAGACCGCaG	3720
tGGAAcGATC CGCTCCTTCC GGTTCGTTAT CTCTGTGCT GGGCATAGAA GAGGATGGTA	3780
CTGAGACCAG CAGAGGTGGG AAAAGTGCAT GTGCGTTGCA GTCTGCaCGC GACGCTCTGG	3840
CAGCAGGGAA AGAAAAGGAG AACAAAGAGG AGCGGGGACA GACCATGTGC TTCTCCGTTT	3900
GTCGTGGACT TTTGCCAACT GTAGCGCTCA AAGCATTAAA GAACGACACC GAGCGAGCCA	3960
ATGTGCACCA GGCAATGATA CAGGATGGGA TTGCGCTGGT AAAAACGCTG CAGTGGGTGT	4020
ACCAGCAGCT TGaCGTGGGT GCAGACGTTG ATGAATGCGC TGTAGCGGAG TTTGTACGTG	4080
CTGCCCGGGC GGTGTCTCCG TCTTTCATTG AAGAAAGCTT TCACACCATT GCAGGATACG	4140
GGGCGAACGC AGCAATGGTG CATTACCGCC CCGTGCCTTT TTCAGCTTTA CACCCTGCTG	4200
CGGGTCAAac GGCAGCAcTg cTTCGCGCGC GTGGTTTTTT ATTATTGGAT TCTGGCGCGC	4260
ATTATCGTGA GGGTACCACC GATGTGACGC GCACGCTGGC TCTCGGTCCT TTGACAGATG	4320
TGCAGCGTGC AGACTACACG CTGGTATTGC AGGCGCACAG TGCgCTTGCC GTGCGcGCTT	4380
TCCTGCAGGG ACCAGTGGGG CCGTGCTCGA CGGAATTGCC CGGGCTCCGC TGTGGGCACA	4440
GGGACGAGAC TACCCACATG GGACGGGGCA TGGGGTGGGT TTTTGTCTTT CAGTGCATGA	4500
GGGTCCCTAT AGTATTTCTC CGAGTGCTCC CGGGAGAGGA GGAAGTGCAC GAGGCATTGG	4560
GGCAGAGCAC ACGGGAGATC CTCCCTTTTT TTCTGAGGAG GCGGCGTGGC AGCTGCGCCC	4620

GGGTATGCTC CTTTCCAATG AGCCTGGGGT GTATGTGGCT GGCTCTCATG GCGTGCGCAT	4680
AGAAAAATCTT ATGTGGGTGG TACAGGCGCA TGAGTCTGAC GCGCagTGTG TGTGGAAGGA	4740
AGGAGGGGAG GGAAAGGAGG AGAACGCGGC GGC CGTGAG TGTACGGGTG CAGATAGGAT	4800
GCAACCGTCA CGATGCCGAA GTTCTATGG ATTTCAAAC GCAACGCTGT GTCCAAAtGA	4860
CACGCGGCCG CTCGTGCGAG AACGATtGCA CGATGAAGAT ATTGCGTGGC TGAATGCCTA	4920
TCACTACGGG TGTATGTAAC CTCGCGCCGT TTTTAGAATc cGTACGCGCG CCTTTTTCG	4980
CACGTGCTGT CGTGCGCTAT AGCGTTTTC TGTGTATTGG TGTATACGC AGATCTTGAT	5040
TTTTGATCAT AAAGGACATT AGCTTAGGCG GGTGCACTGC ATGTGGTGTG TGAAAAGATG	5100
TCCGCGGGCA AGAGGAGGGA ATTGTGATTA CGATTTTCGA AGCGCTGAG CGTGTGCGCG	5160
TCATTCCGGT GGTGACGCTT GAGCGCGTGG AAGACGCagT GCCGCTTGCA CGCGCCTTGA	5220
TAACAGGTGG TATCAGGTGT ATGGAAGTAA CATTTCGAAC GTTGGTTGCT GCGGAGGCGA	5280
TTGCGGCAAT CCGTCAGgAA TGTGCTGATG TGTACTTTGG TGCAGGAACC GTACTGACGG	5340
TAGAGCAGGC GCagCAGGCG CAGGCAGCAG GTGCGCagTT TGTGGTCAGT CCCGGTTTTA	5400
ATCCGCGGGT TGTTCGCGAC TGTTCGGGGC ATGGCGTTCC GATCATACCG GGGATAGCAT	5460
CTGCAACAGA AATTGAGCGT GCGCTTGAGT TTGGTATTTT gGTAGTAAAG TTTTCCCCCG	5520
CTGAGCTTTT GGGAGGTACG GCAATGATGA GTGCGCTCGC AgTCCCTACA CGGCGGTGCG	5580
TTTTGTGCCT ACGGGGGGAA TTCATCTTAA TAATCTTGCT GAGTATGTGG CGCATCCTCG	5640
GGTGCTCGCC TGTGGGGGCA GTTGGATGGT ACCGGCGCAG TCAATAGCGG CAGGAGATTT	5700
CTCGCAGgTT ACTGCACTTT CTCAGCAGAC GTTACAGATT GTCGGGGTAA TGTAGGGGGT	5760
GGTGGCTCAA ACGTTGTCTT TCTCAGAGAG GGCACGTATA CTGCCGGCGG CACTCAGGTG	5820
CGGGAGGTAA CTGGTGCGCA GAAACTCGAG GACGATGGCA AAGATAGTGG CGcTGCTTGC	5880
GCTTATTCTT TTGCTCATAT TGGCAGGTTT TATTTGGTTT GATTATTTAG GAGTCCTCGA	5940
TGCAAAGCGG GCGATTTCTC CGTTGTACCG TCTTTTGGGA CGTTCGGTGC CGGAGGGACT	6000
TGTGTGCACT GCTGATCCGG ATTTGGATGC GGATCGTTAT GCCAAGCGTC TTGAGGCGCT	6060
CGGGGAGCGT GCAGAGGAAT TAGATAAAAA GGACCTGAG CTACAGGAAA AGGAAAAGGA	6120
TCACGAAAGG GTTCTCAGG AGTTGGATGA GCGTCTGCGC GCGCTTGAGG ATAAGGAGAA	6180
ATCCTACAAC TTGCTTGTG CGGAGACAAA CGAGCGTCGC GGAATGTGC GTAAGATTGC	6240
AGAATACGTC AGTGGTATGC CTCCGAGAG TGCGGTAAAG ATTCTGCTGA AACTGATGA	6300
TCAAGATGTG ATTGAAGTGT TTCGTATGGT GGATGCGGCC GCTCGGCAA GGGGTGTTAA	6360

625

CTCTCTTG TG	CCGTATTGGC	TTTCTCTTAT	GCCTCCTGAC	AGGGCAGCTG	AGATTCAGCG	6420
GAAGATGGCA	AATAAACCTG	CTGACTTTCC	CTAGGCGGTT	TATACCAACT	TGATAAAGTG	6480
CTCTTATGTT	TTTTTCTCTC	CTTTCGCCGG	CTGCTTTTCT	GTTTATTTTT	TTTATCCTGT	6540
ATTGGTACGT	TTTCCGCACC	GCGACGCAGC	GGGTCGTTGT	GCTGCTTGTA	GCAAAC TTTC	6600
TTGCTATTGC	AGCTTTTGAT	ATTTCGCTTCT	GCATTCCGTA	TCTCGTTTTA	AGTGC GTTAc	6660
CTACAGCTGT	GGGTGCTCA	TACTCATGCA	GAAAAGTTTC	TTATGGAGAA	AAGTCCTGCT	6720
CATTGCGGGT	ACCTTGTTGC	AGATACTTTT	CTTTTGTCTT	TTTAAACATT	TCTCTGATAT	6780
GCTCTCGCTC	GTGCGTGCAT	TTGCTCCTGC	ATATTTTGCG	CAGCACACAT	GGCACCAACA	6840
TGTAAAAGAC	TGGAATATAT	GGCACCCAGT	GGGTATTTTCG	TACTGTACAT	TCAAATGTAT	6900
GAGCTATGTG	TTTGACGTGT	ATCTGTGCAA	GATACGCAGA	AGAGAGCCgT	TTGCACGTGT	6960
GCTTTTGAT	GTGTCTTTTT	TTCTCAAAT	GATTTCAGGA	CCTATTGCAA	ACGCATCGCA	7020
TTTTTTTACA	CGTCTGCCGC	ACAATTTGCG	CGCTGGTGAA	AGCCCCCTTAG	ATCGTCCTAT	7080
CCACTTTGAT	CGTGCGGTGG	TATTACTGTA	CACGGGGTTG	GTCAAGAAAG	TTATTTTTCG	7140
AGATTTTCTT	TCTATACTTG	TGACTGATAA	AAATTTTACG	CTTCCTTCCG	CATACAGTAG	7200
CACCGAGTTG	CTCTTTGGCC	TCATCAGTTA	CAGTGCGGTT	TTATACTGCG	ATTTTCTGCG	7260
GTACAGTGAC	CTGGCAATTG	CAGTTGGGTT	GCTTTTGGG	TTTGAAACAC	CGGCGAACTT	7320
CAAACGCCCT	TACATATCTC	AGTCAGTTAC	TGAATTTTGG	AGACGCTGGC	ATATTTCTCTT	7380
TTCTCAATGG	TTGAAAGAGT	ATTTGTATTT	CTCACTTGGG	GGTTCACGTT	TTGGGATCAA	7440
AAGAACGGTG	TGTGCACTTT	TTTTTACCAT	GCTGATCGCA	GGTCTCTGGC	ATGGCGTACG	7500
CTTGACGTTT	CTGTGTGGG	GTATGGCGCA	GGGTGTGGCT	TTGGTAATTG	AGCGGGTGTA	7560
TAGGGAAAAA	AGACGGGTGA	ACGGTGCGAA	TGCCTTTGGA	TCAAGTAGTG	TGATGGGAAG	7620
ATGGAAAGCG	CGTGCTATGC	GGTGATACG	CGTCAGTGCA	TTGTTTCTTT	TTGTCaGTGT	7680
TGGATGGCTT	ATTTTTCGCG	CACCGTCTTT	TGCAGAAAGTG	TGGCGGTACG	TTACCTTGCT	7740
GTTCCGAGGA	AGTTGGCATG	GGCCATTCCA	AGTTATCACG	CCATTTACCG	CGTTGCTCGC	7800
GCTGTGTGCA	CTGTGTGTAC	AACTCCCTTC	AGATCGTACG	CGTGCGCGCG	CGTTTGCTTG	7860
CTACTGCGCA	GTGCCCTTAC	CCGTAAAGGC	TTGTGTGCG	GCGTTCTTTT	TCTTTGTACT	7920
GTCGGTTATG	ACTCCATCAG	GTATTGCGCC	CTTTATTTAT	TATAGTTTTT	AGCGAAGGGG	7980
CTATGATGAC	AACAGTGCGT	GTTATATTGC	AAAGGTGTGC	ACGGGGAATA	TGTAGTAATA	8040
AGGGTCGGTA	CAGTGCGAAT	CAGGTACTGC	TTTTTGCAT	ACTTACGCTG	AGCCTGTGGA	8100

626

CGCCATTCT	CGGTCCGGCG	TTGCGCCATC	CTGCCGTGTA	CATACGGCAC	AAGAGCGTGA	8160
AAAACATCTA	CCTTGCAATC	GTAGATCCGC	TCATGCACAC	TGCAGAACAG	TGGGGAATAG	8220
ATACGGTATT	TCCTCTTTTG	CGCGAGAGTT	TTTTGCATGC	GACAGGTTTG	ATACAGCATC	8280
CGGAGTGGA	AGATACGTTT	TATCACTGCG	AGCAACGCTC	TTATGAGCCA	GCTGCTGCCC	8340
TGGCGGAGTC	TGTGCCTTCT	CCTGTCCTTAC	AGGAGGCCGT	GGCCGTTTc	CCTCCGGGGG	8400
TGGCGGTTAA	CGATTCTGTT	GCGGAAAGAA	AAACAACGTC	TCCCGCACGT	GTCTTTTCGC	8460
GTACAGCGCT	TCGTATTTTG	ATGTGTGGAG	ATTCCCAAAT	GCGTTACCTT	ACCGGCGGTG	8520
CGTTGCAGGT	GCTAGGGACG	TCTTCGCACG	TGCAGATTCA	AGAAGTGACG	GTTAGTTCTT	8580
CTGGTTTTGT	GCGGACCGAT	TATTACCACT	GGCCACGAAA	ATTTCTCGCG	CTCCTGGATA	8640
CGCACACCCA	ACAAGAACCA	TATGCAGCGG	TAATTATGGC	ATTTGGTATG	AATGACTATC	8700
AAAATTTTTA	TGATGCGGAT	GGCTCTTTGT	GTGTGACGAA	AACTGCACGC	TGGGAACGCG	8760
CGTATGAGCA	AAAAATGCGC	GCCTGTTTGA	ATATTATTCT	GCACACAGTA	CCGAAGGTGT	8820
ATCTGTTGGG	TATGCCAGAG	ACACGTAACA	AACAGTTGAA	TGAGAAGCTT	GTGTACATCG	8880
AGCACGTACA	AAAGAAAGTA	GTGGCGCAAT	ACGATCCGcA	GCGGGTGCGC	TATTACTCCC	8940
TCAAACCAAT	TGTACCCGGT	GTACACGGAA	CATATGCAAG	CGCGATAAGG	GACACGCACG	9000
GCGTGTGGGT	ACACGTGATG	CACAAAGACG	GCATCCACTA	CACCATAGAG	GGTGGTGCCT	9060
ACGTTATGGA	AACTCTCTTA	CCCCTTATTC	TTGCAGATTT	GGAACGGTCT	CGTCACGGAT	9120
ACATGCGTTC	TTCTCTGGGG	TCGCATGAAC	TCCCTGCGAC	GAAGGGGATG	GAAAGAGCAC	9180
GTCACGCGTC	AACTCGAACA	TAGGGATAAA	CCGCACCGTT	GTATCCTGCA	TGACAGGGGG	9240
TGCGTCCTGT	CAGGGGGTTA	TCGTACGTCC	ACACCGTTGC	CTGCACTTGC	ATAGTGCTGT	9300
TTTGGTCACC	TGAGAATGTT	ACCGTAAAGG	GGAGTGGTGG	GCGCGCCTGC	GATATGAAnC	9360
GTACC						9365

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5019 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

AGGGTGn	Cn	CCGCACGGAA	AATCTCn	TCT	ACAGCn	TCCC	GATTGGTGGG	ATCCTGCTCA	60
---------	----	------------	---------	-----	--------	------	------------	------------	----

627

ATGACGAGTA TATTGCTTTC GAGCTGCTCA ACCTGTTGtC CGCCTCGCTG AAAAAATCCT	120
TCAGCAACTC TTCGTGCCCC GCGTCGAGGT AATCGCTCAT GGGCACAATC TTCCCGCATT	180
CTCAGCCTTT GGTCAAGGCA ACGTCCAAAA GACCCCGCCA CCCGCTGCAT CCCTTGACAC	240
TTCCATCAGC CGAGAATAGA CTCCGCCATG GCGCGCGCG AGGTACGTTT GTCAGGTCCG	300
TTTCTCGCCC TCGGTGGTTA CTCTTGATAT GCCGCGGGAC TGGTCTACT CCTCTACCGA	360
GCGGTGGGGG TCTACGTTTG GATCCACTTT TATCAAAACC AGACCTCTC GCAGCTTTCT	420
ACCCACGCGC GGTCGTCTTG GGTATCGATT GCGGACACG CaGCCTCTTC CTCGGCGCGG	480
TGCTCTTGAC CGTTCGGGAC GTGCGCACCT TCAGAGACGA CAGCACGATG TGGATAGCCC	540
CCGTCTTCT CTGGTCCGCG GCGACCTACT CCAGCATGGG aGmCTGCGGC TTCTCTCTCA	600
GGGCCGTAGC CAGCGGCGCA TCGGGCGTGC TTCTCTTCGC CGTTTGGTGC CTCGCGTcAG	660
AGCTTGGGCG CCGCCGCCCT TAGCGGCGCG TTCGCCCGmG GCTGAGCCTT TTTATAAGA	720
GGGTGcTGC GTAGGCAGCG CGCGCAAATC CGCATGTTCA GCGCAGAGCC ATCTAcAACT	780
ACTcTCAtGC GAgCArGTTT GGTTCACACA CCCGCTTGCC AGTGGTGCAT CGATTTACTC	840
ACGGCGCACC CGCTGATCGT CCCCTTTCCA CACAGTCCAC ATCTTCTTGC caTCGkwmAT	900
GTCTCCGCCG CCGATGATAA AGAAAAGGTC CGCCAGAGTA AAGGCGgCAC GCGCGCTTTA	960
TGGCATAATG CTCCCCGTG CCGTGGTCAA CCAACGCAGA AGGAGCGCCC TCATGTGCGG	1020
AATTCTCTCC ATCGTCGTAA GTATCGCTGT TCTTGACCG CTGGCAGTTG CAAACACCCT	1080
cTgtACGCAC TGTACCGCCC GGGATGCAGA TGGGTTAATC ACGCGGTATC CACCTGGGGT	1140
GCACGGACTA TCTTTGCCGT TCTACATAct ACGGAAGACT TAAGTTTAC AGCGACTACA	1200
CCCACGCTGA GCACCTGCCC ACGCAgTACC TTGTAGTCTC AAATCATCAA AGTGTGCTAG	1260
ACACCCCTGc ACTCATGCGT TACTTTGGcT ATATtGATGC GCCGAGGTG CGCTTCGTAG	1320
CAAAGCGAGA GCTCGCGCGC TTCGTCCCCC TTGTGTCCAC CATGCTCAAA AGCGGTGCGC	1380
ACTGCCTGGT AGACCGGCAT CAGTCAGGAG CACAGGCGAT GCAAGCGCTC GAAACGTTTA	1440
CACACCACGT CATGCGAGAg CGATGGCTCC CTGTGATCTT CCCTGAAGGG ACACGATCAA	1500
GAAACGGCGC CCTGCgCATC TTCCACGCCG CAGTTtCCGT GCGCTCACGG CACGGCTCCC	1560
ACTCCCCGTA GTTGATGCG CGTTGGACGG AGGGTGGAAc cTACGCCCGT TGCTGAAAAT	1620
AGGACAGAAG CTTAAAGGAA GCGCTTACCG CGTCAAAGTG CTCGGCGTTT ACCCCGCACC	1680
CCACAACAAA GACGAACAGC TCTCCCTCCT ACGCGAGGCA AAAGCGCTCA TTCAAGCGCA	1740
gcTAGACGTC TGGCGCTCGG AGACCACCTG TCCTCAAGAC GAGTGCCCTCA CGCGCGCCTC	1800

CAAAGACTCC TAGTTAAAGT CACGCGGCCG ACGCTCAACA CGCCTGCACT TAGGACACTC	1860
AGCGATGTTT TTCACCTTTC CGTTATCAAC AATAGACCTC AGCACCACCT CTCCCCCGCA	1920
CGGACAGTTA AAGCGCTGCG TCGCCGCCCG AGTACGCGAA TTTTGTCTGG CACCAGCCAT	1980
TTTCATACCT CCTAGTAGCT CGCTCGCCAG GCTGCATCAC ATTGTCTTTT TGGTCAAGCG	2040
TATGGCGAAT TCTAGGGGGA AGACACGACA CTCGCCCCGC CTACCGGCGg TACGTACTCT	2100
CTGCATCGCG ATATAGAACC GTGGAATGAG AAAAAATGGC CTCATATTGA CAGAGATTTT	2160
TCCTGTTCCC ATAATGGCAC CCTGGGTGGG GTAGGCGTGG CGCTCACTAA GTCGTTTTTG	2220
GAGTCAAGAT CAACCGGGGA GCTGTTTTCG CTTGCAGATG AGCTCGGTCT TTGCTTGCCT	2280
GAGGATCTTA ATCGAAGACT TGTCAATGGC GAGATCCTTG ATTGTTACCA CAGCGCTCTT	2340
GATTTGAACC CTCCGTGCGC TCCCCAGTCC CTTGAATCAA AGGGGACTTC GTGTGCCTAC	2400
AATACCACCG AAATCCATAT CCTTGCCCCG GACCCGCTTT GGTCTTTTGT CTTTTGGGAT	2460
ATCCACGAGC AACTCTTTTG CACACTCACC CAGAGTCCTC AATTTAGGTC GTTCTTTCTG	2520
CGCGTGCACT CCCTCGGTGG TCATGGCTGG CACACCTCGC TCGACCACTT CGATATTGAT	2580
GTACCCCTCA AAGACAGAAA GCGTTACGTG CACCTGTCTT TGGCCGACGA TGCTAATCGC	2640
ATAGATCTTT GCTGCAAAAT GCTCCAACGC GAACGCATCC TTGCTCAATC CAGAgTTGTC	2700
ACGCTCCAGC GCAGcKTCAT AGAACGGAGT CTTwACCCCG AGGATCCAAC CGGCGCAGAA	2760
GTTCTCAGCC TCTGTGGGCT TCCCCTGCTT GAGGAAACCT ACCCAAGCAC GTCTCTTCCT	2820
GTGTGCTCAT AAGTGGGACC TTCATGAAGA AAATGCCaGT GCACTCTCTT GCATTTGTTC	2880
TCGATTGTAA TCTTCCcTTC GTCCGAGGGG CCGGCGCATC TTCTCTCCTC GCTGAATCCC	2940
GTTTTTTTCT CGAGATTTC TATACCTACC TCCCCCTACT CCGCTTATGC GAAACACTCG	3000
AACGTGAGCG TGTTCCTTTT AACATCTCCC TCGCTATCGG GCCCGTTCTG TCGGAAATGC	3060
TCGCTAACCG CGTGCTTATG GACCGATACC GCGTGCACT CGACGCACTC ATCGAATTCG	3120
GAGAACGGGA AGCCATTTCG CTGAGGAACA GTCTCCAAGA GCGCGTGCAA GCTGAAGCAG	3180
TGCTTCGGTC TCTTCGCTCT CACCGGATT ATTTTGaTCA CTGmGATGGG GCACTCCTTG	3240
AACGcATCAA TCACTTTTTT CgACAGGTT CCATTGAATT ACTCGcAACA ACGGCAGTTA	3300
ATTGTTTCTT ACCCTTCTAC CAAGaCATGc CCGAATCTAT ATCCGcCCAA ATCGAAATGG	3360
GGCTTATTAA TTACCGcAAA CATTTTTCCT CAATTCCCCG CGGTTTTTAT TTACCTGAAC	3420
TTGGCTATGC ACCAGCGCTT GAGCGCACTA TAAATCATA CGGATTCTCG TACACCATAT	3480
TGGAAACACA TAGTTTCCgT TTGGcACTCG CGTACCCCGA CGTGGcATCT TgAGCCkGCA	3540

629

CAGACGTCCA AgGCTTGTGG TGCTTAGGAA AGGAsCGTGT CGCCACkGCA GAAGTGCAtG 3600
GCGCCACgCA TTCCTTCTGT ACACAGGCGG TGTACGGAAA TACAGAACAA GATGCTGGGT 3660
TTATACTGCC TGAGGAGGCT CTGTACCCTT TATTTGAACC ACACAAGGAA CGCATGGCTA 3720
CTGGGTATCT GTACCAGGCC CGTTCAGGCA CGCCGTATGA GCAAGAAAAA GCGCAACGCA 3780
CGTGTGTGCG TGATGCGCGG GCGTTCGTGC GTAATCGGAC AGAAATATTT GAAAAAGTAG 3840
TCCACGCAAC CGCTCCCTTC GAGGCTATGT CGGTGTGCGT ATTCCCTGCA TCACTATTTG 3900
GAGTTGCATG GGCAGAGGGG ATGGATTGGC TTGAAGCCGT ATTTGCGACC GTTGCAGAAA 3960
GCGCGCAAAT GCGnGTgTCC TGTACGGCGG CGCTCACCTG CCCCgCAgTG GGGGTGTCAA 4020
TCATTGAACC CTTTTTTGGA TCTTCACTGG GGGGAGGTTA TGCGGATGAG CTTATTAATA 4080
GCGCAAACGA CTGGATGCAT CCTGCAATAC AAAAAACCAC AGAACGCATG ATCGACCTCA 4140
CAGAGCGCTT TGCACACGAC ACCGGCTTTC GCGAACGCCT ACTGAACATG GCAGCACGTG 4200
ATGTGCTTTT GTGTCAGTCG CTGTTCTGGC CCCTTTTAGG GAACCATTGT CGCTACCCCG 4260
AGTACGCCGC TAGCGAGTGC GCCGACCACC TCAAGGCCTT TACGAGGGTA TACGAGGCGC 4320
TCGGCTCCGG AGAGGTAAGT GCACAGTGGC TAATGCGGCG CGAACGCGAG CTACCACTGT 4380
TCTCTGAAAT TAACTTTCGC TTTTTCAGTA AAAAGAAATG ACACCTCACC AAAAGGCGAT 4440
CTCCCCAGAG TAATACGATC GCATCGACCC AGCGCTATCT ATGCACAGCG CGCCGTCCGC 4500
GGCCAATCCG ACAACACGAC CCAGAATCGG AGGACGTGTT CCCGCACATT CGCGGAAACA 4560
GACGTACTCA CCCTGCTTCC ACAGACACGA CTCAAGCACG CCGATACTCG GcGGCGCCAT 4620
GaCACAGGCA TACAGCCGAT CCAACAGCAC AGGAAGGAAA GCAAACGGAT CAGGGCACCG 4680
CTCGCTCCG ACAATCTGCG CGAGAGAGCA GGCATGCGAC AACTCGGGCG GAAACTTCAC 4740
CTGcAGGAGG TTACACCCAA TACCCACGAG AArCGCTCCC GCGCGcAcCT GGCAGAGCAC 4800
CCCGGnGATC TTACGATCGC ACACCAGGAC GTCGTTGGGC CACTTAaTGc GCGGTGCGCA 4860
CACACCTCCG AGGAAGGCCA TGTATGCAAG AGCGACCGCA TATCCAACAC AGAGCGAAAA 4920
CGCAGGGAAA GCAACACGCC GCAAAACGAC AGTACACAAA AGATTCTTTC CCGGCTCCGA 4980
TTGCCACTTT CTCTGGTCAC CACGAnCACG TCCAGCAA 5019

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3843 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

GTGATCACTC AGGTACGCTA TCACGGTTCT TTAGATCCTA AGAACGTGGA AATTGACGAG	60
CACAGCTATG TGGGTACCCA CCAAGCGGGC AGTCGCGTGT TCTGGGCAGA GCGGCAAATT	120
CTTCTCTCCT CGGTTGACGC GCGCGCCTAC GTCCTGCAGC AGGATGCGCG TGTACGGTC	180
GACGGGGTCA GCATCCCCCTT GGTGCGAGGG GATAACGTGT ACGCTATTAT TTCTAAAATT	240
AATGATTTCAG GCGCGGCAGT CCGTGCGTAC CTTGACCCGG TTACCAACGG TTTGAATATG	300
GAGACATCTG ACGCCAGGCA GTTGTGGTTG CAAGATGAGG ACGAGGCAAA CGTGTTTGCC	360
TCGTTGGGTT TGATTACCGA AGGcAGCGTC CGCCGTACAA TGTGTCAGCA GGTGCACGGG	420
TTTCAGGCGG GTCCATTTTT GACATGGCCA TTGCGGTGCG CAATGCCCTG CTTGCAGGTG	480
ATCAAGAGTC GCTCGGGGGT AAGATTTTAG GAAGTGCAGA TGGTGCAGTT GACAACCTTT	540
CAcTGCGTCT TGCCGAGACA GGAGCGCGGT ACgcACGTGC ACAGGCAACA CTTGCACGTT	600
TTAATAGCCA CATTCGGAAT GTGGTTGCAG CGGAGTCTCG TGAGTCTGAT ATTGATTGA	660
CGCAGGCGAT TACGGATTTG AAAATGTTTG AGTATACGCA CCAAGCAACG CTGAGTACGG	720
TGGGCTCTTT GTATAAGCAC ACGCTCTTGG ATTATTTCG GTAGGGGAAG GAGCCGCACG	780
CTATGGAGAT TCAGACGAAG ACGCTCGGTA CACAAACGGT TGAGGCACAC CAGATTATTA	840
CGTTGGAGCG TGGTCTCTAT GGTTTTGAGA AATATCATCG CTTTGCCTTA TTTGATGCAG	900
TGCAGGTTCC GTTTATTTCAT ATGCAGTCCT TAGACGATCC GCGGTTGTCC TTCATTGCTA	960
TTGATCCGTT TTTGTTTCGT CCGGACTACG AATTGGACAT TGACGATGTA TTGTTGCAGC	1020
CGCTCGATAT TTCTTCTCCT ACCGACGTCT TGGTGTTCGC GTTGGTGACC ATTCCTCCCG	1080
ATGGATCTGC GGTGACTGCA AATTTGCAAG GTCCCTTGAT TGTGAACAAG AAAAACCGCA	1140
AGGCGATGCA AGTGGCGATG GGTGGCGATC GGTGGAGAAC GAAGCACGAT ATCGTCGCCG	1200
AAATGGCAGA AAGAAGGGCG CAGGAACAAT GTTGATCCTT TCGCGCAAGA CAAATCAGAA	1260
AATCTTTATT GGGGACTCGA TTGAACTGAC TATTATTGAG ATTTCGCGCG ATCAGGTAAA	1320
AGTCGGTGTG GAAGCGCCGC GTTCGGTGAA AATATTCCGA CAAGAGGTAT ACGAAGAGAT	1380
CCAGAGAGAG AACCGCGCTG CGTCCGACTC CCCCTGGTCT CCTAACTCAT TGCCTCAGTT	1440
GCCTGTGTAG TTGCAGAGGA TACCCATCCC TCGGGGTGGG AGTGTTTTGC GCGGATGACT	1500
GAGTTCACCT AAATCGCACC GCGTTCCAGT GCGCATTGTA GTGTTTCGATT GCTGCCCCCA	1560
CATCTGTTTT TAGCGTTCCT CGCTCGAGGT CATGCTCGCT GTAGTATGGA GTCTTCTTCT	1620

631

GATATGCTGC	CGCTTCCCGG	TGGATAGTTG	AAGGGAATCC	AAAGGTGTCC	AAAAACTCCG	1680
CGTAGTGTGC	AGGCTCTAGG	AAGAAGTTGA	TAAACGCATG	GGCAAGGTCG	CGATTGCGTG	1740
CCCCCTTGGG	AATGCAAAAG	CTGTCTACGT	ACACTGGGCT	GGCGACATCT	TGTGGTATAA	1800
AGAAGTCTAT	ATGTTTCGTGC	ATTGCCTCAG	GAGTCTCTGC	AAAGAAGGCC	TCTGCAAAGC	1860
CATGAGCTAC	AACAAAGTCT	CCCGATGCAA	ATGACTTTGC	GTATCCGTCC	GAATCAAAC	1920
TTACCAAGTT	TGGTTTCCAG	TGGTCGGTGA	CAAGTATTGC	TGCCTGCGCA	AgCTCTTGTT	1980
CGTTTTTTGT	GTTTACGTTG	TAGCCAAGTG	AAGCAAGTGC	AGCACCCATT	AcTTTCGCGCA	2040
TATCGTCCAT	CATGCTCATA	CGATACGCCA	GGTCTTTGCG	TGAGAAGATA	GACCACGTGC	2100
GCGCGTATGA	CGGAACTGCT	TTTTTGTTTA	CCGCAATGCC	TGCCGCTCCA	AGATAATACG	2160
GCACCGAATA	TTCCATTTTT	GGATCGTAGG	CTATGCGAGC	ACGGACACTC	TCTTTGATAA	2220
ACTGTACGTT	GGGAATCTTG	GATAGGTCAA	TTTTTTCCAA	CAGATGCTTG	CGTTTCATGA	2280
TGCTGACAAA	GTCACCCGAA	GnGCCACTAA	ATCATAACCA	CTTGACCAA	TGCTCAGTTT	2340
TGCAAAACATA	TCTTCATTTG	AAGCGTAATC	ATCATAGACT	ACCTGCACGT	TATACTGTTG	2400
TTCAAACTTT	TTAATGAGGG	ACGTCGGGGT	GTAGTACGTC	CAGTTATACA	GGTACAGGAC	2460
ATCCTGTCTG	GTCTGCAGGC	ATGATCCCAT	CCAGAGGGAG	AGAAAAAGGA	GAGAArGAAT	2520
GCgCGAACTG	CTCACACAAA	AACGTTTCAT	GCTTTGCTCC	TTACGAGATT	GTTTGCAGAA	2580
AAGTAGTTAC	TThGAATGGA	CTATTGTTTT	TAnAGAATTG	CGCAGGAGGT	AGGCGACCCC	2640
TACAATCCCT	GCCATCATGA	TCAGGGAAAG	GGCATTGATG	ATaGGAGAGA	CCCCATAGCG	2700
GATCATTGAA	AACACATACA	GGGGGAGTGT	GGTGGAGCCC	GGTCCTGCAA	CGAAAAAGGT	2760
GATGACAAAA	TCTTCCAGAG	AAAGGGTTAC	TGAAAGTAAA	AAGCCAGACA	GTATGCCTGG	2820
CATGATGGCA	GGGATCACGA	TTTTTCCTAG	CGCTTGCCAC	TCGTTTGCAC	CTAAGTCTTG	2880
CGCCGCTCT	ATGAGAGAGA	GGTCAAAGGT	GTCGATGCGA	GTAAGGATGA	GCAGGAGCAC	2940
GAAGGGCAGA	CAAAAGGTGA	TATGAGCGGT	GATGnATGTT	GCGCGCCCCA	GCGGCAGGCG	3000
TACTAGGGAG	AAAAAAACGA	GCATTGCCAT	ACCTGTGATA	ACCTCAGGGA	GCAGCATGGG	3060
CAGAAGGCTC	ATTACCTGCG	CATATAGCCG	GCCTGAGAAA	CGATACCAAC	GAATTGCGAT	3120
GGCAGCGGCA	GTCCCCACAA	TTGTTGCTAC	AAGTGCAGAA	ACAGATGCTA	TAAGCACGCT	3180
ATTAAGAAAG	GAAGACCACA	GTTTTTCTGA	ATAAAAGAAT	AGCTCTGTGT	ACCAGCGCAG	3240
CGAGAAACCG	GTCCAGATAA	GGGATTTATC	CTTGTTGAAG	GAAAAAAGCG	CAATAACTGC	3300
AAGCGGCAGA	AATAGGAACG	AGACAACTGC	CGCCAGCAGC	ACAGCAGAGA	AGGAACACCG	3360

632

TAGGGGAgTG	CGTGCGCGCG	TGTGGATCAG	ACGGCAATTA	GGCATATGAG	CGGCGTCCTC	3420
CGCAAGGGGG	AGGTGTTGTA	TTGCAGGCAC	CGCTTTCTGC	AAGTATCCAG	AGTACTCCTA	3480
CCCCCCTGC	GAGGGTAACG	AGCATCGCGA	AGGCCGAAGC	GAGTGGCCAA	TTTCCCACGA	3540
TACGTACCTG	GTCCACAATT	CGGTTTCCGA	TAAGGTAGGA	ATCCTTTCCT	CCCACCAGGA	3600
GGGGGACGGT	GTAGGAACCG	AAGACAGGAA	TGAAGGTAAA	GAACACGGCG	GTGGCAATGC	3660
CGGTTTTGAT	GTTGGGAAGC	AACACGCGGA	TAATGGCACC	CGTGGGGGTA	GAGCCTAGAT	3720
CGCATGCAGA	TTCAAGGAGG	GAGAAATCGA	AGCGATCGAT	AGCGGCGAAA	ATAGGAAAGA	3780
TAGCGTAGGG	CAGGAACATA	TAGGTGAGCA	CCACAATGAC	TGCCCCGTTA	TGGTACAGGA	3840
GCG						3843

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2072 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

CnTCATCCGG	CCCCAGAGGG	AAAAAACGCG	CGCCGCGTTT	CCCGTTGTTT	CAGGCCCCACC	60
AGCnCGGTGC	TCCACGTTCC	AGTGTACCCG	GTAGTGCGCA	CGTACTATGC	GCGCATGAGA	120
GATTGGGTGA	TCCGTGCTGT	GCGCGCTCAT	CTTTTTTGCC	AGAAGGAGTG	CGCATGGCCG	180
TGCACACCCG	CCGGCACAGC	ACCACGCAGG	CGGAAAGCTC	ACTGCAGCAG	ATAAgGGGGG	240
AGCATGTTTG	AGCAACTGAG	CGCGAgcTTT	AAACGTATCG	TAGGAGCGCT	GGGAGGACGC	300
GCAACTATCA	GCGAACGGAA	TATTCAAGAA	GCAGTAGAAT	CAATTAAGCG	CGCACTGTTA	360
GACGCCGACG	TGCACGTTTC	CGTAGTGCGT	CGCTTTGTGA	ATCAGACCAT	ACAACACGCG	420
CAGGaCAGAC	GGTGCTTGCG	TCGGTTAGCC	CTGCGCgCA	ATTCATAAAA	ATTGTACACG	480
AAAGACTAAC	TGCCTTCCTC	GGTGAACATA	CGCGGTCGCT	GCATCTTAAG	GGGCCCCGATA	540
CGCAnTCGAT	TATTCTCTTG	CTTGGGCTCC	AAGGATCGGG	GAAAACTACC	AGCGCgCAA	600
AGCTTGCTGC	GTACCTGAAG	GATGCAGGTC	GCTCCCTCT	CCTGGCCGCT	TGCGATCACG	660
TTCTGCGCGC	AGCGAGTGCT	CAGCTGGCCG	TTCTCGGCAC	GCACATTGGC	GTTCCCGTGT	720
ACCAGCATGC	GcTGCCGCAC	GAACAGCAGC	CGTGTGCTCT	TGATACgGcG	CGCGGTGCGc	780
YTTCAGTACG	CGCGCTCACA	CGGCAATGAC	GTACTTATCA	TTGACACTGC	TGGCCGTCTC	840

633

```

CACGTGGATG CCGCGCTCAT GCAGGAGTTA ATCCTTCTCA AAGAAACACT GGTTCCTGTG      900
GAAACACTCC TTGTTGCAGA CGCTCTAACC GGTCAGACTG TGGTGCGCAT TGCAGAAGAG      960
TTCCATGCCG CGGTGGGTAT TTCAGGCGTT GTGCTCAGTA AGTTTGATTG AGACACCCGC     1020
GGCGGAGCTG CACTGTCTTT GAAAAGTATT ACCGGTCAGC CACTGCTGTT TGTGGAACC     1080
GGTGAACGAC CGCAGNACTT TGAACCGTTC CATCCCGAGC GAGCCGCCGG AAGAATTCTG     1140
GGTATGGGGG ACATCGTTTC TCTCGTGGAA AAGGCGCAAA AAGCCTTTGA TGCACAGGAA     1200
CATGCGCGTG CGCAGAAGAA AACGCAATCG CACGAGCGTT TCACGCTCAG CGATATGCTC     1260
GACCACCTGC AAACATATAGA AAAAATGGGA CCGCTGCACT CGTTGGTGA GATGATTCCC     1320
GGTTTAGCGG TAGCCGTTTC TGCCGATGCT CTTGACGCGC GCGCGTTCAA GCGTCAAAG     1380
GCGATTATTC AATCGATGAC CGTGCAAGAG CGTGACAATT TTCTCATTAT CGGCCCTCA     1440
AGGAGGCGGC GCATCGCGGC AGGGTCAGGC ACTTCGGTGG CTGATGTTAA CCGTTTAATT     1500
AAGAATTTTC AGAGGATGCG CACGCTCATG CGCAAGACTG CATGGCAGTC ACGCCGGGCA     1560
CACCTAAAG GAGATACACC CTATGGATGG CCACATCGCT AGATACGCCG CCGCGCCCT     1620
TTTCGCACTC AGTGCGCTGT GCsCCCCgct TCGCGCGCAG AAGACGCGGA CCACTCCTGG     1680
TCCCCCGTAC ATACCCACCC CTACGATCCT AACTTTTCC AGTCGGACGC GCAGcGTGCC     1740
GCCTTCCACA CCTTGGCGGC GGAACACCTT TCCTTCCTTA CCGGTCACAT GTGCTTCTTC     1800
CGTCCTATCC CTACCCGCGA TCCTTTCCTC ACCCGTGCCT ACGAAATCTC CCCACATCCC     1860
CGCACACAGA AACCCACCGT GCTGCTCGCC TTGACTCGG ATATCATCTA CCTTCTTTTC     1920
TAGATCACC GACCAACAGA TTTCCCCGCC CTCCGCTTCT TTCAAAACGC ACCTACTTTC     1980
CAAGAACTTC CGAGCACCTT CTACCCCTAC ATTGCCATGC ACAGCGACGC CGTTCTCGTG     2040
CGACATCCAA CGCCGCGCCC CCCTACCCTT CC                                     2072

```

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

```

ATGnTATGAT CACATTCATC ACATCTCCTA CATTTTCTTG CGCACACGAA AGCTCCACGC      60
TCATGATAGG CTCAAGCACG TATGGCTCAG CGGCTACACA CGCCTCACCA AATGCTTGCA     120

```


634

CCGCTGCAGC TTCAAATATA AAAGGCGAAG ACGTCAGTTC CTGATACTCC ACCGACAGGA	180
GATGCACCCC CACGTCTACA CACGGATACC CACTCTGAAT ACCTCCATCC CACGCGCCGc	240
GGATAGCATG CTCTACCGCT CCGATAATTT CTGCCGGAGC AGTATGCGCC GTGCACACTG	300
TGCCCCGCAA CTCTTTTACC TGACAAAAAA ACTCATTTC CGCACCAcgC TTCCGCGCCT	360
CCACACGCAA GgTTAACCCCT GCCATATATT CTTTGCCACC GATTACTCGC TGTACTCGCA	420
GCGTACGCTC AACTGTTTTTA CGAATAGATT CACGGTACGT CACGTGCGGC TTACCAACAC	480
GTACCTGCAC ATTAAAATCC TCGCGCATCC GGGTGGTGAG CACATCAAGA TGCAACTCCC	540
CCATACCGGA AATTAAAAGC TGCCCTGTCT CTGCATCTTC CCGAACCGAG AAAGTTGGAT	600
CCTCTCGCGA AAGAATACCA AGTGTCTCCT GTAACCTATC GCGCGATGAT GCGTCCATTG	660
GCTCAAGCGA CACAGAAATA ACCGGTTTCAG GAAAATGCAT AGACTCCAGC ACTACCGGAC	720
ACGAACCATC CCCCACGCTG TCCCCTGTTT GTGCAGATTT TAGTCCCACA ATTACCGCAA	780
TATCCCCCGC CTGTATGCAT TCAACGGTTT CAGACTTATT CGAATGCATA CGCAAAATGC	840
GATACACCCG TTCACGTTTC TTTTTCCTAA TGTTAACGAT ACTGTCCCCC GTACGCAGTT	900
TTCCCGAATA CATGCGCACG TAGCAGAGTA AACCcGCTTC ACGTTCGTAC TGAATTTTAA	960
ATACAAGTGC CAGCAACGGT CCTTCAGCAG TAGGAGCGAT AAAACAGGC TCCTTTTCT	1020
GTACGTGAAA ACCTTCTACT GCTTTacGCT cgCGGCGCAG GCAAtACTCT AmCACTGCAT	1080
CGAGCaGTGG TtGCACACCC AAGTTATGAC GAGAAGAACC GCACAAAAAA GGAACATATC	1140
GwCCGtCGCG CACAGCCTTT CTAATTTCTG msTGCagTAA CTGCACTGGA ACGTGCTCCC	1200
CTGCAAGCAC AACTCGGTT ACCTCATCCG AATATATGGA AATGACATCA AGCATTTTTT	1260
CTcGCGcttc gGcCTGGGCA ATACGTGCGC TTTGAATAGG CCGGTACTCC ATCTGTTCGC	1320
CACTACTTGC CGCATCCCAG AAAATCTCTT TCATGGTGAT CAAATCAATT ACCCCCTCAA	1380
AAGAGGTACC AGAACCAATG GGTATCTGCA ACGCGACTGC ATCTATACCG AATTTATTGT	1440
GGACTTGGTC CAATACTGAG AAAAAGTCAG CACCGATCCG ATCCATTTTG TTAACAAAAC	1500
AAACACGCGG GATATCATAA CGATCTGCCT GGATACCATA CGGTTTCTGT CTGTGGGCTG	1560
TACTCTTCCT ACCGGCACAC AATACCACCA CTACCCATC TAACACGGGG CAACGCAnTT	1620
CGACTTCTGC AGTAAAATCT ACATGtCCCG GcGTAcAATA AtGGTAATGT CTACTTCACG	1680
CCACCGCACC GTCGTTGCAG CACTCTGAAT GGTGATACCG CGTTCCTGTT CCTGTACCAT	1740
CCAATCCATC GTTGTGCGAC CATCATCAAT TTCCCCATG CGGTGGATCT TGCCCGTGTA	1800
AAAAAGCATA CGTTCAGTGG TAGTAGTCTT ACCAGCGTCA ACATGTGCCA TAATGCCAAT	1860

635

ATTCTCATC TGCTGTTGTC TCATATCTTC CTCTTTATCA CGTACCTGTA CGGATAAAAA	1920
ACAGTGCACA GGACTACTCC CCACCATCAT AGCAGCGGGA AAGAGAATAC CTA AACGTA	1980
AAACAGTGCA CGCTACACCG CACGCGCAT CAGTGACAAA TCACAAATCG TCTGTGAAAA	2040
CAAAATCTGc AATTAAATGG GGTGGTACCG AATCTTTCAG TTTCCTTACA ATAGACTGCA	2100
GCACACGCAC ATCTTCGGCT TCACTTAACA GAGACTTTTT TTGACGCAA AATTCAACCG	2160
CCTGAATATA TTTTTTCGCG TGCACCAATA CGTTTGCATA CTCAAGAATA CGTTGAGTAT	2220
TTTTCTGATC ACGCTCATA AACTGTTGAT AAAGAAGTAG CGCGCGAGCT GTTTCACCAA	2280
AAGAAAGCa cCATAnCGTA CGCGGCAGCA ATGGTTGCAT TGGCAGAATC CGCATCGTAT	2340
AACGGTTGCA GTGCATGAAC AGCaGTTTT CAATCATCT GCAATCCACA CACACGCGCA	2400
AAATTATACT GCGCTGCATG ATAGTACGCA GGGTCACGCG CTGCACGCAT ATAATAATCA	2460
CGCGCTCGT CATAACGATG CAGCTGCACA TACGCATGGG CAAGATCAAA ATACTCTGGC	2520
GCAAGAGACG ACTCAGGCTT TCCGCATGCA AATAGTCCTG TATAAACAG GTGAAACAAA	2580
AAAAAGCAAA AACACTGCTT ACCGTTTCATC AGTCAGCGAG AACCTAATAC CGTTTCCTCT	2640
ATCTTGCGGA GCTGGGACCG GTACAGGCCA GAAATATTTG AACCATAGTC TGCCAAAAGC	2700
TGGATAATAT TCCGCGGATA GTCTTCAACA TCAACCCCGT TAACTCGATC ACCAGCATCG	2760
CCAAGACCAG GCATAATATA CGCACGCGCG TTGAGTACGG GATCCATCCA CAGCGTATAC	2820
ACCGTGCAAT TCTCTAGGGA ACGCACTACA CGAATCGCAC CTTTCAGTGC AGAAATCATG	2880
TGAAAACAGC TGATAGATTT TGGTTTCACA CCGAGATCTT GCAAATAACG CACTATGGTA	2940
ACCAAACACTAC CACCGGTGGC GTTCATGGGA TCGGCGAAAA CCAGATCCTT ACCATCCAAC	3000
TCTCGTGCAG AAAAGTATGA TTTATCCAGA TCAAACACAT ACTGcATATC GCGCTCATCA	3060
CGGAGaTCAT CTCGCTTGaT TTTAAAAAGC GCAAACGGcG TTACGTACCC ATGcGAAGAA	3120
TATTCTTCTA TCTCCTTAGA AACATCATC GAaGGTAACA GCGCTCCTCG TAACATGACA	3180
CACATCACCG TGTTCCTCAAT TTTATAATCC ACGTTTGCAA TTTTATGTAC TGCATAGTTT	3240
TGTACAGGAA AAGCAACCGG TGTTTTTGTA ATAAGATATG TTTTATGC	3288

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

AGCCGTTGCG TCCGnTGGGA GTGGATTcAG ACTGTGGCGn CAGTGGAGGT GGTGGAGCAC	60
GGGGAGCATC .CGTGGTTTTT CGGCGTGCCA GTTCCACCCG GAATTTTGTT CTCGACCGAA	120
CCGGGCTCAC CCTTTGTTCC GGGCGCTGGT GGGCGGGGCG TTGGAGCGAA AAGACAGTCG	180
TTCTTGACGC GCGCAGGTAT TTTTCTAGA CTCCTCTGTC CTCTCAGCC GGTGAAAGA	240
GCTTTGTGTG GCGGTGCGGG TTTGTGTTGC GCGCGCTCCG ATGCGGTTGC AGGTTTGAGG	300
GAGTGGATAT CCGTTTTGTG GGGAGGGATG CGGCATGCAG GGAGTTATGC GATGGCAGTG	360
AAGCGGGCAC GGGGAAAGAT TGTACGTCGG CTGGGGATTA ACATTTTTGG GAATCCAAAG	420
TACACGCGGC TTTTGGGCAA GAAGCCCGCG CCTCCAGGCA AGGAGCATGG GGTGAAGCAG	480
CGGGCAAAGG TGTCTGTGTA CGGGGAGCAG CTAAAGGAAA AGCAGAAGTT TCGCTTTGcg	540
TATGGAATGT CCGAGCGACA ATTCCGTAAT CTTTTTGCTC AGGCACATCG GATGAAGGGC	600
GTGACGGGTA ACAATATGcT GTCGCTAATG GAGCGGCGGC TGGATAACAC GGTGTTcAGG	660
ATGGGCTTTG CGATCAGTCG TGTGCAGGCG CGGCAGATGG TGTCACATCG TTACTTCCTT	720
ATCAATGGGA AGACGGCCAA TATCCCTTcC ATGCGCATTA GCGCGCATGA TGTCATCACT	780
ACTAAGAACC GGAAAGGTAT TCATAGCATC ATTGCTCACA ACCTGACCCT TTCTCAGGGG	840
CAGCGCGGTT CCTGGCTAAA CGTGGATGAG GAGCAGCTTT CGGCAACTGT CTCTGAGCTG	900
CCGCGTGCGC AGGATATCCA TCCGGTGCGG AATATCCAAC ATATCGTGGA GTACTACTCG	960
CGGTAGGATC CTTTGCCACT TTAGCTGGCG TTGCTCAATT ATCTCCCAAG TCTTACCAGG	1020
GACTTTGGGG CGTGGAAGGA TGGCGGCGGT GTATGGATGA TGGTCCCTTG AGGGTTGTTG	1080
TGCTTACCTC ATTTGTcATA CTCGTAGTAG TCTGTGCCGT TCGCTGTGT ACTTTTTTTG	1140
TGTTCTCAA AAGCCCTGAT CAGGTGATGA CTCCCCATAT CGTGGGCAAG GACTTTGTGT	1200
CTGCTGCTAT AGAGATGCAG GCAAAGGAGC TGTATCCCCG CGTTCAGTTG CGGTTTTCTA	1260
CCCGTGAGAA GCCTGGTGTT GTTCTTGAAC AGAACCcACC TCGGGGGGCC ATCGTCAAGG	1320
CTGGGCGCTA CGTGGACCTC GTAGTGAGCC AACAAGCAGT GACTACGCAC GTTGAGGACT	1380
ATCGGGGATT GCAGGTTGAA GAAGCGGTGG CGCGCATCGC TGCTGCTGAA GTTGAGCGCC	1440
GCATCTCAGT GAAAACACCC CACTTATATC GGTTCAGCAC TGGCGCAgCT GGcACCATTT	1500
TGGAGCAGGA CCCTGCTCCT GGGCGGTTTc TGTCTGCGGA TGTAGAGTTG CGTTTTGTCG	1560
TCAGTAAGGG GTCTGAGCGC GAGCAGACTA CAGTCCCCCT ATTGGTAGGA TATAGTTTGC	1620
CTGAGCTGTA CCGTGTTATG GCGCAGACGG CGCTCACCTT GCAGTTTACC GTATCTCCCC	1680

637

CGTCTCCTTC TGGGGAGAGA AAAGACGGAG AAGCACGTGG AAGAACGCGT GCCAATGCGC	1740
AGGACTACGC GCGGGTTTCA GCACAGGATC ATGACCCTGG TTCGCGCGTT GAAGCCTTTC	1800
GCGCCATGCA GGTGCAGGTG CTC'TTCCAG AGCGTGGAGA GGCTCACGAA ATATACGGTA	1860
TCTTAGCTCT CGATCTGCCG CGTTATCCGT ATCCTATGTC CTGTGTGTG GATGTACAGT	1920
ATCCAGGGGG GGTGCGTACC GCGCTTGCAA TGTTTCAGCA TCCGGGGGGA CGTTTCACCA	1980
TCCCTATGG ATTGCCTGCA GGGGCGACGC TCTTCCTAAC GGTGGGGGGG AAGGAATTGT	2040
TTTCTGGAGA GGTGGGTGCA TTGCCTCATG CAGGTTCCCTA GCAGACGTGA TGGAGCACTG	2100
CGGGTGAAA GGTGCGATGG CTGCGTGGTC TGGCGCAGcG TGTGTTGTGC ACTGCTGGTG	2160
GCGCTTTTGT GTCTTGCCGT CGGCTGCGAT TCCCTTGATT TGCTCGTAGA TAGCGATCTG	2220
TCTCTTTCGC GCGTGCGcGT GGCAAAAACG CTGGTTATGG GAGTGAGCGA TCGTACGCCG	2280
CCGATGTGTT TTCGCTATCC GAATGGGGAG AtTGT'TGGTT TTGATGTTGA TCTTGCGCGC	2340
GCGGTCTGTC GTGTATTGGG GGTACGCCCTT ATCATTCGTC CCATAAAGTG GACGCTGAAA	2400
AGGAATgcGC TGCCTGTGG TCTTGTGAT TCGCTTTGga CGGCGTTTGC CGTAaCGcTC	2460
GGCGCCGCAC TGAGTTTMTA CTTTCCGAGC CATATCTGCG TACTGCGCAG GTACTCCTTG	2520
TGCGTGAgGG CAGGTTGCAT CCGATT'TGG CACACGTGGA ACGGGAATTG GGGCAGCGTA	2580
TGACAGGTGT TTCGGCTGTG CATACGCGCG GTGATATTTT GCCTATGCGC TCGTCGCATA	2640
GACAGGCTCG CATCGCCGTG TTGCGCGGTG GTcCGGTACC GGGAAATGAG AAGTGGCAGT	2700
TTGGATT'TGA ACCACACGGG AAGGTTGTGT GGTACCGACA CCGGAGTGCC ATGCTTGrAG	2760
GChTGCAC CCGGGCGGTG GACGCGGCAC TTGTGGATCT GGTGAGGCT CATGACGCAG	2820
TGCATCGTCA GGGTGCGCCT CTGAGGGTGA TGCGGGTACC GCTTGGGTG AGCCAGTATG	2880
CGGTTCATT TCGGCGTGAG GATCGTGCGT TGCGTGACGA AATTCAGCGA ATCTTGTATC	2940
GTATTGCTGC CTCCGGTGAG GCATACCGTA TTGCAGAAAA ATGGTTTGGT GTTGSTCAGT	3000
CGGTATTGG GATAGAATAA AGGTGCAAGG CAGCGGTGCG TTTT'TGCAC TGCGCTTTTT	3060
TTGCGTGTGT GCAGGGGTGG GGGGATGCT CTGGTCGTGT ACTCCTCGTG CAAGGGTGTT	3120
TCACGCGCAG GATGCGTCGT TCGATGAGGC GCGCGTGCGG GGTACACTTG TGGTGGGCGT	3180
CGGTCGGGGC TTGGCACCTT TGGTGGATGC TGCCACTTTC TCTGCCTTCT CTCTTCCTTC	3240
TTGGTTGTT CCTCCTCCTG CGCGGTGTTT GTTGCTTTTG CAGGAGGCGC GCGGCTACGA	3300
TGTTGAGCTG TTAGCTCAAG TGGCACGTCG TCTCCATATG GACGTGCAGG TGAAAGTCGT	3360
TCATTGGGAT GAAAAGGAGC GCGCCCTCCA TGCGGGGGTA ATTGACTGTA TCGCAGACGG	3420

638

ATTACCTAT ACTGCAGATC ACGCGCGCAG ATTTGCACTG ACGCAGCCGT ACGTACGCGA	3480
TGTGCGCGTC TTTGCGGTGT TGCGCCAAGC CCCGTACGCA ACGGTTCAG ACCTGCATGG	3540
AAAGCGGCTC GGGGTCCACG CATgACCGAT GTGGAAGAAA ATGATGCATA CCACGCGTTG	3600
TTTGGGCAGG TGAAAACGTA TGCCCCACTAT GTTCAGGCAC TCACTGCTTT GTCGCGAGCG	3660
GAAGTAGATG TGGTGGCGCT GAATTTGGTG ACGCTCTGCG CAGTGACGCC GCACCTGCGG	3720
gCTTGATATCG AATTTTGGAT GAACCGATAG ACACGTGTGA ATACGTGTTT GCGTTTCGTG	3780
CGGATGCGCG TGCTTTGCGC GACATGGTTG TGCGCACTCT GTCGCAGCTG CAGCGAGAGG	3840
GTTTGTGTC AGCGCTCTCA AAGCGGTGGT TTGGCAGCGA TATGTCCATC ATCGACCGCT	3900
AAGGCGGGTG GAGGGGGAAT ATCGGTGGAT CCGTTGAATG CCGTTATTGT GGAGGGAAAT	3960
GTCGTTCCAT CTGCTTCCGC GCGCGTGCCG GAGGgGCCGT GTGTGCGTTT TGCATTCAAA	4020
CGCAACGGCG CGTGCAAGGG GAGGGGAGGG TGCACACAGA GGTTCGTAT TTTGAAGTTG	4080
AGGCATGGGA TGCATTGCG CGCGTGTGTG CGCAACAGGT GCGGCCAGGA GTGGGGTTGC	4140
GGGTGGTCCG CCGTCTCAAG CArGATCGTT GGCAGCAGGA GGACGGGGTG CGAGTGCAGC	4200
GGGTAAAGAT TGTCGCTGAG CATGTAGAGT TTCAGACT	4238

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

TTCCGTTTCG GGATTGAAGA TTTCAATAGG TTTTCCTGAA TC GTTACCGG ACCACAGTGC	60
CTTTTCCTTG CGTTGTGTAT TGTGTGCGAT AACGCCATTT GCGGCAGCCA AAATAGTTCC	120
GGTGAACGG TAATTTTGCT CTAAGGTAAT TTCTGTGGCG TAGGGGAAGT CTTTTTCAAA	180
AGAGAGAATA TTGTCGTGGT GTGCTCCACG CCAAGAATAA ATTGATTGAT CATCGTCCCC	240
TACTACACAG ATATTTTGTG TAGCGAGCAT TTTCATTAAA CGGTACTGCT GTGCACTGGT	300
GTCTtGGAAT TCATCCACTA AAATGTAATG ATAGCGACTC TTATATGAAG CAAGGATATC	360
AGGATATTCA CTGAAGATCT GGATtGGCAG TACGATCAAA TCGTCAAAGT CTACCGCATT	420
AAATAATTTT AACGCAGtAT GATATTCGTG CCAAAGAGCA CGTTCCTTGT GCTGTAGCTC	480
TTTTAAGTTC TTACGCTGCA TTTTAATAGC GGAAAAGAGC GTgTCACGC AGTTTGTGTC	540

639

AAGAACTTCT GGCAGGAGAT GTACTTCCTT TGcTGcTTCG CGAATGAGAG CACGTTTATC 600
ATTTTCATCA TAAATGCTAA AGTTCTTCCT CCAGCCGAGA ACATGGATAT GTTCTCGCAA 660
AATCGTAACG CAAAAGCGT GAAAAGTACT GACGGTCGTG TTGCGTAAAG GTTTGCCCCGT 720
GAGAGCTTTA ATACGTTTCA ACATCTCGTG TCGCGCCTTG TTAGTGAAGG TCAGTGCAAG 780
AATGCGCGAT TGCAGAATAC CGCATTTCGAG CATATACGCG ATGCGCGCCG TGATTACGCG 840
CGTTTTCCCT GAGCCTGCGC CGGCGATAAT GAGAAGCGGT CCCTCaAGTG TGGTAACGGc 900
TCGACGTTGC TCAGGATTAA GTGTAGAGAG CATAGACGCA CAAGCGTAGm AnAATAGGGC 960
GGAAAAAAGA ATATCCGTAT GTGGAAGGGc ATAGACTGTG GGTAATACTT CAGATTGGGT 1020
AGAGATGGAT GGATTGCGCT ATGTGTATGC CGCGCAnGGT GCGGCCCCCA TGCCTGCTCC 1080
TACGGATAAT CCTGCTTGTG ATGCGCACAT GTCGCATGAC GTCATAGCGC GTACTGCCCA 1140
AGCAGTTTTT GGTATTCTGTG CGCTGTTTTCC TTGGCAGCGC TTGTAATTG CTAACATACT 1200
GGATGCGGCG CATGCGTGTA CACATACAAC TCCGTTCGCT GCGGCAGGTT CTTCTCAAAC 1260
CGATGCTACG AGGGTGACTC ATGTGGATGA CGCGCACCTG AGGATAATTT CGTCGGTGCC 1320
ATGCAAGACA CACGTTTTGA TCAGGATGGC GTGTCACGCG CACATCAAGT GGTGCTATTG 1380
CCGACAGgTG CAGGAAAATC GCTGTGTTTT CAAGTACCTG CCCTCTTTTT AGAGGGGCCG 1440
ACGCTAgTGG TGTACCCACT GTTATCGCTC ATGCGTGATC AGTGCCGTCG GATGCAGGCA 1500
GTGGGATTTT CGGTCATCTT GTTACGTGGT GGACTGAATG CGCAAGAGCG CGCGTACATG 1560
TATGCGCATt GGATAgTGTG CTGAgGCGTA TGGCCGGATG CGAGgCGTTA cGCcTCctGc 1620
ACACCAGACG GCAGAATTTT CCCTTGCGTA TTCGATCTCT TTTGATGCGT CACTCTTCTC 1680
TGATGACGTG AGTACCTTCT CGAAGGTGGT ACATGTGGAT GAACGTCTTG CTCAGAAAAG 1740
GACAGAAAGT CGAAGAGGTG TATGCATCAT CGCAAGTCCA GAGATACTCA CACAAcCgck 1800
CTGCGCCACG CGTGCGTGCA TGTCGCGTTG CGCATTGGT TATTGATGAA GCGCACTGTG 1860
TGTCCGAGTG GGGAGATTCG TTTCGTCTG ATTACGTGCG ACTAGGCGAA TTGGTGCAAG 1920
ATCTTGCGCC TCAAGTGGTG ACTGCATTTA CGGCGACTGC AAGTCAAACA GTGCTTGCGC 1980
GCATCATGGA AGTGCTGTTT GCGGTCGTG CGCACGTGTT GCAGGGAACA GTAGATCGCC 2040
CGAACATTCG ATACACCGTA CGCACGGTGC TGTGTAAGCA GACGGCACTG ACTCAACTTG 2100
TAGCGCGTTG TGTGCGCCCT GCAGTTATTT TTTGTGCTCG TCGGTACAG GTGGAGCGTG 2160
TAGCCCACCA TTTGCGCACG TGTCTTTCTG ACACACAGAT ACGTTTTTAT CACGCAGGtT 2220
GCAGAGGGAA GAAAAGAAA CAGTGGAGCG ATGGTTTCAT ACCCATGATT CTGCCGTTTT 2280

GGTAACTACT TGC CGCGTGGG GAATGGGAGT TGATAAGCCG AATGTACGTA CGGTCATTCA	2340
CGTGGATGCG CCACTGACTG TGGAGGCGTA CGTACAGGAG GTTGAAGAG CAGGACGGGA	2400
CGGAATGCGT GCAGACGCAT TTTTATTGTG GTCACCTCGA GATGCTCGCT CGATAGAAAC	2460
ACTGCCGCAT GCACAACGGG TGC GTGCGCA CGTGTGCGC CACTTTGCTG AAAGCGGACG	2520
TTGTGCGCCG GCAGTTTAC TTGAGTCTTT GGGGGAACAG AATGTGTGTG CCGGATGTGA	2580
TGTGTGTGCA GGC ACTGCAC GTTTTGTATG TGAGGATGTA GAAGCGCTCT TACAGTTTTT	2640
GAAAAAGAAT GCGCGCAGAT TCACTGTATC ATCGTTGGTG CAGCACCTCG CGCTACATCA	2700
GAAAGTGCTC AGTGTGGCGG ATGTACGTGC CTTGCTATAT TACGCGCTCG AAACAGGACG	2760
TGTGAAAAAA AAACATTAC TCTTGTGGG TGATGTCTCG TATGTGCAC GTTAACGATT	2820
CTGCGAGCAA ATCGTATCTG CAGGAAAGCA AGAAGGATGG CGAGAACATA CAGTTGCCTT	2880
GTATATTCCG CGAGTTACGC GCATTTTAT GGCCGAGTGG TTAGCATTAC TTCTACAGGT	2940
TTTTTATGCA ATTTTATATA CTGAGCCGTC GTTCATGTGT CTCCGATACG GTGTGGTCTA	3000
GGTCCGTAC GTGCGGGCAC GGAACACATC GAGCGGACGC GTCTGTTCTG GGAGGATATT	3060
ATGAAAAGGT TTATTCCCA TCGGGTGATT CACGCGGTGT GTATCGGGCT TGCACTTGTA	3120
GGTGTAGGA AACTCGATTG TCGTGCGGG GATTTTGAGT TAACGATTAT ACATATCAAC	3180
GATCATCATT CGCATTTGGA ACCAGAACCC TTAGAGCTTG CAGTGGCAGG GGAAAGACTC	3240
AGAGCGGCTG TAGGCGGTTA TCGGCGCTT GTGCACGAGA TACAACGGTT GCGTGCAGG	3300
TCGAAGAACG CATTGGTACT GCATGCAGGA GATGCACTCA TAGGTACGCT GTATTCTACC	3360
CTCTTTAGAG GCGGTGCGGA CGCGGTGCTG ATGAACCATG CAGGATTTGA TTTTTTTACC	3420
CTTGGAATC ACGAATTTGA TAATGGGAAT GAGGGACTCA AAGAATTTCT GCACTATTTG	3480
GAAGTGCCAG TTCTCTCTGC AAATGTGGTT CCTAATGCTG CCAGCACGTT GCATGGCTTG	3540
TGGAAGCCGA GCGCTATTGT GGAGCGTGCA GGTGAGCGTA TTGGGGTTAT CGGACTTGAT	3600
ACGGTAAAGA AAACCGTGGA GTCATCCAGT CCCGGTAAGG ATATCAATTT TATTGATGAG	3660
ATAGAGGCGG TCGTCTGTC AACTGTTGAA ATGCAGCaG AAGGAGTAAA TAAAATAATC	3720
CTCCTTTCTC ATGCAGGTTT TGAGAAGAAC TGTGAAATTG CTCAGAACAT TTCTGGTATT	3780
GACGTCATCG TGT CAGGTGA TACCCACTAC CTTTTGGGG ATGAATCACT CGGACGGCTA	3840
GGTCTTCCGG TAGTTGGTGA ATATCCAGG AAGATTATGT CCCCTGCAGG GGAGCCTGTG	3900
TATGTGGTAG AGGCGTGGGA GTATGGTAAG TGTCTGGGCG AGCTGAACGT AGTCTTTGAC	3960
CGAACAGGAG TAATAACGAG TGCAGTAGGC ATGCCGCGTT TTTTGTTACA TACGAATACA	4020

641

TTGCAAAAAA	AAGGAGCGGA	TAGAAAAAAT	TATCCTCTTG	AGGAGGCAGA	GCGTGAAGCG	4080
CTGCTTGTGG	CAC'TGAGGAT	GACGCCAGAG	ATTATATTTG	CGCAGGAGAA	TGATCAGATT	4140
ATATCTGTGT	TGGAAGAATT	TAAAAAGGAA	AAGGAGGCGC	TTGGTGCACA	GGCAATTGGC	4200
GTAATTACCG	GTGCCCTCAAT	GCGAGGkGGn	TCTGTGCATC	GAGT'TCCCGA	TGCACAGAmT	4260
CCACAGGGTT	CGGTTGCAAC	GCGGTTTGTA	GCAGAGACGA	TGCTCTCAGA	CATTCAAAGT	4320
TTTGGTGC GG	GGAAGgTAGA	TTGCGTAATT	CAAAATGCAG	GCGGTGCGCG	GTCAAATATT	4380
CAGCCTGGTG	AGATTACGTA	TAATGACGCA	TACACGCTCC	TCCCC'TTAG	TAACACGCTG	4440
GTGTTGGTGG	ACGTCAGCGG	TGCAGAGTTG	AAACAAATTA	TAGAGGATGC	ATTGCAGTTT	4500
GCACTTGGTG	ATGGTTCCAC	GGGAGCCTTC	CCCTATGGGG	CGGGTGTCGG	GTATGAAGCG	4560
CGCCAAGAAC	CAGATGAACA	TGGCAAACGA	GTGATAAAGC	TTGAGGTGCA	AAAAAAAGAT	4620
GGAGCGTGGG	TGCCAGTAGA	TGAGCGCGCG	CCGTATCGGT	TGGGTGTGAA	CTCGTACATT	4680
GCGCGGGGAA	AAGACGGATA	TAAAACGCTC	GGAGAGATTG	TCAGTACGCG	CGGAcTGAGG	4740
ATACGTATCT	GCGTGATGCG	GAGTCTTTGA	TTAAGT'TTTT	GCGTGCGCAT	AAAAATTTTC	4800
GTGCATACAC	AGATTCCAAT	GTGATATTCC	GTCTTAAATA	GTAGGAAGTA	ACTTACATTA	4860
GAGGcCTGTA	AAGAACTACG	TTCTTTACAG	GCTGTGCCAA	TCTGCT'TTTC	CGGGAAAGAC	4920
AAAGGGTATG	CCACGTTAGG	AGCGGAAAGA	AGGGTGCTGC	ACATAACCTT	ATCTTTGCGA	4980
TTGACCGTGG	TATACTCCTT	GCACCTTATG	CAAGAGAAAA	AAACGCTTTA	CCTTCTTGAT	5040
GCCTACGGAC	TTATTTATCG	GAGTTACCac	GCGTTCGCGC	GTGCGCCGTT	GATTAACGAC	5100
AGCGGTGCGA	ATGTTTCTGC	CGTATATGGT	TTTTTTTCGA	GTTTGACACAC	GCTCCTGTGT	5160
CACTATCGAC	CCCGTTATTT	TGTTGCTGTT	TTTGATTCTC	TCACGCCTAC	CTTTCGGCAC	5220
GTACAGTACC	CAGCCTATAA	GGCAAAAAGG	GATAAGACTT	CTGCAGAGCT	TTATGCGCAA	5280
ATTCCCTTTA	TCGAAGAAAT	CCTGTGTGCA	CTGGGCATTA	CAGTTT'TGCG	TCATGACGGC	5340
TTTGAAGCTG	ACGACCTCAT	TGCAACCCTA	GCAAAACGAG	TTGCGGCTGA	GCACTGTCAT	5400
GTTGTGATTA	TCTCCTCAGA	TAAAGATGTA	CTTCAGCTTG	TGTGTGATAC	GGTGCAAGTG	5460
CTCAGACTTG	ACATAGATCA	TAAGTGGACA	TGTTGCGACG	CTGCGTACGT	ACAGCAACGG	5520
TGGACGGTCA	TGCCAACACA	ATTACTTGAT	TTGTTCTCTC	TCATGGGAGA	TTCCTCCGAC	5580
AATGTGCCTG	GTGTGAGAGG	GATTGGTCCT	AAGACGGCTG	CACATCTTCT	CCACTGTTTT	5640
GGCACACTTG	ATGGTATTTA	TCGTCATACC	TATTCCTTAA	AAGAAaGCGc	TGCGCACGAA	5700
GATAGTGTGT	GGGAAGAAAG	ATGCATTTTT	TTCTCGTTCA	CTCATTGAGT	TGCGTGACGA	5760

TGTACCATGT	GTTTTTTCGC	TCGAAGATTC	CTGTTGTATT	CCGCTCGATG	TAACGTCTGC	5820
TGCACGTATT	TTTGTGCGAG	AAGGATTGCA	TGCGCTTGCA	CAACAATATC	GTGCTTGTGT	5880
GCAAGAAATA	GATACAGAAG	CAACAAACGA	TACATTACAA	ATGACAGAGT	CTTCTGTGCT	5940
CACGTCTGGT	CGATGTGCAA	ATGAGTGTTT	CTTATCTCAG	GTAAGAGGA	GGGCTAGTAC	6000
ACCGGAGGTG	AaCTCCGTAT	TGAAGTCGGA	GTTGAAGACG	AGTGCTGTGT	CTGGCGCCAT	6060
ACCTATAGAA	AaTAGAGATC	TTAGGCAGGA	TGTTATGCTT	gCACGCAGTG	CaGGTCATTA	6120
TCGTGGTGT	ACTGACCCTG	TAGAACTTAA	ACGTATTATT	GATTGCGCGT	GTGCGAATGG	6180
TGTGGTTCGG	TTTGATTGTG	AAACGGATGG	ATTGCATCCG	CACGATACAC	GTCTGGTCGG	6240
ATTTTCGATC	TGCTTTTCAGG	AAGCAGAGGC	TTTTTATGTT	CCTCTTATTG	TTCCGGACGT	6300
TTCTCTTCAT	ACCGAGTCAA	CTCAGTGATC	ATGTGCACGT	AGCACTAATG	TCGAGACTGA	6360
AAAGGAGTGC	ACAGAACAGC	ATGGGGTATC	TGCATCTGCT	GTGCAGGATC	CGGCATATGT	6420
CCAAGCTGTC	ATGCACCAGC	TTGACGTCT	TTGGAATGAT	GAGACGCTCA	CACTTGTTAT	6480
GCATAATGGA	AAGTTTGATT	ATCACGTTAT	GCATCGTGCA	GGCGTTTTTG	AGCACTGTGC	6540
ATGTAATATT	TTGATACGA	TGGTTGCAGC	TTGGTTGCTG	GATCCCGATC	GCGGTACATA	6600
CGGTATGGAT	GTACTTGCCG	CATCATTCTT	TCAGATCAGA	ACGATTACAT	TTGAAGAAGT	6660
GGTAGCAAAA	GGGCAAACCT	TTGCGCACGT	CCCTTATGAG	TGTGcAGTCC	GCTATGCAGC	6720
GGAGGATGCA	GATATTACTT	TTGCTTTATA	CCATTATTTA	AAACTCCGCT	TGGAACAGC	6780
AGGATTGCTT	TCTGTGTTTG	AGACCATAGA	AATGCCGCTT	TTGCCTATCC	TAGCACGTAT	6840
GGAAGAAGTG	GGGATTTTTT	TACGTAAGGA	TGTTGTGCAG	CAGCTCACTC	GATCTTTTTC	6900
AGATTTGATC	CAGCAGTACG	AGCACGATAT	TTTTTCTCTT	GCCGGTCATG	AATTTAATAT	6960
TGGTTCTCCG	AAGCAACTGC	AGACAGTCCT	TTTTCAAGAA	TTACATTTAC	CGCCCGGTAA	7020
AAAGAATACT	CAAGGTTATT	CTACTGATCA	TTCTGTATTG	AAGAACTTG	CACGTAAGCA	7080
TCCCATTGCA	GAAAAAATAT	TGCTCTTTAG	AGATCTTTCA	AAGTTACGTT	CGACGTATAC	7140
CGAATCGCTT	GCAAAACTTG	CTGATCAAAC	AGGGCGTGTA	CATACTAGCT	TTGTGCAAAT	7200
TGGTACCGCA	ACTGGAAGGC	TTTCGAGTAG	AAATCCAAAT	TTACAAAACA	TTCCCATTA	7260
AAGCACAGAA	GGAAGAAAAA	TAAGGCAGGC	GTTTCAAGCT	ACTGTTGGGC	ATGAGTTAAT	7320
TTCCGCAGAC	TATACACAAA	TAGAGCTGGT	CGTGTGGCC	CATCTATCTC	AAGATAGAAA	7380
TCTTCTCAAT	GCATTTTCGAC	AGCACATTGA	TATTCATGCA	TTGACTGCTG	CATATATTTT	7440
CAATGTGTCT	ATAGACGATG	TACAACCTGC	AaTGAGAAGA	ATCGCAAAAA	CTATTAACCT	7500

TGGAATCGTG	TATGGAATGA	GCGCTTTTAG	ATTGAGTGAC	GAACCTAAAA	TTTCTCAGAA	7560
GGAAGCGCAG	AGCTTCATTT	ACCGTTATTT	TGAAACGTAC	CCGGGGGTGT	ATGCTTTTAG	7620
TACACAGGTT	GCAGAGCAGA	CACGTAAAAC	CGGCTATGTG	ACTAGCTTGG	CTGGAAGACG	7680
ACGCTACATC	CGTACTATCG	ATAGTCGCAA	TACGCTTGAG	CGCGCGCGTG	CCGAACGTAT	7740
GGCGTTGAAT	ACTCAAATTC	AGAGTTCTGC	GGCGGATATT	GTGAAAATTG	CCATGATAGC	7800
AATCCAGCGT	GCGTTTGCGC	GCCGACCGTT	ACGTGCACAA	TTGTTGCTGC	AGGTACACGA	7860
TGAATTGATT	TTTGAGGCGC	CAGCTGCTGA	GACAGCGATA	GTGAAAGAAA	TTCTCTTTGC	7920
TGAGATGGAA	CATGCTGTTG	AGCTCTCGAT	CCCCTGCGT	ATACACGTGG	AGTCTGAAA	7980
TAGTTGGGGT	GATTTTCATT	AGCATACCCA	TCTGAGGGAT	GCAACAGGGC	ACGTTATGAG	8040
GTTACCTCGG	CGCGTAGTTC	CTTAAAAAAT	GATGCTACCA	CGCACAAACAT	AATCAGCGCT	8100
AAAGGAAATG	CCGCAATGAT	GGCTAAACTT	TTCAGGTGCA	TGAGTGTGGA	CTGGGAGAAT	8160
ATGAGAGAAG	CGGGAAGGAG	AATGCACGCA	ACCGCCCAA	ACGATTTTCAT	TATTTGACGT	8220
GGTTCTTCTC	CCGGTGCAAC	GCTTTTTTGC	GAATAGGAAG	CGATGATGAG	CGTTAATGCG	8280
TCAAAAGTAC	TTGCATAAAA	GGCGATCATG	GTAGCTGCCA	ACAGCGCCAT	AACGATGTAC	8340
GCGCAGGcAG	TGTCTGAATA	ATTGCGATAA	TCACCTCAGC	GGGTGTATTTC	CCCGCGCGCA	8400
naAGGTACGC	GGCAGGAAGG	AGGTGGTGCG	TTTGTAATA	GAGCCCGTAG	TTCCCTAAGA	8460
CGATGAAGGA	GCCGTACGTA	CCTGCGATAC	CCCAGCAGAG	CCCTCCGACG	ATGGTATTCC	8520
GGATGGTTCT	CCCTTCGGAT	ATCGCGCCGA	TGAAGAATGG	GGTTGCAACA	GACCACGTGA	8580
TCCAATACGC	CCAGTAAAAG	ATAGTCCACC	GCTGTGGAAA	TCCAAGCGTC	CCATCCGTTT	8640
CCTGTAATGA	AATACGAGAA	GGATCCATCC	ACGTTGCCAT	AAGAAAGAAG	TTTTGTAGCA	8700
TTTTCCTTAT	CGCGGTGATA	CCCGTCTCGA	TAAGATACAC	GGTTGGTCCT	GCACACAAGA	8760
AGAAAACAAG	AACGGTACTA	AAGCAGTACA	CCGCGGCACG	cgAGAGCTTT	GAGATCCCCT	8820
GGGTACCCAG	CAGTACTGCT	GTGGTGTA	CCAACGCAAT	AACGCAGAGC	AACGCTAAAG	8880
CGAGCAGCTG	GGTGTTAGAA	ATACCGAACA	AGAGAGAAAC	CATGAGCGAA	AGGAGGGGCG	8940
TTGCTAAGGA	AAACGTGGTT	GCAACGCCTA	GAAGCAATCC	CACTACAGAA	CAGATATCGA	9000
TTGCTTCTCC	TATTATTCCG	TCTACGTACG	CGCCAGCAG	CGGACGACAG	GCTTCAGAAA	9060
TTTGTGTGT	GTGTCGCTTC	TTTACATGCA	ACATGTAGCC	GAAGcaCTGC	GAGAAGAACG	9120
TAAAAAGACC	AAGGTATGAT	GCCCCAATGG	AAAAGGGGAT	ACGCTGCCGC	CCATTCTTGT	9180
CTTCCGTGG	GAGGGGAGTG	TTCTGCTATA	AACGGAGCTT	GAGTGAAGTA	GTGCGCCCAT	9240

TCGATGAGCG	ACCAATACAA	AATATCCGCC	GCCATGGTGG	ACGTAAAAAT	CATGGAGCCC	9300
CACGTAAAGT	TGGAATAGCG	TGCGGTGCGC	GTAGTACCCA	GATACACCGC	ACCATACCGT	9360
GAAAAAGCAA	TAGTCAGCGT	CGTTCCTAAA	AAAAACAGTC	CGGTAAGGAT	ATAGAAAAAG	9420
CCCAGTTTGT	TTACCAGTAT	ATTCAAGAGG	GTACCGATTA	CCCGATGAGA	AATGTCAGGA	9480
AAGGAAATAA	ATAGGAGTGC	GCACGAGATC	ACGATTCCCA	ATGGGATGAG	AGAGACGCTG	9540
AAGTCACATT	TTTCTTTCTG	CATGATCTGC	CCTATGTGTT	TTCAGGAGCG	TCTGAACTGC	9600
TTCGTAATAT	TCTTTTGCAT	ATCGGTACAT	TTTCAGTCCA	TAATCTCCAA	ACGAGATACC	9660
AAGCGCTGT	TTGTAGCTCG	TCCACAAAGA	CCACAAAAAT	CCCCAAGAG	CAATATAGCA	9720
AAAGACGCGC	AGGCGCTCTT	CTCCGTGCGG	ATTACGCTGA	AAATAACGAT	ACATGAGATC	9780
TTCTATCTGG	GCGGTGTAA	AGTGGGCATA	CAAAGAGAAC	ATCGCGATAT	CCACAAGCGG	9840
ATCACACATG	CCCGCATATT	CCCAATCGAT	GAGCTGGGCA	CTGCCATCGC	AAAGCAGGAA	9900
GTTATCTGGG	GTTAGATCGA	CATGCGTAAG	TACGCACGGT	TTGTCCACTG	AATCGACAAT	9960
AGCCAAGAGT	GTATTCATTT	TTTCTCTCAC	TGAACGATAG	TCAGCGTAAA	GAATACTGTA	10020
CTGGTCGAGG	GCAAGCTTTT	CGTAATACGC	AATACGCGAT	CTGAAGTCGA	ACCTATGGGC	10080
AACACAAATA	CCTGATTGAT	GGAGTTTGCG	CGCAATCCTC	ATGCACAAGT	CAAGGTCTGC	10140
CGGATCACTA	GGGTTTGCAC	TGCGGCAGTC	TTTGTGGAAG	ACGGTGATTT	TAATACCACG	10200
GGCAGGCTCA	AGGTGAACGA	GAGTGTCAAC	AATATTAAGG	GGCTTAATTG	CTTCATACAC	10260
GGCAGCTTCT	TGGAAGCGAT	TGACAAGGAG	TTCGGTACCC	TCTCCAGGAA	TTCTGAATAG	10320
GTACGGCTTA	TCATTCAGCT	CAAAGATAAA	AGATTTGTTC	GTCAATTCCTG	CTTTAAGTGG	10380
ACGCAGCTTA	CCGATTGTCA	TTTCGGGTTG	GTTGAAAACA	TGGGAAATGA	CGCGCATCCA	10440
CTCGTTATCG	CTCGAAACCA	TGTACGCAAA	ATCAAACCTG	CGCAGCTCAT	CGAGCGACTC	10500
AAATTCGTAG	ATAAGGTTGT	CAGCCTGTTT	GTTGGCAAAC	ATGGTAAGGG	ATTTTGTATT	10560
GCGCATAAAG	ACGTCTTCCC	AGAACCACGC	GCGGTTTTCT	GGGCGCATGT	AGGCAGCTTC	10620
GATGAGGGGG	ATGATCTTTT	TAGAAAACGA	TGCAGAAAAG	TAAGCTGGAC	CGTACATGAT	10680
CCACCCACTT	CTGCCACCAA	TTTTACGGC	GGTAATTTTG	TCGTACAATC	CGGTTTTTAA	10740
CACCCATTCC	TTTGTTTTCC	CTTGTGTCTT	GACAGCCGTA	TACCAGGAAT	CCCACTCATG	10800
GGAGTGATAA	ATGTTTTCGC	GTAGCCAGTT	ATCGCTTGAG	AGTATGTAGG	TATTTCGAAG	10860
TAAATGACGG	GCGTGGTAGA	GGGTGGATAG	GTTGTTGGCA	GTTTCATAGT	CAGGGTTATA	10920
GGTGAGCGTC	ACGTCATGCT	TGTCGACGAG	GTACTCAAAG	GCCTCTTTGA	GGTAGCCgAC	10980

645

GACGACCGTG ATGTCAGTAA TGCCGACTTC GTGTAAGTGA CGAATTTGAC GCTCAATCAT 11040
GGGCTCACCA AAGACTTTCA GCAGGCCCTT TGGAGTAGCG TATGTAAGAG GCACGCAACG 11100
GGAGCCAAAG CCTGCAGCCA TTATTACCGC ATTATGAACC CGGCAAGACT GATACTGACT 11160
ATGTGCAAGG GGGGTGAGAG AaCGCGTCCG CGCACCAAAG GTCCCGTGGG TTTCAAGGAG 11220
TCCTGCAGAC TCCATAGCGT GTAGAAGGCG ATTGGTGTAA GCCAAGGACA GGCGCAACGC 11280
CTTGCGGATG TCACGCTGGC AAAGCCGAgG CGCATCGCGC AAAAGCTGAA AAATCTGGAA 11340
AAAACGACGC CCCACACTGA GGAAGTGTAC GGGCGTGTTC GCCC GCCGTC AAGCACGCAA 11400
AAAACAGGGG AAAAAGCACC CCCCCCCTG CTCGCTTCCT GCACACAGCT GTGAGGAGCG 11460
CATCCTTCGC TCTCCTAGAT AATATTTTTC ATCACAATCG GCTGTCCTGT TGCATCAAGG 11520
GCGTCGCGCC ACAACGATCC TTCAGGATTT ACGTGTTCG GTTGGCACAC CACCACATCG 11580
ATTGGGAGGT GTACAAACTT ATTGTGCACC AAGCCAATGA TCATTTTCGT TTTACCGCAC 11640
ATCGCCGCAT GCACCGCATT GTTACCGAGG CGTTCGCAGT AAATCGAATC TATGGGCGCA 11700
gcAACCGCGG aACGAATCAA GTAGCTCGGA TCGATGTACT TTAAATTGAT GTGTATACGC 11760
TTTTCTTTGA AATAGACTCC AATCTTTTCT TTTAAGAACA AACC GATATC CGCAAGGCGC 11820
TTGTTACCCG ACGCATCCGT GCCGCTGcTC ACGCGCAAAC TACCTCCTTG GGAATCACCG 11880
GAGGGCACAC CGTCCGCATT TACCATTAGG TCTTGCCCCG CACCTTCTGC TACAACGAGC 11940
ACCGCATGCT TACGTAGCGC GATTGCGTTC TCTAGGTGAG CCAAAGGCC ATTGGACCG 12000
TCAAGGTCAA AGCTCACTTC AGGGATGAGT ACGAAgTTTG TCTCATGGCT CGCAATCGCC 12060
GTGTACGTAG CGATGAATCC AGACTCACGC CCCATGAGTT TGACCAGTCC AATGCCGTTA 12120
ATCTGTGAAC GAGCCTCCAT GTGCGCTGCG GCAACTGCCT CTGTTGCTTT GACAATAGCA 12180
GTATCGAAGC CAAATGACTT TTGAACAAAA GAGATGTCGT TGTCACCGT TTTGGGAATG 12240
CCGATGATGG AAATCtTAAG GTTGCGGtGT TTTATTTTCGT CGGCAATCTC TTTTGCTCCC 12300
TTCTGACTCC CATCCCCCCC AATGaTAAAG AGAATGTGCA gGTTGAGCCG CTCGATACCA 12360
TCGAAGATGT CAAnCAnAAG GTTCCCCCA ACGCGnGAnG TGCCTAAGCA G 12411

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 971 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

ACCACCGCAA CAATCGGGAT ACCAACTCGC CTCGCTTCAC GGATAGCGAT AGTCTCCTTA	60
CGCGTATCAA TGATAAACAC TACACCCGGC AGCTCCTTCA TTTCCTTTAT GCCGCCAAA	120
TTCTTTTCTA GTTCGCGTGC TCCTTGCGTA AAGACGCCAC CTCCTTCTTA GAGAGATGCT	180
CGAAmGTACC GTCTATCTCC ATGCGTTCTA TCTTCTTGAG ACGCGAAAGA CTCTTCCTTA	240
TGGTGGA AAA GTTAGTGAGC ATGCCGCCGA GCCAACGGTT AGTCACATAA AACATCCCAC	300
nAGCgcTGCG CTTCCTTGGC AATGGTTTGC TGGGACTGCT TCTTTGTGCC CACAAACAAA	360
ACGGACTTGC CTGAGGAAAC AGTCCTGCGC ACCATGTCGT ACGCCTCGCG GATGGCCGTA	420
ATCGTCTTTT GCAGATCAAT GATGTGAATG CCGTtACGCT CCGCGAAAAT ATACTTTTTC	480
ATCCGCGGAT CCCACCGCCT GACCTGATGG CCAAAATGAA CCCCAGATTC AAGCAGATTT	540
TTGATAGTCA CCACTGCCAT ACCATTCTCT CACAGAGAGC GCCGAGGCTC TCATCCTTCT	600
CTCTTTCACC ACACGCACAC GCGCCGGGGA TATTCTCGAG AGGACAGAAA AACGCGTCCC	660
CTCACACACG GTCACCTTGA CTAAAATCAG ACGTATGGAA TACGGTTGCC CGCCTCTTCT	720
GTGGACCTTC CCAGGCCCGC AGCAGGTTAC AGAGCAGGGA AGATTAGCTC ATTCGGATAG	780
AGCGTTGGCC TCCGGAGCCA AAGGCGnTGG GTTCAAATCC CGCATCTTCC ATCCTCTTAC	840
CCACGTAAAC GGGCGCCCCG CGmTrACGC TCCTTCCAGT CAAGCTGGCA ACTCAGGGGc	900
CGTCCGCCCG CTCTCCTTCA GCAGGTCACT TGCCGCCAGA AACGACTCCC TTCAnCACTT	960
CGAGCGCGCG A	971

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1985 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

AGTGCCGACG CGCGAGAACG TATTTTTGCC CATCTTGAAA TGCGTGCGC AGGTGCACGG	60
CGCGTCACCT ATCGCCTACG CCACTGGGTG TTCAGCCGTC AGCGCTATTG GGGAGAACCC	120
ATCCCTCTTG TGCACTGTCC TTCtTGCGGT GTTGTA CCTC TCCCTGAGAG TtGCCTGCCG	180
CTTTTGTTAC CCGAAACCGC CGATTTCACT CCCACGGAAG ATGGGCAGGG CCCCTTGCA	240
CGAGCGCGCA CGTggTGCGC GTTCCCTGTC CGCAGTGTGC ATCTGACGCA GTGCGAGAAA	300

647

CAAAACACAAT	GCCCCAGTGG	GCAGGATCCT	GCTGGTATTA	CCTCCGTTAT	ATGGACCCCC	360
GCAATAAGAC	TGCCTTTTGT	GCACCCGAGA	AGGAGCGTTA	CTGGGCgCCA	GTGGCGTTAT	420
ATGTAGGTGG	TGCAGAGCAC	GCCGTACTGC	ATTTACTGTA	TGCACGCTTT	TGGCACAAGG	480
TATTGTACGA	CTTAGGTCTT	GTAAGCACGA	AAGAGCCCTT	TGCGCGGTTG	GTGAACCAAG	540
GCATGATTAC	GTCGTATGCA	TATCGCAGGA	AAAATGGCGC	GCTTGTACCT	CACGACGAGG	600
TGCACACTAA	TGCTCAAGGT	ACCTACGTGC	ATGCTCGTAC	GGGGGAAAAA	CTCGAGTGCG	660
TTGTGGCAAA	AATGTCAAAA	GCGTTAAAGA	ATGTCGTCAA	TCCTGATGAC	ATGATTGCAG	720
CGTACGGTGc	tGACGCGTGC	CGGGTATACG	AGATGTTTCAT	GGGACCTCTT	GAGGCTTCCA	780
AACCGTGGA	TACGCAGGGG	TTAGTGGGGG	TTTTTCGGTT	TTTAGAAAAA	ATTTGGGTAC	840
TTGCGGGGCG	CGTGGCGGCC	GCAAACGGTA	TTCCACAAGA	CTCTCGTGCA	GAGCCGCCAG	900
GTGACCTGCA	CGCACAGAAA	AAGTCTTGCA	GCATGTACGC	CCTCGAAACG	CTGTTACACC	960
GGACTATTCA	AAAAGTgaCg	ACGATACGTC	GGCGCTTAGT	TTTAACACGG	CAATCAGTCA	1020
GATGATGATA	TTTGTAATG	AwGgTACGCG	GGTGGCGCGG	AGGATGCCTC	TTCCCTCTAA	1080
AATGTGGGAG	ATGTTTGTA	AAATCCTCTC	TCCCTATGCA	CCACATTTGG	CAGAAGAACT	1140
CTGGGAAATG	TGTGGGCACA	CGCACACTAT	CGCATATGAG	CCTTGCCAC	AGGTGGACCC	1200
TGCGCGTGTG	GCGCCGCATG	TGTGCTCCGT	AGTGGTGCA	GTGAACGGTA	AAGTGC CGA	1260
CACCTTCTCC	GTAGCGCCGA	ACGCTCCAAA	TGAGGAACTC	GAGCAAAAGG	CGCGGGAAAC	1320
CGCCGGTGCG	CGTAAGTTTC	TTGGTACGCA	GCAGCCAAAG	CGCGTAGTGA	TAGTTCCCAA	1380
TAAATTAGTA	AATTTTCGTT	TGTAGTCCGC	ACTGCTCCTG	CAGCGTTGTG	CAGTACCTGT	1440
GTGGTGCCCT	ACCCGCGTGC	ACTACAATCG	CGTAAAGGCA	CAGCTGCATC	AGCGGCCCTT	1500
GGAGAGGCGT	CCCACCTGAG	CGGATCATTG	CGTCTGTCTG	GAACAATCTA	TCCAAAATAG	1560
CATGCGTATC	GCTCAGGGTC	CAAAGAGACG	CAGCGCGCTG	GTATTGCGCA	ATCATACGCC	1620
GAGAAGTGAA	CCCATAGCGC	TTTAGCGTTG	CAGGGTGCGT	TTTGTCTCTC	GGTATATGGT	1680
GCCAATGCGC	AAGGCGACGG	AACGCGTAAG	naGtCCTGCA	AGGATTTGTA	CAGGGGCAAC	1740
GTCTTTTCGAA	CAAAGCAGCG	TGTTGAGAAT	CATAAGTGAA	TGCTCAAGAT	CTCGTTTGGA	1800
CAGCGCATCG	AATAAGGTAA	ACGATGTCTC	TTCTTTTGTG	TGCACCAGCA	ACGAACTAAT	1860
GTCGTGCGCA	gTGATGCGGc	GTCCTTTTTc	AAAAAAAAGA	GAAAGCTGCG	TACAAAACAGT	1920
TTTGAGCGCA	CGAGTGTTGT	TCTCCACCAA	CTCAAGAAGA	GATTCGATAG	CCTCCCTGTC	1980
AATGC						1985

648

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1043 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

AGGGAGTGGC TTATGGGATA CGGTTTCATCA GCTGAGGAAA CGTCTTCTAC ACCGCATGCG	60
TCAGGCCAAA GGAAGGTTGG TTTTCTGTCC CTGCGCACCA AGCTCGCGCT GGTGTTTGGG	120
CTGCTTGCCT TCGTGTCTGG TCTGGTCCAG GCGGTATAT TGGTCGTTT TGC GCGTAAC	180
TCCATAGTTG GGGAGATTTC TAGTCACCTT GCTGGCCGTG CTCGGGATAC CTCCTCCATC	240
GTGGAAGGGC GGATCGGCGC GCTGTTCCAG TTTTGGGAAG GTTTGGCACG TCTTGAAGTT	300
TTGCAAGGCT CGTCCGACAG GCGCCGTGCC CAGGTGGACA GGCTAAAGAA GGAAGCGTTT	360
TTTAACCGGG ATATCGCGCG TCTTGCGGTG GTAGATCTCG CAGGCGTGTT GTACGGGGAG	420
GACGGGCGCA CGCATTACGT ACAAGATCGA AAGTACTTTC AGCGGCGGT TAAAGGCCGT	480
TGTTACGTCT CTGCGCCCTA TCCCTCGCGT TCGTCGGATG ACATGGTCAT TACCTTTTCC	540
ATCCCGGTAT ATGACGAAaT CGGCGGGTTA TgCCGTGCTC GTAGCGGaTG TGATTtGGAC	600
GTGGCTGTGT GATATCACAG GGGATTTTTT TGTAgGgGGG TGGGGAGAAT CGCCGTTATT	660
GACGAGGTTG GTACCGTTGT CGCGCACCCA CGTCACGAGG TAGTGGCGCA CAGACAAATT	720
ATATCCGCCT GGCAAAGGAA GACCCGGCCA CGTACGCGTC CGTCGAGAG TTCGTTGAGA	780
AGGTTATCAA GTCAGACTCT ACTGCCTCTC ACGTGTtCTC GTATGAAGGC TTAGAGAAAA	840
TCGGTTCATC TGCCAAGATG AAGAGCACAG GATGGACCGT CGTGGTGTtT GTGCCTGTCT	900
CCGAGTTTAT GGGGCCTGTG TACACCCTGG CAGAACTACC TGCTTGCGGT GGGTATCATG	960
TGGTACTCTT CTCCTCATG TGGTGTATGC CGTTGCGCGC AAGATTGTGC GCCCGCTACG	1020
CTCTACCGTC AGGTGTTAGA AGA	1043

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

ChTCTnTTAT TTATTTTGAA AAAGACACGT TGCTTTTCCT GCGCGAATGC GTCAGAATGG	60
CGCGGTCCCT ATGATATCGT GTTCGGTGCG CAGGAGGCCG AGATGGGAGC CTCAGGTCGG	120
CGCTGCGTTT CTTGCTTTG CGCTCTTACC GGTCCTGGCG AGCGGACGTG GTATGCAGGC	180
GGCAGTGGCC ACAGCCGAG GGTCCAGTGG TTCCGGCAGT GATGGCAAGC ACCCCGGCAA	240
GGAACAGTTT CTCCAGTTCC TCATTCCATC TGGCGGTGCG TACGAATACC TCGGGGTGAG	300
CTTTACAGCG CTGGCAGATG ACGCCAGCTT CTTTGAAGCT AACCCTGnCG GCAGCGCCGG	360
GCTCAGCCGC GGGGAAGTTG CTCTGTTCCA CCACTCGCAG ATCCATGACT CACACACCGA	420
AACGGTTTCG TTTGCGCGAC GTACGCAGAA CACCGGCTAC GcGCCTCCGT GCGCGCCTTC	480
TCTTCTGAGT CAGATCTCAA GTCCTTCTTC GGGGGCAACA GTGGTGCAA TAAGAACGGC	540
GGACACCAGG GCAAACAGGG AAAAGGCTTC GTGGCAATAG CCAATGCGTC TCACACCTTC	600
TGTGGCCAGT ATCGCTTTAA GGGCGTAACT TTGGCTGCAA TTTCAAGATG GGATTCCGCA	660
AGGtAAAAC GACAGCCACG TGACCGTCGC GGGTGACTTG GGCCTGCGCG CTGCCTTTTC	720
TGTGGCAAAG AACTTTGGCT CAAATGAGCC GAACATGCAC GTGGGGTTGG TGCTCAAAAA	780
TGCCGGGATC TCGGTAAAAA CAAACAGTTG CCAAGTCGAA CACCTCAATC CGGCCATTGC	840
CGTCGGCTTT GCCTACCGGC CGGTGTATGC GTTTTGTTC AGTCTCGGGC TGCAGCAAAC	900
CCTCACCAA AGGGAGTCGC CGGTGTGCAG TGTGGGTTC ATGTTTTTTT GTACCCAACA	960
CGTTACCCTC CTCGCTCTG CTGCGTGTGA AGGAGGGGCC TACGCCCTCT CAGGCGGCGC	1020
AGAAATCCGC ATTGGCTCCT TCCACCTCGA CATGGGGTAC CGGTACGACC AGATTTTCCA	1080
AGCCGCCCAC CCACACCACG TGTCAGTAGG GCTGAAGTGG CTCATACCCA ACGGCGGCAC	1140
CCAGGCGGAT CAGGCCCTCT TGGTCAAAGA GTCCTATCTA GTGGGGCTGC GCTTTTATGA	1200
CCAGCGGCGC TACCAAGAAG CAATTACTGC GTGGCAGCTG ACGCTGCGCC AGGATCCGGG	1260
CTTTGAACCG GCTGCTGAa GCATCGAgCG CGCACGACGC TTTTAAAAAC TACACGAAAA	1320
ACTTTCTCTC TTTGATATTC TCAACTAGCC TGCCGTG	1357

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

CACCGaCCCT GrAATaAAGC GTTACAAAAC CTACTCCTAC CATAAGGGCG ACAAGCAGTA	60
TGAATACAAA ACTGTAAACGC TCTTGATGTA CATTTTCTCTC GATGGAAATC ATCGGTCTCA	120
TCGCTCTTTC CTCAAAGAG GTTCAAGCCG CTCGAGCGcA AcACTGCGTG AACCTTTCAC	180
CAGAACAAAA TCACCCCGCC GTAATTGCGC GTCTAACGTT TCTTGACGCG CAGACAGTTC	240
CTCTAGTGCA AAGGCGTACA CGCGCTTCCT CCCCCAGGAA ACTTTTCTTA CCGCACGACA	300
AAATTCGGGA CCAAACACAT AACTGCACG CGCGTCAGAA GCGGCTGCCA AAACACACAC	360
CCGATAGTGA GCTTCGGCAG CGGTAACCTC TAGCTCTCCC ATGTCACCGA GCACATATAC	420
TTTGTACT GCAGAAATAT GCGCACACAA ATGAAGCGCC GCAGCCATTG AATCAGGATT	480
CGCATGTGTA CAATCGAGCA AAAAGGTCAG CGACGCACAC ACCACATGAG AGCGGCCAAA	540
GGGCGGTTTT ACCCGCTCCA TCCCCGCTG AATTTCTCTA GCAGGAAGTC CTACCTGTGC	600
GGCAAGCGCA ATCACTGCAA GCGCATTCTT TGC GTTATGC ACCCCAGGTA GTGGCACGCG	660
AATCCATCGT CCTTGATATA ACACGCGAGA ACCACGTAAA CCTCATCTA TCACCTCAGT	720
TGCTAGACCA CGCCCCCCT GATCGTAAAC TACAACCTA CCGTACGGGA TATTAGACAG	780
GAATACagAT ATGCATCGTC GGGGACAAAA CCCACGCTGT GTTCAGTAAA TTGAGAAAAA	840
ATCTCTTTTT TCTCTTCCGC AATGCTGTC TGC GTGCCA GAATGCcTAC GTGCGCACAA	900
CcTACGTTGG TAATGATCGC GTAATGAGGA ACAAGTATCT GAGCGAGCGT ACGCATCTCC	960
CCCCGACGAT TCATCCCCAG CTCAAAGATT CCTACCTCAT GTTCTGCACG CACAAAAAAC	1020
AGCGACTGCG GtAAACCTAt CTCTGAATTT AAATTTCTCTG GCGTCGCAAC CACCCGATAC	1080
CGTTCACTGA ACACCGCGCG AGCcATTTCT TTTACGGTTG TCTTTCCGCT TGATCCGGTA	1140
ATGCCAATCC TAATAAGCGC AGGAAACTTT TTGCAGTAAA AGGAGGCAAG ATCTTGCAGC	1200
GGCTGAGCG TGTCGTGCAC CGCAATACAG GCAGCTCCAA AGCGAGTGCA CCAAGCAACA	1260
TATTCCCCAG CATGGGGGtA CCTTTGATCT ATAAGCGTTG CAACTGCGCC CTTCTGCAGC	1320
GCTTCTTCAA CAAACGTATG TCCATCTACG TGCGCACCAC GGAGCGGAAT AAACAAATCA	1380
CGCGGCACAA CCGCACGACT GTCAAAGGAA ACCCCGTCAA AACC GCGCGC CCCTCGTGCA	1440
TCGCACACGC GAGCCCCTTG CACTGCCGCA CATACCTCAT CAAA ACTCAG AAGCATGAGG	1500
GGAGGAGTCC TTGTGCGCAG GACGCAGCTT AATGCGCACA ATTTGCGCGT GCGACGCCCC	1560
GTGTAAGTGC AGTTTCTCTA CCGCGAGCTT TTCAATACGA TCCGCTTAG ACAGGATCGC	1620
GATCCCAGAA ATCTTACGCT TATTTTCTGC GATAATACGG TGTGCTCTG CGTCGTACTC	1680

ACGCACCACA CGCTCAACCG CCTGATAGCG CGAAGCCTGC CACACCCCCG CACACAGCAA 1740
CACGGGGATA CTCACCGTAA AGAACAACGC GCTCACCTTT TGCACCGTCA TCCCTCTTTG 1800
CCGGCGAGGT ATTCCCcTTC GCTGCTTTTC TCTCATCGCC CCTTTCTCAC GCATCAGCCC 1860
AGTCTCTTAC CGTTTCTCAA TGACGCGTAA CGTAGCACTC CgcGAAGCGG CATTCGCAGC 1920
ACGCTCCACA CACGAAGGTA CAAGCGGCTT CTTGGTAATC AGCGATGCAC GCGCCACACC 1980
GCCGCAGCTG CATATCGGCA CACGAGCCGG ACAGCTGCAG CGTTTCGCCC AGTGCCGAAA 2040
ATGTACCTTA ACAATCTTAT CCTCACGCGA GTGAAACTA ATAACCGCAA GTCGACCCCC 2100
AGgCGCAAGC GCCGTAAACG CTGCCGTAAG AAGGCGTGCC AAACGCTCAA GCTCCCTGTT 2160
CAyCGCAATG CGCAATGCTT GAAACGCCTT GGTGCGCGGA TGGAGCTTCG GCAAAACCCC 2220
AAGAACACgC GCCGCTTCCC AAAmCGCGCC GTyCGCATCG GCGGCaCCAC GCGCGCAACG 2280
ACTTCTGCAA ATGCGCGCGC AGAGcAAAAG GGCGCCTGCC cGaaCTGCGc GCACACCGCC 2340
TGCGCAATCC GACGCGCGTA ACGTTCCTCT CCCCCTTCAA AAAACAATTG TGCCAAAnCG 2400
TCTGCGGCAG CCGATTcAGG AGGTCTGCAG CGGTCTGGGA GG 2442

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

ATCCGGGATG CGCGGCCCCC TGGGGGAAAC GGAAATTGAA ATTGCGGCCG GGGCAGCCCC 60
GGTGTGCCGC TCGCCgTGCG CGAACGGCAC kTGCACTCGC CACCCGCCGG TGCAGCGGGT 120
GGGGGAGTGG AACGCCTGTC TACCGAACGG CGTCTTTCTG TACTGCACGG CACgACGCGG 180
CTGAACCCGA AGCAGACGCC GTGCAGTAAC GCGCCGGcgC GCGCGCGCGC GTGCCGGCAG 240
ACGGCGCTGG TGGGACAGTC CGCAGGCGGC GCGCCGCTAC CACGCGATTT TAAGGCCGCA 300
CACAAAGGTG CCAAAGTGCT TATCTGAGGA AATATCTTCG GTAATTAGCA TGTACGGCGC 360
GGTGGCCAGC CGCCCCTGCT CCCACCGGGC GTCAAATCC ACTTTTTCTA TTGGGCTAAC 420
GGTGAACCCC ACGTGGTACT GCATTGCCTT TTCGCGTAgc AGATTGTTAG CTTTGTCGGT 480
GTTGAAACGG TTAGTGTTTC CGTACACCAC CGCGTACGGC TTGAGCCAGG CGTGGGAGCC 540
GAGCGCAATC TGATAGCTCA GCCACGTTTT GCCCAGACC GGCAGgTTGA TAGGCCCCCT 600

652

CATTGTAGTC TTCTTGTAAT CGATGCCCCC GTTGTTTACG TAGGAGGTGT AGGTGAAGGG	660
AATGTACAGG CGCGCCTCCA CCCCCGCGTT CAAGCCGGTG AGCAGGTGCG TGTAGGGGTC	720
GCCGGACTTT GTTTCTAATT TTAAGAATGC GCGCGAGTCC AAGTAGTCTG TAAGCTGCCT	780
GGAAAAGACG CGCTTGCCAA ACATATTGGC GCCGGCGGTG GCAAAATACG CGCCGGAAGA	840
AAGCCACTTC CACTGCATGC TCAGCAAGGC GTCAGcGcCC AACTCGTGCA CGTGCAGGCG	900
GTGCAGCCAC GCAAAGAACG TGACGAGCGC AATGGCCGGG TCCGGCTTTT TAAGGAGCTC	960
GGCGAATCCC TGGGTGAGCT GGTTTACCAC CGCTCCCAGG CCCAGTGTGC TCTGAAGTAG	1020
ATTGGAGAGT TTTCCCTCCA AATGGGAAAC CACcAGTGCC AcTTGCGCTA TGAaGGCAGC	1080
GCCCCGcAcTT TTTTGACAAA AAAcTCTCCG ACGCCACCGT TGGCCATaTC TGGGCCATTG	1140
TGCCCCAAAT cGGTTAACGy TGCAtTmAGG CTTcTGCCGm CTTGGsCTGC AgTTTACCGT	1200
CTTCCCTATA TCCGCGTCGC TCCGGTGAAT GTTTCCCACA TCAAGCGCCA GCACGAGCCG	1260
AAACCCGTAC CCGGGGTCA GCGTCAGCCG TCCGCCGGCG CTCCACAGCA GGCGGTTTTT	1320
CTGCTCATTG TTTTTCCTT GCTCAGTCCC CGTGGTGTAT TGGGGCTCCA GCGTGGCGTT	1380
CCCCGCCAGC TCCATCTTGA TGCGCTCAGC GCGGTGGTGC GTGTACGTAA GCGTGGCGTC	1440
TGCTCCAAAG CCGTACTTGC TGTGCGCAGT ACCACTATCC CACATACCGT TTGACGCAA	1500
CGAGAGCAAG CCCACGTCCA ACCCAATGCC AtGCCGCCGA TATCCTGCGC ACGGTAGCCG	1560
AGCTTGCCCC CATAGCCGCC AAAGCCGGGs CATAGCGCAC GTCCTCCTGC TTGTAGTCGC	1620
TGGTCACGAA CGGGTCCCAC aGtGCGCAA GTTAATAAAG CAGTTCGGGT CCTTGCCAAT	1680
GGTCAGGTAC GCGTTGTAGC AGTGGAGCGT TGCTTCAAAA GACGCTTTGG GTTTTTTGAG	1740
CGTAAAGGCC TGCCCCGCC TGGGGGATTC AAAATCAACG GTCAGGTCCT TGAGCCGCAG	1800
TCCGCCACA CGCCTGAGCG CGCCCCGCCG CGACGCAGGT GCGTGGCCTT GGGCACGAGG	1860
GGGAGCGAGA TTTTCAAATC ATTGGTGGTG CGAAACCCGT GCGTGACTC GTTnnTTGCA	1920
C	1921

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 658 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

653

GTCAATTGCA TTAAGGTTAT CACGCGCGCC CACACCCTCG GCTATTGCGG CGGGGTGCGT	60
ATGGCGGTGC GCATGGCAGA ACACGCCCGC GCCCACCACC GCGGGAGtTC TACACGCTCG	120
GTCCGCTCGT CCACAATCCC GTGACGCTCG CCCGTTTGCG CGCGCGTGGC ATTGAGTGTC	180
TGGATCCTGC TCATCTATCT TTTGCGCTGC ACGCTCCTGC GGcACCGGGC GCACGCCGCA	240
TGCAGTGGAA GAAAAGACGG CCGGTACCGT GGTGATTAGA GCGCATGGCG TGGCACCTGA	300
GGTGTATGAG GCCCTCGAGC GTTCCGGAGC GCAGGTGGTG GACGCCACCT GCCCGCGAGT	360
TAAGGAAAGT CAGCGGCGTG CTCAGGGTTT TGCCGCGCAG GGACTGCACG TTATTCTCGC	420
CGGGGACCGC AATCATGGGG AAATCGTTGG CATCGAGGGG TATGTGCGCG CGGGAGCTGC	480
GCAGGCGTGC ArCCAATTGC CAGGCGGCGC ACCAGACGGC ATGCTGCCAC AGGTGCAGTG	540
CTTTGTGGTG CAAAACGCGC GTGAgGCTGC CGCGTTGCCG TGTtTagCGC GTGCAGctTC	600
CTTgCCCCAA cTACCATTAC ACaGGGTGAA TAmGACGCGA TyGCCGCTGC GGgCGTAA	658

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 763 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

TTCTGCAGTG TACGTAAAT CGGACGCATA CTATGGGAGG TGAGCATTGA TAAGGCGTAG	60
ATATCGTGGT TGTACGCAGG AGCGTGGATA GTAAGTGTG GTATGCTATT TGCATCGTGC	120
ACTTCAGGGG CGTGGAAGGC ATCAGTAGAT CCGTTGGGGG TTGTGGGATC TGGTGCAGAT	180
GTGTACCTGT ATTTCCCTGT AGCGGGGAAC GAGAATTTGA TTTCTCGTAT TATCGAGAAC	240
CATGAGTCAA AGGCAGATAT TAAAAAATA GTGGACAGGA CTACCGCGGT ATACGGTGCT	300
TTTTTTGCCC GATCAAAAGA GTTTCGTTTG TTCGGAAGCG GTTCGTATCC ATACGCCTTT	360
ACTAATTTGA TTTTTTCTCG ATCCGATGGC TGGGCATCTA CGAAAACGGA ACACGGAATC	420
ACGTACTATG AAAGTGAACA TACGGACGTT TCGATTCTCG CGCCGCATTT TTCTGTGTG	480
ATTTTGGTT CCTCCAAAAG GGAGCGGATG AGCAAAATGC TGTCTCGGCT CGTTAACCCC	540
GATCGACCGC AGTTACCGCC TCGCTTTGAA AAAGAATGTA CGTCGGAAGG TACGAGCCAG	600
ACTGTTGCAC TCTATATAAA AAACGGGGGA CACTTTATTA CCAAACTGTT GAATTTTCCG	660
CAGCTTAATT TACCACTTGG GGCAATGGAA CTGTACTTGA CCGCGCGGAG GAATGAGTAT	720

CTTTACACGT TGAGCTTGCA GCTGGGGAAT GCAAAGATAA ATT

763

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4968 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

GGCCCCAATC CCATAAAATA CTCTGGTTGT GTTTGCTGCG TATGACGTGA TAGTCAGCTC	60
TTCCACCGTA AATGAGATCG CAAATACGGG GCGGGGTGCG ATATACAATG AGCATACAAG	120
GATCATGCAT TCGTATCGTA AACGGTACAG TTTGATCTGC GCTCGATTCTG AGTACGGACT	180
TTCTACTACT CACAACCTTC AAACCTACGGG AATCGCTTTT GTCGACAATT AAAAGTTGAT	240
ACATAACGGA GTGAAATACT TCACCAACCG ACAGTATAAC CCCATTGTGT TTTCTAGTTG	300
TGTGAGATTC AAATCCCAAG GATGGCACGG AACTGAGTAC GCGCCAATAC ACCTGcCTTA	360
ATCGTATAAA GCTTGCAGGT ACCACCACGT CGCTAAAAAC AAATACAAA AGCGCACTGC	420
ACAAACCAAT CGACAAAAGA GGAATATCA AAAACCGCGG CGAAACGCCC AGCACTTGCA	480
GCGCAAgcAG TTCAAGGTTG TTACGCAGCC GCCCCAACCC CAAGAGGGAA CCGAcCAACA	540
CGGCAAAAGG AGTAACGTAA ATCAACGCAG CGGGAATGGA ATACAGCAAC AGCCGGACCA	600
CGTCCGCAGC GCTCACGTGC TTGGTAAGTA ATGTCTGCGC AAAAAGCAGT ACGTTGTTCA	660
CAAAAAAAC CAAGAAAAG CACAGCACGC CCACCAGGAT GTGTTTGAAC ACTACCTCGC	720
ACACGTACAC AAAAAGCACT CTTCTCCACA TCTAGGTAAC TACAGAACCC CTGTGGATCC	780
GTACCCTCCT TTTCCCCGTT CAGTCAGCGA GATACTACCG GAGCGCACAT ATTCAACACG	840
GAGCACAGAA GAAATCACCG CCTGCGCGAT ACGATCTCCA TGGGAGACTA CGAAAGCAGC	900
TAGCCCAAGG TTGACAAGCA ACACGCGTAT TTCCCCCGG TAGTcAGCGT CTATCGTTCC	960
CGGGGAATTT AAAACCGTCA CTCCGTATTG GAGTGCTAAC CCAGAGCGGG GACGAATTTG	1020
CATCTCCAAC CCCACAGGAA GCTCCACACA AACACCCGTG GGGACGAGAA CCCGGCCCAG	1080
GGGATGAACC TCAAGCGGTC CTCCGGGAAG AAAGGCCCGC AAATCGGCTC CACTTGAGCC	1140
TAACGTCTGG TACTCGGGAA AAGAAGCTCC CGGATACAG ACAGCTCGCA CACGGATCAT	1200
TTCGTCGTGT CCAGACCTCC AGACTTCCCC TCAAGAGCAT CGATATAGGA AAGATTCAAA	1260
CGACCCATCC TGTGATATC AATCAACTTC ACACATATCC GCTGACCCTC TTGCAGCACA	1320

655

TCGCTGACTT	TGGACACGCG	GCTGCGCGAC	AGctTTGAAA	CGTGGCAGAG	TCCTTCCTTC	1380
CCTGGAAAGA	TCTCCACAAA	AGCACCGAAC	TCTACGATTC	GTTTCACTAC	ACCCTGATAC	1440
ACCCTCCCTA	CCCGAGGATC	TTCAGTAAGG	CCCACCACGG	CGACCTTTGC	GTCGAAAACG	1500
GACTGCGCAT	CCCTTCCGGA	GACGGTTACG	GTACCGTCAC	TATCAGTGTT	GATAGTCACC	1560
CGATACGGT	CAGAAAGCGA	CTTAACGGTT	TTCCCCCAG	GACCGATGAG	CGCGCCGATT	1620
TTTTCAACCG	CTATTTTAAA	ACTCTCAATA	TGCGGCGCAT	AGCGAGAAAT	GTGcACGCTC	1680
GGTGCCTGa	TTGTCTGATT	CATGACAGAA	AGAATATGGA	GCCTACCTAC	ACGAGCTTGC	1740
TGCAAAGCCT	CCTTCATCAG	AGACGCAGAC	ACCGCCTCTA	CCTTCACATC	CATCTGAAAA	1800
CCGTAATGC	CGTCACACGT	ACCTGCTACC	TTGAAATCCA	TATCACCGAG	ATGGTCCTCC	1860
TCACCCAAAA	kaTCCGAAAG	AATCGCATAT	CGCACGCCAT	CGGTGATGAG	CCCCATCGCG	1920
ATTCCCGCAA	CAGGCTTTT	GATTGGGACC	CCTGCATGGA	GAAGAGAAAG	CGTCCCTGAG	1980
CACACAGTCG	CCATGGAGGA	AGATCCATTC	GACTCCAAAA	TTTCTGAAAC	CACACGCACG	2040
GTGTAAGGAA	ACTGTTCTGG	ATCCGGAATG	ACTGCCGAGA	GGGAACGATG	CGCTAGACAC	2100
CCGTGCCCAA	TCTCCCTCCG	ACCAACCCCC	ATTCTCCCTA	TTTCCCCCAC	TGAAAAAGGA	2160
GGAAAATTAT	AGTGAAGGAT	AAAATTCTCC	CGTCTATCCC	CTTCGATGTC	GTCGTACACT	2220
TGCCCCTCCG	ACATAGCACC	GAGCGTGACC	ACCGCGAGCG	ATTGAGTCTC	CCCCCGGGTA	2280
AACACCGCAG	ACCCATGCGG	ACGCGGCAAC	ACCCCGACCT	CACAGGCGAT	GGGCCGAATG	2340
GCATCAATGG	CACGGCCATC	GATGCGCAAA	CCCCTGTCAA	GAATGTTTCA	CCGTAGTATC	2400
TCATACTCCA	TCTCGTGGAA	CAACGCGTCG	AACAACCTGC	GCTGCACATC	GTTCTCAAGC	2460
TGAGCAGCAT	ACTGCTGTGC	AACATCACGC	TTCAcCGCGT	CGCAGGCACT	GcgCCGCTCA	2520
CCCTTCCCCT	GTGCATACAA	AGCCTGCGCA	AGACGCGGAT	AGGCGAGCTC	ATAAATACGA	2580
TCGCGACCTA	CAAGcTGCGC	AGAAGAAGGG	ATAACCGTCT	GTTTCTCCTT	GCCACACAGT	2640
CCACGCAGAC	GCTCCTGCAT	ATCGCAAAGG	GCTTTAATAT	GCTCTTGTGC	CTGTTGAGC	2700
GCGCCGAGCA	TGAGGTCTCT	GGACACCTCT	CGCGCACCAC	CTTCCACCAT	GGTAATGCCC	2760
TGCCTAGTGC	CTGCAACGAC	AACCTCCATA	CTGGCGGCAT	CAATCTGAGA	AAAGGTAGGA	2820
TTAATAACAT	AGGAACCGTT	CAGATATGCA	ACGCGGACTG	CAGCAACCGG	TCCATGGAAG	2880
GGGATATCCG	AAAGAGTAAC	GGCAGCTGAA	CTGGCAACAA	TAGCCAAGAC	GTCATGAGGA	2940
TGGACCATAT	CCGACGATAT	GCACGTAGGG	ACAACGTGTA	TATCACGTCC	AAACTCCTTT	3000
TCAAAGAGCG	GCCGCATCGG	ACGATCAATG	AGGCGCGAAA	TGAGAATCTC	TCTGTCTTTC	3060

656

GGACGGCCTT CACGCTTGAT GAAGCCGCCA GGCATCTTCC CCACCGCATA ATACTTTTCG	3120
TTGAAGTCAA CAGTGAGCGG GACATAGTCG AGCCCTTCCT GTCGCTGAGC AGAGGAGCAT	3180
ACGGTCGCGA GAATCGCCGT ACCTTCACAC TGTAATATACA CGGACCCGTT CGCTTGCCGC	3240
GCCAGATACC CACTTTCAAG GAGAAGGGGG TGGTCCCCAA TAGTGCCGGT TATGCTGTGT	3300
TTCATACGTT TCCTAAGAAC AGAATGTATC GCAGGCCGCA CCAAGCCCTG GCACAGCCAC	3360
CTGCGAAGCT AGACAAAGAA AGCAGAACGG ACAACCGTCC TATGCACAAC CCCTCGGCGG	3420
CACGCACTGC GAAACTTCCC CATGCAAAGC CCCTACTTCC TCAAACCGAG GCTTTTGACA	3480
AGCGAACGAT ACGCCCCCAT ACTCACGCGC CGGGAATATC TCAACAGGCG ACGACGACGC	3540
CCCACCAGAA CGAGCAACCC CCGGTTGCTA CTTTTGTCTT CGGATGAACC TTACAGTGGT	3600
CAGTCAAcTG CCTAATCCTC TCAGTGAGAA GAGCGATCTG CACACTCGAA GATCCTGTAT	3660
CCTTTTCTCC TGAGCCGTAC TGCTGCACTA CCGAAGCAGT ACGTTCCTTT GTCAGTGCCA	3720
TTCTCCTTCT CCTTTCTTAC TCGAACTCGA TAGAGTCAAG CGCCTCCCGC CCATGCGACA	3780
GCGCCTCGGT ACCGAGCCTC AGCTGCACGA GAGAGGAACC CACACTAAGT GCGCACGCAG	3840
ACCCACCCCA CTCCCCGTGA CAAGGGTACC GCATACTCGC CCTCAGGTGG AAGCGTCTGA	3900
CTCACACGCC CACGCTCGGn GCACAACGTG CGGGCACACC CCyCGCTCTG CTGCCAGGGA	3960
ATTACCTCCC CGTCAAGCGA AAACGCACGC CCCAGCAGAC GCCGCGCGCT CTCAAAGTCT	4020
GCGCAGCGcA cckCACGGGT ACCGCGCTCG AACTCACCCG AACTCCCTCG AGAGTGTAGT	4080
GACCCACCGC GTCaGACAAA GCTATGCGCA TCACCAAGCC GACGCAGCTC ACGGACCCCG	4140
GTGTCCAGCC CATGTCCACA CCGAAAGTCG ACACCAACTG CGAGGTAGCA CACCCTCACT	4200
GCACGCAACA GGGTGTGAA GAAGACACCA CCCGGGATTC TAGCAAAATC CTTGGAAAAG	4260
TCAATGAGCA CGACGAAATC AAAGCCGCGC GCACGAAAAT AACGGAGTCG CAAACGCAGC	4320
GTTGACAGAT CCCCCTCGTA AGAAGAGGTT TTGTGCTTCC TGGGAGGATG AGTAAAGGTG	4380
ATCAGCCCGG TGCACCGCGC CCGATCGGCC ACAGGAGCGC ACGCAGCGGC AAACACCTTA	4440
TCGAAGAGAA AAGCATGTCC CCGGTGAGGA CCGTCAAACC CCCCACCGA TATTGCTGCT	4500
CCCCGATCAC ACGCTATACA TGCACCCTCC TGCAACTGAG ACCAACGAAA AATGCGnCAC	4560
GCCTCACTCC GTACAAAATA CCGCCATCAT ACGAAAACCC ATTCGCCGCT TTCCTTATTA	4620
TCCAAGACAG CGACCCTCGG AAAACACCAA CGCACGTTCC CCGGGCTTCG CGTACCAAAC	4680
GACTGGAACC AACATGCGCG TATTCTTTCC CCATGCAAAA ACCGCGAACG CATACTGCGC	4740
ATGCACTGAA CACGCCGTAA GTCCAATACG ATTCGCAAAAG TCCACATCAC AGCTAACCAC	4800

657

TGCCTGCTTA ATCTCACGCA CCGTCAAGTC TTCACACCCG AAAGAGACTG AATCGGTCGC	4860
CACGCCGCCT GAGGACGGAG GCGGTGGAGC ACCCACAATCA AAGCAAGCGG CACCGCAAGA	4920
CGCACGCTCT TTGCCCCATG TCCAGGACCC GAGACGAACA CACCCGCC	4968

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6086 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

AGTTTCGCGC GGGCTAAAGT GGGTTGGTCG CGTGTGGGTG CCAGCGCGCT GTACTTGTCG	60
CGCGTTATTT CGTGCATTGA GCGTTCTAAG GTGGTTTAGC GCTTATGAAG GAGAATTCCTT	120
GCACGGCGTG CAGCAGACGG CTCGCCCTGT TCGTGGGCGC TGCGGTGCTT GTGGTAGGCT	180
GTTTCATCAA GACGGATGTC ACGCTCAACC GTGACAAGCC CCTAGTGTTT TTTAACCGAC	240
AGCCCTCTGA ATCCCTCAGG GGGAAGGTTG ACATGGCTGC CATGAAGTGG AACGACAAAA	300
CCTATTACGT GGGTTTGTAC GCTAAGTTTG GTGGTTCTAT ACAGGGAAAG ATGATTCTAG	360
ACTTCCTCGC CTCTTCTGAG TCCTCGGTTG ACCGCAACGG TGACGGCATC ATCGGTTATG	420
TGCTTTGCAT CCGTGACGTC GGGCACAATG ATTCGAAAGT CCGCACCGAG GGTATTTCGCC	480
GCGCGTTGGG CACGTGGACC GGCTCCTCGG ATCCGGGACA GGCGAAAGAA GGCCAGGCAG	540
TGGTAGGAGG GAAATCCTAC AAGGTGGTGG AGCTCGAGGG AAAGGCGATG ACGGGAAGTG	600
ACGGTTCCAC TTGGAATACG AATTCTGCAA CCGAGTCAAT GGGAAGCTGG GTGGCAAAGT	660
TCGCGGATAA GATAGACCTG GTCATCTCAA ACAACGACGG GATGGCAATG GGCTGTCTGC	720
AGGCGTCCAA TTATCCGCGG GGGCTGCCTA TTTTCGGATA CGACGCAAAT GCGGACGCGG	780
TCGAGTCGGT TGGTAAGGGT GAGCTCACGG GGAAGTGTCTC TCAGAACGTC GACGCGCAGG	840
CTGTTGCAGT GTTGCAGATT ATCAGGAATT TGCTCGATGG CTCCAGCGGG GAAGATGTGG	900
TCGCCAACGG TATTTCAAGA CCTGACGCCC ATGGCAACAA GATAAGCGCG CCCGTGCAGT	960
ACTGGGaaAGA TGTAAAGCG ATTATGCGCG ATAACTCGGA GGTCACGAgC GCmAACTGGA	1020
AAGAGTACAC CAGGGGAGCA CGGGATGCAG GGGTGCGACA GGTAAGTGCG CCGACGAAAA	1080
AGGTGCTGCT CACTGTCCAC AACGCGAGCA ATGATTTCTT TGCTTCTGCC TATCTTCCCCG	1140
CACTGAAGCA TTACGCTCCG CTCCTGAATG TCGATCTCAC TGTCGTGCAG GGCGATGGCC	1200

AAAACGAGCT AAGTTGCCTT GATAAGTTCA CTAATCTCGA CATGTTGAC GCGTTCGCGG	1260
TaAACATGGT AAAAACGAAC TCGGGCGCTG ACTATACAGA CAAGCTCAAA TACTGAGCAG	1320
CCGGGTTTGG ACGTGCCTTG GGTAGCTGCT GTTCCTGGTG CACGTCCTGT TCGTTGAATA	1380
GGTAGGGTCT ACCGACCTCG CACCGCTTTC GCGCGCGAGA GGAGTGATAG TTGCGATGTG	1440
CGATGTACTC ACCATAAGGG ATCTTTCTAA GTCTTTTGCG AGGAACAGGG TTCTCAACGG	1500
GGTGAAC TTC CGTATGGGAA AGGGTGCCGT GGTGGGGCTT ATGGGAGAAA ATGGTGCGGG	1560
AAAATCCACG CttATGAAGT GCCTCTTTGG AATGTACGCT AAGGACACTG GTCAGATTCT	1620
CGTGGATGGA AGCCCGGTGG ACTTTCAGTC TCCCAAAGAA GCGCTAGAAA ACGGTGTCGC	1680
CATGGTCCAT CAGGAGCTCA ATCAATGCCT TGATCGCACT GTCATGGACA ATTTGTTTCT	1740
CGGCAGGTAC CCTGCCCCTT TCGGGATAGT TGACGAGAAA CGCATGTTG ACGACTCCCT	1800
CACTCTGTTT GCTTCCTTGA AAATGGACGT AAACCCGCGG GCCGTCATGC GCAGcATkTC	1860
TGTcTCTCAG CGGCAGATGG TAGAGATTGC CAAGGCGATG TCCTATAACG CGAAGATTAT	1920
AGTCCTCGAC GAGCCTACTT CCTCTCTCAC GGAGAGGGAG ATTGTCAGGC TCTTTGCCAT	1980
TATACGAGAC CTGAGCAAAA AAGGAGTGGC ATTCATCTAT ATCTCCCACA AAATGGATGA	2040
GATCTTTTCA ATCTGCAGCG AGGTGATTGT GCTGCGGGAT GGTGTCCTCA CGCTCTCACA	2100
ATCCATAGGG GAAGTGGAAG TGAGCGACCT CATCACCGCT ATGGTCGGGC GCACTTTGGA	2160
CAAGCGCTTT CCCGACGCTG ACAATACCGT CCGTGACGAT TATCTTGAAA TACGAGGTCT	2220
TTCTACAAGG TATGctCCGC AGCTGCGGGA TATTTCCCTT TCTGTGAAAA GGGGCGAGAT	2280
TTTTGGCTTG TACGGGCTGG TCGGTGCGGG GAGGAGTGAA CTGCTTGAAG CGATTTTCGG	2340
CCTGCGTACC ATCGCAGACG GTGAGATCTT TTTAGCAGGA AAAAAAATTC GCTTGAAGAG	2400
CAGCAGGGAC GCAATGAAAC TCAATTTTCG CTTTGTGCCC GAGGAACGTA AGCTCAACGG	2460
AATGTTTCGA AAGGGGAGCA TAGAGTATAA CACCACGATT GCAAATCTCC CTGCGTATAA	2520
GCGTTACGGT CTACTCTCAA AGAAAAAGCT GCAGGAGGCA GCGGAGsGGG AAATAAAGGC	2580
CATGCGCGTG AAGTGCGTTT CTCCAAGCGA GCTTATCAGT GCGCTCAGCG GGGGTAATCA	2640
GCAGAAAGTC ATTATTGGAA AGTGGCTCGA ACGCGATCCC GACGTCCTCT TGCTTGATGA	2700
GCCGACCAGG GGGATCGACG TGGGTGCGAA ATATGAAATT TATCAGCTCA TCATTGCTAT	2760
GGCGCGTGAG GGAAAGACAA TCATTGTGGT TTCTAGTGAA ATGCCTGAAA TTCTTGGAAT	2820
CACCAACAGG ATCGCAGTCA TGTCCAATTA TCGATTGGCT GGGATTGTGG ATACAAAGAG	2880
TACCGATCAG GAAGCCTTGC TCAGACTTTC TGCGCGATAC CTGTAGGGAG GAGCAGATAC	2940

659

ATGCGCGATC	GTACACAGTG	TGTGGCGGTG	CCAACTCAAG	CGTTCAATGA	GATTTTAGAT	3000
CAGGACGGTC	AGCTCACCGC	GTACGCCCAA	AGGCTCGAGC	AGTTACGAGA	GCGCGGTTCC	3060
CATAGGGTTG	CCTTGCTCCG	CGGGGAGCTT	GCGCGCATAC	GGCAGGATCA	GGTCTTGGGC	3120
ATGCCGGAGA	AAAGGGTGCA	GGTTGCGGCG	CACAGGCTCA	AGATTTCCGA	AGCGCAGGCC	3180
GTTCACAGAC	AGTrmAAAAAC	TGAGGAAACG	CAgTTGGtTA	GGAArGsTGT	GCGCGGTGTA	3240
AgGGGGCTCt	TTCGAGACTT	TGACTGCTCT	GTGCGCGACG	CGATGCGCGA	ACAGCGGCTC	3300
TTGCTAAAGC	AAGTTGCGAC	GGTGCaGCAC	ACCTCTGCCT	CATCTGACCA	AAGAGAGCAC	3360
TGTCTGGCTC	AGCTCCGGCA	ATGcmAGGAG	GCGCGACACC	ACGCCTACCG	TTCTTGGTTC	3420
GAAAGaGct	GCGCTGCGGA	ACGGGAAAAT	GaCGTTTATC	GAGCGCGTGG	TGCGTGCTCT	3480
TAGAGAATAT	TCGTTCAATT	TTGACGCAAC	CCAGTCTTTC	CTCGCAAATG	GTTTGTACAT	3540
TGCTATTGCG	GTATTCTTTA	TTGCGTGCA	CGTagTTGCA	CCTTTCTCTG	GTAATGGCAA	3600
TCTTCTTACC	ATTCCCAACA	TTCTCACCAT	ACTGGAGCAG	TCTTCAGTGC	GCATGTTCTA	3660
TGCGGTGGGA	GTAGCAGGTA	TTATCCTGCT	GGCAGGAACT	GACCTCAGCA	TTGGGCGTAT	3720
GGTGGCAATG	GGGTCTGTAG	TCACGGGTAT	TATTTCTTCAT	CCGGGACAGA	ATATCGTTAC	3780
ATTTTTTGGA	CTGGGGCCGT	GGGATTTTAC	CCCTGTCCCC	ATGGCTGTCC	GTGTAGTCAT	3840
GTCACTTGcA	GTTTCTGTG	CACTTTGCGT	TTCGTTCAGC	CTATTTGCAG	GATTCTTTTC	3900
TGCTCGCCTC	AAAATACACC	CTTTCATTTT	AACTCTTGCA	ACGCAGCTTA	TCATCTACGG	3960
GGTTTTGTTT	TTTGGGACAA	GTGGTACGCC	AGTTGGCTCT	ATTGACCCAT	ACATCAAAGA	4020
CCTATTCGGT	GGGCGGTGGA	TTCTAGGCAC	CATGCAGGGC	ACACTCGTGA	CCTTCCCAAA	4080
GCTGATAATT	CCTGCCACCA	TTGCGGTGGC	CATCGCGTGG	TTCATTTGGA	ACAAGACGAT	4140
TCTAGGAAAA	AATATGTACG	CCGTTGGAGG	GAATGCTGAG	GCAGCGAATG	TTAGCGGCAT	4200
CAGTGTTTTC	GGGGTGACTA	TGAGCGTTTT	TGCAATGGCA	GCTGTGTTTT	ATGGCTTTGG	4260
CGCGTTTTTT	GAGACGTTCA	AGGCAAATGC	AAGTGCGGGC	ACTGGTCAGG	GTTATGAGCT	4320
CGACGCAATT	GCCTCCTGTG	TGGTAGGGGG	TATCTCCTTC	AACGGGGGAA	TCGGAAAAC	4380
CGAGGGTGCC	GTGGTAGGCG	TAATCATTTT	CACCGGTCTT	ACCTATTGTC	TGACTTTTTT	4440
AGGCATCGAT	ACAAATCTTC	AGTTCGTGTT	CAAGGGTTTG	ATCATCATCG	CTGcAGTTGC	4500
ACTCGACAGT	GTGAAGTATC	TGAAACGCCG	CTAGTTCTTG	CCCcGCTGGG	CGGGAcGTCA	4560
ACGTTCACAA	TACGAATAAG	CCGGGCGCCT	TTCTGGGcCA	TTGTTCCCTC	TTTGGCTAAC	4620
TCAGGGTGTG	GGCTGACaG	AAGGCcTCCG	CTGTCCGAGC	TCTACCGTGC	TTCAGATGAG	4680

660

CCcTTTtCTT TTCTCAGTAG TTCGAACGnc yTCGCGCGCA ACTTGGAGGA TAGGGTAATC 4740
 TCTTACTGGA TCCGCAACCC GAAATCCACT GTACCCAGAT TGCTCAAAGT TCTTGGTATC 4800
 TCCCACATCC CcTGGTCCTC GTAACCTCAG ATCCTCTTCG GCGATAACAA ATCCATCCGC 4860
 aGTACTTCCC ATAAaTTTTCA GCCTGCGTTT CGCACACTCA GTCATTTTCGT CCCCATGCAT 4920
 TAaGAAACAA TACGACTGCA CATCACCCCG ACCAACCCGA CCACGCAGTT GATGTAGTGC 4980
 AGAGAGGCCA AAAACTCCGC gTGCTCTATA ACGATACAAT TCGCATTTGG TACATCCACT 5040
 CCCACTTCAA CAACGCTTGT AGCAACCAAG ATATGGACGG TACCTTCGCT GAAATACTTC 5100
 ATGATACGCT GCTGCTCTTC CTCAGTCATT TTTGAGTGAA TCATCGCAAC AGCATATCGT 5160
 GCAAAATAAT TTTTtagata CATATACATA CATTGCACCG ATTTTAAATC GGTTAATCCT 5220
 ATGTCATGAA TACGTGGATA AATAAAATAT GCCTGCCTAC CTTTTTCTAT TTCATTTCCC 5280
 ACAAACTCAT ACACCTTTTC TGCTTTTCGTC TTTCTTGCAA TATACGTAAT CaCTGGTTTT 5340
 CTTCCACCAG GCaTAGATTT AATTATTGAA ATATCTAAAT CACCAAATAC AGAAAGTGCa 5400
 AGCGTACGTG GAATTGGAGT TGCGCTCATC ATAATAATGT GTGGAGTCTT TCCCTGAGGG 5460
 TTCCCTTCCC TTCCTTTCTG AATCAAGGCC GAACGCTGTA ACACTCCAAA ACGATGCTGT 5520
 TCGTCAATGA TAACCAACCT CAGATCATGG TATCTTACGC TCTTTGAAAA CAGCGCATGT 5580
 GTTCTACAA CTAAATTGAT TTCTCCTGCA ACAAGAGCTT CGAGCAAGTA CGCCCTTCCT 5640
 TCACTTTTCA CATTACCTGT CAGGAATGCA AGTCGAATCC CAATAGGAGC AAGTAATCGA 5700
 GCTGCaGTGT CAGCATGCTG GCGTGCAAGT AATTCAGTTG GAGCAAGCAG TGCGACCTGT 5760
 CCACCTTGTT CAATAATTTT TAAACAAGAA AAAAACGCCa CTAACGTTTT TCCTGATCCA 5820
 ACGTCTCCCT GAATTAGCCG TGCCATCGGT TCTTCTCTTT CAAGATCCTG CGTAATTTCT 5880
 GTAATTACTC TTTTCTGATC CACTGTCAAC TCAAATGGCA AACACCGGTG AAGTTTCTTC 5940
 TGTAACAAAG ATAATTCAGA AACAACGAC GGAATAGCCG ACTGCTGATC AGATTCTCCC 6000
 TGTGTAAGAG GCAATCTCCC CCGCTTCTGT AAAGAGCGCA TACCGATAGT CATTTGAAGA 6060
 GAAAAAAATT CTTCAAATAT CAAAGA 6086

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20757 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

GCAGCGGCCG GTGTGGGCGC CCACCGGCGG GCGGTATGCG TCTTTGGACG GTGCGTTTAC	60
CGCGCTGGCA ATGATGCAAG TTTCTTTGAG GCAAATCCGG CAGGAAGTGC GAACATGACG	120
CACGGGrAGC TGGCTTTCTT CCATACCACT GGCTTTGGCT CGTTTCACGC CGAAACGCTC	180
TCTTACGTTG GCCAGTCGGG CAACTGGGGA TACGGCGCGT CGATGCGTAT GTTTTCCCT	240
GAATCTGGGT TTGACTTTTC TACCACCACG GAGCCCGTGT GCACACCTGC TTCGAACCCC	300
ATTAAGCAGC GCGrGGCAAT TGGAATCATC AACTTTGCCC GCGGTATCGG AGGTCTCTCC	360
CTGGGAGCCA ACCTGAAGGC GGGGTTCGCG GACGCGCAGG GCCTGCAGCA CACCTCTGTC	420
TCCAGTGACA TCGGCTTGCA GTGGGTGGGG AACGTTGCCA AGTCCTTTAC CTCTGAAGAG	480
CCCAACCTGT ACATCGGGCT TCGGGCCACC AACTTGGGAT TGACCGTAAA GGTCTCGGAC	540
AAGATAGAGA ACTGCACGAG TACCTGTGAA AAGTGTGGTT GCTGCAAGGA GAGGTGCTGC	600
TGCAACGGCA AGAAGGCGTG CTGCAAGGAC TCGGACTGTA ACTGCCCCTG TCAGGACTGC	660
AACGACAAAG GTACGGTGCA CGCAACAGAC ACCATGCTGC GTGCAGGGTT TGCATACCGG	720
CCCTTCAGCT GGTTCCTCTT TAGCCTTGGT GCCACCACCA GCATGAATGT GCAGACCTTG	780
GCTAGTAGTG ACGCCAAGTC GCTGTACCAG AACCTGGCTT ACAGCATAGG CGCCATGTTT	840
GATCCCTTCA GCTTCCTGAG CTTGAGTTG AGCTTCGCA TCAACCACAA GGCTAACATG	900
CGAGTGGGAG TGGGTGCAGA GCGCGCATT GCCCGCATT AGCTGAACGC GGGATACCGC	960
TGTGACGTCA GCGACATCAG CAGTGGGAGT GGGTGCACAG GCGCGAAGGC TTCGCACTAC	1020
CTTTCCTTGG GTGGCGCGAT ACTGCTCGGC CGAAATTAAT TCATAATATG CCGGGCGGCC	1080
CGCCGGTGCC CTGCTGAAGA ATGCGGcCGG cAAGACGTGG AGGGGGTTTT GCCGCTTTTT	1140
TGGTGCGGCG GCCGTGTGTG TCGGCTGCGC CAGTACGCGT AGGAGGACGA TTGGTGTTCG	1200
GTTTTCACAG CGTCGGTTCG CGCGGGCTCT GCTTGGGGGC CCTCCTGCTC TCCCyTCGCA	1260
TCgTGTTGGC ACAGCACGTT GCTGACGCTC CTTTGGGCGC ACGCGGGGTT GTTCCGCGCA	1320
GnTCCTTGCC TCGGCGCACG CGGGCGGCC GGGCTACGAC GCTGCGATCT CGGGGCGGCG	1380
TGGTCAGTTC CgCGCGAGCG GGGGAACGCT CGTGGTCACC GCGCAGAAAC CGAAGGTCAT	1440
GGCACGAAAT GACGTGGACT ACCGTCCGCT CTCCCTGCAG GCCGGCGGCA GACAAGGCTC	1500
GTGGACCTT GTTGCCACgC AACGGCGGAT GACGCCAGCT TCTTTGAAGC GAACGCCGcA	1560
GGAAGCGCCA CCATAcCGCG CATGACGCTC GCCTTTTTTC ACACCATGCG CATTTCGAC	1620
TCCCACATAG ACGTACTTTC CTTGTGCGGG CGGGCGGGC GCACCGGCTA CGGCGTTTCG	1680

662

GCACGCGCCT	TTTACCCAGA	CATGTCCAGC	AAAACCACCG	GCTTCGTGGG	AATTTTAAAC	1740
GTATCGCACG	CTTTCTCTTC	CGCCTATCGC	TTTAAGGGCG	TGAGCGTGGG	CGCAAACCTT	1800
AAGGTGGGGT	ATCGCCACAC	CCGGGGGGGG	GGGTAGCAGC	CAGTCAAAGA	GCTCCAACGG	1860
GAAGGAGAAC	CACCACATAG	TCCTGACCGC	GGACGTAGGG	GTGCGCGGTG	CGTGGACGGT	1920
GTCTAAAAAC	TTTGGTGCGC	ATGAGCCAAA	CCTGTGGGCA	GGAGTAGCAT	TCCGCAACAT	1980
TGGCGCGTCA	ATCAACGCCA	CAAACCTTCA	CGGAAATAAC	GGCGCCGGAG	GCAGCGGCGG	2040
CGGTGGAGGG	GGCAATGGCG	ACGGGAAACC	TGCCCACGTC	ACGGACTCCC	GCGTTATCCT	2100
TGCGCTTGCG	TACCAGCCGG	TGCGGTATTT	TCTTTTGTGC	GCCGGGCTTG	AGTGGCTCTA	2160
CAATGTGGGG	TCTATCAAAG	CCGTCAATTC	GCTCCGGTAT	GGGGCGGCGT	TCATGCTTTT	2220
TCCGCTCAGG	CAATTGGCAT	TCAGCTCGAG	CGTGGTTATG	AAGGGGATGG	GTCCACAGCA	2280
GGTCCGCGCG	AGCGCAGGGG	CAGAAGTGCA	GTTTTCTCAC	GTGCGGTGCA	CCGCCTCGTA	2340
TTCGTATCTT	TGGAGTGCGA	CACCCACACG	GCCsCACTAC	GTTTCAATTG	GGGTAGCCGG	2400
TTTTCTCAAA	CCGGTTCCCG	AACAACCCCT	GTGGCAAGAG	GTGTACCGCT	CCTATTTGCG	2460
CGGTGCGCCA	CTACCACGCG	CAGCTaCGCA	GAGGCCATCG	CCGAGTGGAA	GCGCACGCTG	2520
CAGCAGGGCG	TCAGTTTTGA	GCCTGCGCGG	GAAGGCATCG	AGCGCGCCAC	CAAGCTTTTG	2580
CAGCTGAACC	AAAAGGTTCA	CGATTTTAAAC	ATTTTCTAGC	CGCGCCGCCG	cGCAtCATCT	2640
GCTCCGTCCT	GTGCCACGCT	GCCGGCACCG	GCGGAAAGTG	GGGGCGGACC	CCTTACTCGA	2700
CCGTCACCGA	TTTTGCCAGG	TTCCGCGGCT	GGTCAATGTC	AGTCCCyTTG	AGCAGGGCAA	2760
TGTGGTATGC	CAACAGCTGC	AGCGGTACGG	CGTAAAAAAT	CGGCGCGGTA	AGGGGAGATA	2820
CCGAAGtACG	GTGACTATCT	GACTGCACGC	CCCTTCCGGC	GCGTCCGCCT	CGGGCGTGCA	2880
TACCGGGCCA	AAACGCTCCG	GCACGTCCGT	AAAGATGTAG	AGCATCCCGC	CGCGCGCGCG	2940
AACTTCCTCG	ATGTTTGAGG	CCATTTTTTC	AAACAGGACG	CCAGGTGACG	CCGGCGCGAT	3000
TGCAACCACC	GGCATCTGCG	CGTCCACTAA	TGCAAGGGGC	CCATGCTTTA	GCTCCCCCGC	3060
TGCGTATGCT	TCGGCATGGA	TGTACGAAAT	TTCTTTTACG	TTGAGCGCCG	ATTCAATTGC	3120
AATCGGATAC	AATTCCCCAC	GCCCCAAAAA	GAGCgCATGC	TGCGCATGCA	CAAAATGCCG	3180
CGCGCACCGc	GCAACGTCTG	CCTCACACTC	AAGCACGTGC	TCCACATCCT	GAGGCAGTCG	3240
CTGGAGCGCC	GCAGAGAGCG	CGTCCTCGGG	CTCtTGCGTG	AGTATCTTTT	TTGCCTGCGC	3300
AATCATGCGG	GTGAGCACGA	GCAAGCACAC	CAGCTGGGTG	GtAAAAGAtT	CGTTGAAGCA	3360
ACCCCTATTT	CTGACCCCGC	GTGGGTGAGC	AGCAtGCGTC	CGACTCACGC	ACCAACGTGG	3420

663

AACGTGCCCC GTTGCAAATG GCAATCGCAC AGAGATACCC TTGCGTTTTT GCCAGGCGCA	3480
GTGCGGCAAT GGTGTCAGCC GTTCTCTCCG ACTGAGAAAT CGTCAGTACT ATTTACGCG	3540
CGTGACGAC GCTCGTGCGA TAAGGTACTC TGAGGCAATC TCCACCTGAC ATCCCACCCC	3600
TGCAAATGCC TCAAACCAGT AACGCGCCAC TAACCTGCA TGGTACGAGG TACCACACGC	3660
GATAATGCGC ACCCGTGTTA TCCGTCTAAA CAGCCGCTCA AACGTCTTAC ACGAGGTACC	3720
GTCCAAGACC CGGTCTCTCC CGAACGTCCG CACCTGTGCG CGAGAAGACG AAGAAAACGA	3780
CATATAGGCA TTCAGCGTAT GCCGTATAGC GTGTGGCTGC TGCCATATTT CTTGATGCaT	3840
ATGGTGACGG TCGGTACCCT TATCCTGCGT ACAAAGCTGC ATCTGATACG TAACAACAGG	3900
ACGCGCCACA ACGTTTCCCT GCGCGTCGTG GACGCACACG CTATCTCGGT GGACGTCTGC	3960
GATGTCTCCT TCCTCAAGAT ACAAAAAACG CTGCGTAACA TGCGCAAGcG CAAGsgGGTC	4020
TGACGTAACA AAATTTTCCC CACAGCCGAG TCCTACCGCC AACGGACTGC CAGAACGCGC	4080
AgCAATCAAC CGCCCAGGAG ATGCAGCGTC CATGCAAAGT AACCCGTAGt ACCCCGAACC	4140
TGCGTCAACA CTTTTTTTAC CGCAAGCAGG AGGTGCGCCG TGTACCGCAA CTCCCAGTGC	4200
AAAAGATGCG CGAGCACCTC GCTATCAGTT TGTGAATGAA AAAAATAGCC ACGGGTCACT	4260
AGCATTTTAC GCAAAGACCG ATGGTTTTCA ACAATACCGT TGTGAACTAT CGCAACGGAT	4320
TCAGAACAAT GCGGATGCGC ATTGCTGCA CACGCTTGC CGTGCGTTGC CCACCGGGTG	4380
TGCGCAATGC CCATGGTCCC GCAAAGAGGA CTCTGACCTA ATAGCGCGCA GAGCGACTGA	4440
ACACGACCCT CACAGCGTAA AAGGCGGAGc GCACAGTCCG AGCCAACGAC AGCGATCCCT	4500
GCAGAATCAT ACCCGCGGTA TTCAAGACGA CGCAGCCCCT CAAGCAAGAG ACCTGAGACA	4560
TCACGCCCCG CCACCATCCC AACGATTCCA CACATAGACG CCTTTTCAGT GCAAAAGCAC	4620
ACGGGAGAAC GTTAAACTCA AACCACAGA ACACACGCAC GCGTAGGAAC CATCTGACT	4680
CAACCAAGCC ACGAGCCGCC TCGCAGGCTA CGGTCCAGCG CACCAACAGG GAGACTCACC	4740
ACCTCCCCCA AGGGGAGACC CGACGAACGA GCAAGGTAAC CCACAGGTCA CAGGCGATCC	4800
CATGCCCATC CGTTGCCTTG CTGCACATCG CTCACTTTTT CGAAGCTGAA TCTGGGAGTA	4860
TTTCCTGTAA CTCTATCTCA AAAACTAGGA GCGCACCTGG AGGGATAACC CCCTCGATAC	4920
CACGCTCCCC ATACCCCAAG GAAGAAGGCA CATAAAACCG ATAGGTAGAA CCCACCGGCA	4980
TCAGCTTTAA GCCCTCAGAT ACCCCAGGCA CCATACCATC CACCGGAAAC TCCGCAGGCT	5040
TATCTCGAGA GGCATCAAAC ACCGTTCCAT CAAGCAGCGT CCCCTTGATC TGAGTGCGCA	5100
CCCTCTGAcC GCCTGCGGCT TTGGACCATC TGCAGCCTTT ACCACCTCGT ACTGCAACCC	5160

664

AGAGGAAGTT	ACCTGCACAC	CTGGCTTCTT	CGCATTCTCT	TCAAGAAAGG	CCTTTGCCTC	5220
CTGCGAATTC	TTCTCTACCT	CTTTTTGCGG	ATATGCCTCG	AACGCACGCT	GTAGCACGTC	5280
CTGCGCATCC	GCAAGTGCCT	GCTTATCCTT	GTCTGCACTG	ACTGTCTTCT	TTAGACCCTT	5340
CCACACCTGA	CCCAGGTCAA	CGTCTAACTT	CGAATCCTGC	AGCGTCACCC	CCATGAGAAC	5400
CCCAAAGGCA	TACCCACAC	TCTTCTTTGA	AAGCGGCGTC	TTCTGcCGCT	CCTGCTCCTG	5460
CACCTTTTCG	GGATCGAGCT	GATCAGCAGT	CAGCGCCTTC	TTATCCGCAG	CCTCCCCGGC	5520
AGAGGACACC	CCCTCAGCAC	CCTTCCGACA	GGAAAAATA	CTCATACCCG	CAAGGAGCAG	5580
AAGCGCAAAA	GAACACACCC	CTGcAGCTTC	TTTTTTCAAA	ATCACCGCTC	CTTTTGCGCG	5640
CTCATCCGCG	CCGCCCCGAG	GCGACCAGCC	TACCCCATCC	GTACTTCACA	CGTCAAGGAG	5700
ATAGCTAATG	CCCCGATCCT	TCCTTGAGCC	ACACCCACTT	TTCAGGCATC	GTACGCACCA	5760
TGAACCTCTA	TTTGATTGG	GCTGCAGCTG	CTATACCCGA	AACCCGGCTT	ATCCTACGCG	5820
AAACGCAACA	GGCCTGTACT	CTCTTTGCCA	ACCCTTCTGC	TGTGCATTGC	TTGGGAAACG	5880
ATGCGcGCGA	TGCGCTCGAA	CGAGCACGAC	ACACGTGTGC	CCAGAGCTTA	GGCATCAATC	5940
CAGAACGCCT	TATATTCACT	TCAGGCGGGA	GCGAAGCAAA	TCAACTTGCC	CTCCTTTCTG	6000
TCCTTACTCG	TCTTCCTCAC	GCAGAAATCA	GCGTCAGTAT	GCTAGAGCAC	GCGTCGGTCA	6060
CTGCACTTTT	GCCCCGGCTT	GAGCGGTTGC	AGGTATCCGT	ACGCCACATC	CCCGTCAATG	6120
CCCGCGGTTT	CATTACCCCT	GAGGCTGTAC	GTGCAACGCT	CAGTCCCCGT	ACCACGCTAG	6180
TGTGCGTGAG	CGCCGTACAT	AGTGAAACCG	GCGCCATCCA	GCCGCTCCCT	GCTATTGCGC	6240
ACGTGCTTGC	ACATACAGGC	ACACGCGGAC	GCTCTATCCA	GCTCCACGTA	GACGCCGCAC	6300
AGGCCTTTGG	GAAAATACCG	CTCAATCTGT	ATATGGACCT	TCCGCGCATA	GAGGAACATG	6360
CACAGGAAAA	CAACGCGCCA	CAGACACCAC	CGGGCTACCC	CGCACCCACT	GCACAACGCG	6420
CGCTTACCTA	CTCGGTAGCA	ATCAGTGGCC	ACAAAATAGG	CGCACCACGG	GGTATTGGGC	6480
TACTGTGCGC	ACACCGTTCA	TTTACCCCTT	TTGTCTTGGG	AGGCGGACAG	GAAAAAGAGC	6540
GCCGCCCCGG	AACTGAGAAC	CTTGcAGGTG	CGCTCGCGCT	CGCCGCTTGC	GTGCGCGAAG	6600
GCGCCTTCTT	CCGTACTCTA	CATACCACTC	CGGAAGGCCC	TACACCGCAT	ACGAAGCCCA	6660
CAGCTCCTGC	AGGGTTACGC	AGTGTcCGAG	GCGGTACGTG	CGCCTTTGTG	CGTGCACTCA	6720
GCGATTTACC	GCGGGTGCAA	CTAGTCCCTG	CAACGCGCAA	AGAAGACGAA	GCGCACTTCT	6780
CTCCCTACAT	CGTCTGCTGT	GCGGTACAAG	ACGCCAGCGG	cGAGGCATTA	GTACGTGCAT	6840
TCTCAGACGC	AGGTGTGTGC	ATCTCCACCG	GTTCTGCCTG	CTCGACAAAG	AAAGGTGGCG	6900

665

TTTCAACACG	CCTTCTGCGT	GCACTCGGGG	TAGAATcCCg	cGCAAgCGCG	GCGtGCTGCG	6960
TTTCTCTTTT	GGTCCACACA	CCACCGCCGA	AGATCTCGAT	CGGGTCTTAA	CGCTTTTCCG	7020
TACCCTGCTG	CAAAAACTAT	GACCGCTCCA	CACAGAAAGG	GTACACGCAC	AGGAAGCACT	7080
CAAGCGCCGC	ACACAACCCC	TTATTTTGTC	AAAATTTTTA	ACGGATTTAC	CACCGACCCG	7140
TTCTTAAATA	CTGAAAAATG	CAAAATGCGGA	CCAGTTGCC	GACCGCTAGC	CCCCACGCGC	7200
CCAATGGTCG	TCCCCTGGAC	TACCCGCGCC	CCACGCCCTA	CCATCACCGA	ACTTAAATGC	7260
CCATACATGG	TTTGGTATCC	ACCGCCGTGC	ACGATGATCA	GGTAATTCCC	GTAAATTCTG	7320
CTATATCCAA	TTTCTGCCAC	TTTCCCATCG	AGCGTTGCTT	TCACCTGCGT	CCCATAGGGT	7380
GCGGCTAGGT	CAATCCCATT	GTGAAAGCTC	CTTTTGCCCTG	AAAAGGGATC	TGAGCGGTAC	7440
CCAAACCCAG	AGGTGCGCCG	CCCGCGAATT	GGATACATGA	ATAACTCCCC	CAACACCTTC	7500
CTCAAAATCAA	AAGCAGATAA	TTTTGCACCC	GGAATAAACA	AACGCTGTCC	AACTGTTAAT	7560
GCACGACTGA	CTAAATCATT	CGCATCCAGC	AACGTATTCA	GGGGCAAACG	AAAGAGACTG	7620
GCAATTGCAC	TAAGCGACTG	CCCCTTTTGT	ACCGTGTGCA	TGAGTCCATC	CATGGACGGA	7680
ATAGTAATTT	GATCCCCTAC	CGATAGTCTG	CGCGCGTTTG	AAATTCCGTT	CACCGACAGC	7740
AGCGTCCCCA	TATGCTTGAG	TCCTGcGCgC	ACAAtTGGcA	CTAATAGTAT	CTCCCTTACG	7800
TACGGTGATC	GTGCGGTAGc	TCACCGTCGC	AAGCTGCGTA	TCCAACGCCT	CTGCAAGCGC	7860
GGCAGGTTTC	GCGCCGCCCT	CGCGCGTTTC	TACCTCCTCT	GCACGAAAAA	CCCCACGACG	7920
CAGCGCATGC	GCCAGGTGCT	GTCTGTTTCA	AAACGCACCA	GCGCAAgCCT	TCTGCCACCG	7980
GTAAAGTGCA	mCGCCACGG	GATACACAGC	ACCATGAGCA	CAAAGAGCAG	CGCGCAAGCC	8040
AACGCCGCAC	ACAACGGCAC	ACAAGAAGCA	TCCTGCAAAG	AACGTACAGG	CACCGAAAAG	8100
GAAGGAAAAG	AAAAACGAGG	CACCcGGTGC	GCGCAAGCGG	CGTGCGTGCA	CTCTTTTCTC	8160
TCCGGAAAAA	ACGCATCCCC	CCTATACaCT	CctGCGGCTC	ACCCGAACAG	AACGGTTTGA	8220
AATACTGCTG	AGCAACCCCG	AAGCGTTGAG	CGCCTGCGCA	CGTATCAAAC	GCGCTTCTGC	8280
ACGTGTGCTC	CATTTTGCGT	AGCGCGCGCg	TAAGCCCCGC	CCTCCTCCGA	GTCTCCCACT	8340
GACTCGGCTG	CCTGACTCAG	GAATATCGAG	GGTATCAGGA	CTTTCATGAA	ACGAAATTAT	8400
CTCTTCCTCA	AGGGGAAAAC	GGGGAACAAG	ACGGTTACGC	GTACGAGCGC	GCGCACCCCC	8460
GCTATCGGAA	AACGCACTAC	TTGAAAGAAC	TGCGCGGCGC	ACTTCTGCAG	GGCTCGGACA	8520
CACGCTGAAC	GGCTCACATC	CCCGCGCATG	ATCCGGAAct	AAGTCCGCAC	CCGTGTACGT	8580
AATCACGTCC	ATAACGGGCG	GTATCGGAAC	ATTTATTCCA	GCGGTtGAGC	ATTTGCCTG	8640

666

CAGCgCCACA	GGcGGCGGaG	TCCCCAGCAG	CGTGCCACTT	GTTTTTGAAC	CGCACGGCGC	8700
ACGCCCCGTA	TAAAGAACAC	ACCTCGCCGG	GCGCAACCGC	CGAGGGTGTC	TTTCCCGATA	8760
AAGCAGAGTT	CAGTGAAGAA	AATGAAAATC	GTAAACCTGC	CGGTTTAATT	GCAAAAGCTT	8820
CGTTGCACGC	TCGATACCTT	CTCGCGCCGG	CTCAAAGCTA	CCGGCACGCT	GCAGGGTGCG	8880
GCGCCATTCTG	GCAATCGCTT	CCTCATAGTG	cTGCGCATCA	TAGTGACGCA	GCCCCCGCAG	8940
gTATGAAGTG	TATACTTCCT	TTTCCAAGTG	CTTGCCTCGG	TCTCGATTAA	AAAATCCTGC	9000
AATTCGCGAG	GAAATGACAT	GCTCATCCTT	GTCTGACTCA	TAGGTGTATG	TGAGATCCAC	9060
ACGCACCCAC	GTACTTTTGA	ATTCTACTCC	TGCACTTGCA	CGGATATCTG	AGGCGAGCCC	9120
GGTGAGAAAC	ACATTTGAGC	CAAACGCAAC	GTA CTGCACC	GGCAGGAGCA	GGAaCGctAC	9180
GCCGTATCTG	AATCTATTGT	TGTCTGCAAA	TTCTTGACAG	TTGTACTTCC	ACTCAATCCC	9240
CGTGCCAAAG	AGAAACCACC	GTATCGGTTG	ATACGCACAT	GCGAGAATAA	AACTCGAGTT	9300
TGTAGCGTGC	ACCGTCCTGC	CGCCACTCAT	GCTAGAACCG	CTGTTGGATG	CGTCCACCTC	9360
AAcTGAAAGT	CCAACGTTTT	TGACAGTACC	GCCCACCCAC	AGATTCCGGCT	CATGGGAACC	9420
AAAATTCTTG	GCCACCGACC	ACGTCCCTTG	CAGACCGATG	TCTGCGGTCA	CCACCACGTG	9480
CTTCTTACCC	CCCTGGTTTT	TTTTATTCTT	CTCCCCGCGG	GCTGAAGAAT	CGCGGTAGCC	9540
AACTTTACAG	TTGGTTCCCA	CACTGATGCC	TTTAAAACGA	TAGGCAGACA	AAAAACGGTG	9600
CGCCACATTG	AAAATGGCAA	CGCCGCCTAC	TGCCTTTCCC	TCCATTGTCA	GGTAGGGATA	9660
CTGAACACTC	GCAGAAAAAC	CGTAGCCGGT	CCGTCCTATG	CTGTGCACAA	GTGCAATCGT	9720
ATCTGTGTGC	GATTGATTAA	CCCGGGCAAA	GTGAAACCCT	CCCACCAGGA	GATAGGGGAA	9780
CGCGGCACTC	CCTGCTGCAT	TCGCCTCAAA	AAAACCTTGA	TCGTCTGCTA	AAGCGGTAAA	9840
TGCCAAGCCG	AGCATTTTCAT	ATCTGCCGCC	TGTCCTCAGC	GAGAGGGCAC	GACGGCCAC	9900
TCCCTTCTGC	TTCTCGGATG	TCTTTGCTGC	CATTGCAACA	ACCGGCGTCA	CGGACGTTCC	9960
AGACACGGCA	CGCCGCACct	GCGGTGCGCC	GGCACTCGTG	CGCGAACTTC	CCCCAGAACT	10020
TCACCCCTT	GCGAAGACCA	CGCGCCCAAA	GAAGCTGTCC	GCGCAAAAAG	CGGGGCAAGA	10080
CACAAGGCAG	ACATCCCAAT	ACGCATCCCC	AGAACCCGAA	CTGATAGAAA	gCTGCGGCAC	10140
CGCGCACCGC	AGCACATCCG	CACGCGCCAC	CGCTTGAACA	AGCTCTTCTC	CGCCTCATCC	10200
GTACCACTAG	ACTACCTCAC	CGCATCCGCT	CCGTGCAACC	CTTGCGcACA	GTCCCTTCCC	10260
TTTCCCAyTA	CtGCGCCCTT	ACCAAGTCCC	CGATTACGTC	AGAGAATGGG	GCAAAaGCGC	10320
AcTCCAcGTA	cGAAGGGCTA	CGGCyTCTTG	CAGTGCGCCA	CcTGTAAGCG	CGCAACACcT	10380

TCTATATCTG	CAaTTGTACG	CGCTATTTTT	AATACCGCAT	GTCTCCGCG	CCCCGATAGC	10440
TGCTCCTTTC	CTACTGCACG	ATGGAAGTCC	CGCGCAGCAT	CaTCTGTCAA	CATACACCAA	10500
CGCTGCACAT	TCTCAGGAGA	AAGACGCGCA	TTCCGGTATC	GAATCCAATC	TTCCACCGTT	10560
GATGACCGCC	CGTTAATCGG	CGCACATAGA	CAGCTCCCCT	GCCGTTCCcCA	cTGCGCTTCA	10620
AGTGCGCACG	CAACCGTCTT	GcgCAAGCGC	GCGGTACAGC	ATGCCGGTTC	GGACAGCAGC	10680
GTATGCGAAG	CAGGcGGCAG	CACCTCCACC	CGCAAATCAA	CGCGATCTAA	AAGAGGCGCA	10740
GTcAGctTGC	GCCAATACCG	CTCCAcCGCC	TGAGGCGCAC	AGGTGCATAC	CTTGTGCTGC	10800
ACCCCAAAAT	TCCCACATGC	ACACGGATTG	ACTGCCAAAA	GCAACTGAAA	CCGTGCAGGA	10860
TACGTGCTGC	TTTTTCCTGC	GCGACTGACT	GTTATCTGCC	CTGTCTCAAG	CGGTGTGCGC	10920
AscgtTCTCTA	ATACCGGACG	CTTAAATTGC	GTGCGCTCAT	CTAAGAAGAG	CACTCCCCCA	10980
TGCGCAAGAG	AAATTTCTCC	CGGAAGACAG	GTGCTGCAC	CCCCAATTAT	TCCTTCTGCG	11040
CTCGCACTCG	AGTGCGGCGT	GCGACACGGC	GGACGCGcCAT	GAGCGGGTCC	TGCTCAGCAC	11100
CCTTTGGGAG	GAGGCCTGCA	ATACTGTGTA	CTCTTGTAC	CTCAAGTGCC	GTACGTGCAT	11160
CCAAGTCTGG	CAGAAGAAGC	GCAAACCTAC	TCAACGAAAG	CGTCTTGCCA	CACCCAGGCG	11220
CCCCGTACGC	AATAAGATGA	TGTCCTCCAG	CAGCTGCAAT	CTGTAGTGCC	CGGATCAGTT	11280
TTCTCTGTCC	CCGCACGTCT	TCAAACCCAC	CGGTAACCCC	CAACGCAGCG	TGTGGCCAGT	11340
GCTGCACCGG	GCGTTCTTGC	CCTGTTCCCC	CGGCAGAATC	AGATGCGTCT	CCCCTGGACC	11400
TGCCAACC GA	AAATAGAAAT	GGCGATACAC	CCGGCGCTGT	CCCCTCAGGG	CGCGCGCCTG	11460
TCTCTCCAC	CGCACCCGGA	CACCGCTTTG	GGAACAACGC	CATAATTGCC	CCTGCATCCA	11520
TACCCGCGTC	CTGGTGACA	GACGCACCTG	TATCTGCCGG	AAgGTGCACG	CGATGCGCGG	11580
TGTCTTCCAC	AGAAACCTGC	TTCCCCCTCC	ACAAGAGAAC	TGAGTTTGAC	TGACCCACC	11640
CAGGAGCGGA	CTGCTCATGC	GGCGCATCCT	GCGGTTCTAC	AGCTAGCTGC	TGGCAGGCAA	11700
CAAGAGCTGC	ACGAAGTTCT	TGCACGGCAA	AAACGCGCAC	TCCAGGCGTG	ATACGCGCTT	11760
CTGCCTCATT	TTCTTTTGGC	ACGATGTAAT	CGTAAATGTG	CGCGCTTAAT	CtGCGGCAAC	11820
TGCTGCAAgC	GTGCCACGCA	CTGGCCGGAT	ACGTCTTGAA	AGCTCAAGCT	CTCCGAGTAC	11880
CATCACACGG	CGAACCTCGC	GTGcgCATCC	GCGCGCACCA	CCTGTCAGTT	CCGGCGTTTC	11940
CTCTGCAGAG	CTCGCGTGTA	CCTGGGCGCG	GAgcACTGCC	AATGCGATGG	GCAGGTCAAA	12000
CGCACTCCCT	TCCTTTTTTCA	GATCTGCAGG	GCTCAGATTG	ATGAGAATGC	GCTCCTGAGG	12060
AAAGGGAAGC	GCTGCATTGC	GGATAGCAGC	GCGGATCCGC	TCCTTCGCTT	CTTTAACCGC	12120

AGACCCTGGC AGTCCCACAA TATCCACTAC CGGCAGTCCC CTCCGAAGAT CCACTTCCAC	12180
CTTTATGACC TCGCCTTCAT ATCCAAAGGC GGAAAAGCTC ATAATCTGCA CCGTTTACCT	12240
CCCATGCGAT GCGCAGGACG CAGTGCATA CACGCGTGTA CTGTGCATGG AGCTGGGCGC	12300
TACACCTGCC ACCCTGCCTA CGGTAGCCGC CGCATAACCG ATACCCATAA CGATAGCCGA	12360
TCAACCTGCA TAGCCAACGC ACACCCGGAC GTACCTACCA AGGAACGTAA CAAAAAAGGC	12420
GAAAAAAACC TCAAGTCCTT TTCCGTTTTT CCGAAAATAG GATTGGCCCG TTTCTGCTCT	12480
CGTGCGGTGC AsGGGCCCCCT GCAGGGCACG GACGTCTTGC AGGAATGTCA GAGATTCCAC	12540
GGAGGAATGC ATGATTATCA ATCACAACAT GAGTGCATG TTCGCGCAAC GCACACTCGG	12600
GCACACCAAT GTCCAGGTTG GAAAGGGCAT CGAGAAGCTT TCATCCGGcT ACCGCATCAA	12660
CCGCGCAGGG GATGACGCTT CTGGTTTGGC TGTCTCAGAA AAAATGCGCA GCCAAATCCG	12720
CGGCCTCAAC CAGGCATCCA CCAATGCCTC AAACGGTGTC AACTTCATTC AGGTTACCGA	12780
AGCCTATCTG CAAGAAACCA CCGACATCAT GCAGCGTATC CGAGAGCTTG CAATTCAAGC	12840
GGCAAACGGC ATCTACTCTG CTGAAGACCG CATGCAGATC CAGGTGGAAG TTTCGCAGCT	12900
TGTGGCAGAG GTAGACCgCA TCGCTAGTTC TGCCCACTTC AACGGCATGA ACTTGCTCAC	12960
GGGCCGCTTC TCCCGCACTG AAGGTGAGAA CGTCATCGGT GGCTCCATGT GGTTTCACAT	13020
CGGCGCTAAC ATGGACCAGC cATGCGCGTG TACATCGGCA CTATGACTGC GGTGGCGCTG	13080
GGCGTACGAA ACGGCGTGGA TGAGTCAATC ATGTCCATTG AGACTGCAGA CTCGGCCAAC	13140
AAGAGCATCG GCACCATCGA TGCTGCTTTG AAGAGAATCA ACAAGCAGCG TGCGGATCTC	13200
GGAGGCTACC AGAACCGTAT GGAGTACACA GTTGTCGGTC TTGACATCGC TGCGGAGAAC	13260
CTGcAGGcAG CTGAGTCTCG CATCAGGGAC GCAAACATCG CAAAGCAAAT GGTGAATAC	13320
ACTAAGAATC AGGTGCTCAC CCAGTCTGGC ACTGCAATGc TTGCGCAGGC GAACACCAGC	13380
GCGCAGTCGA TTCTCTCAAT TcCCCGTAA AGcCcTACGc CGCGTGCGCT CTTGTCCAAA	13440
AAGGGCAAGA GGAGTACACT GGGcCACAGG GGCTGCCCTG TGGTGCCCTT CTAGAATGAT	13500
CTTTGAAAAG ATTTCTCCcT TGCAGGCCTT CGTGTGGGCG GTTCTGAGGC TTTTCTAAA	13560
AAGCTTCAGA ACCGTTTTTC GTGGCGCGGT GCGTCAGGG TGCGGCGTGC TCGCCTGCGT	13620
CCGTGCATAC GGTTTTCCAC CCTATGGATC AAAGGAATAG AGGTGGAAGG ACTTCAGGGA	13680
GGGTCAATG ATTATCAATC ACAACATGAG TGCGATGTTT GCGCAACGCC AGGGAGGCAT	13740
CAACGGACTT GCAATTGCTA AGAACATTGA AAAGCTTTTCG TCTGGcTACC GCATTAACCG	13800
TGCAGGAGAT GATGCTTCTG GTTTGGCTGT CTCAGAAAAA ATGCGTAgcC AAATCCGCGG	13860

CCTCAACCAG	GCAGGGCAAA	ATATCCAAAA	CGGTATATCC	TTCATTCAGG	CTACCGAAGa	13920
TACTTGGCGG	AGACAACTGA	AATCGTCCAG	CGCCTGAGGG	AGCTTGCAAT	CCAGGCGGCA	13980
AACGGCATCT	ACTCCGCCGA	GGATCGCATG	CAGATCCAGG	TGGAAGTTTC	ACAGCTTGTC	14040
GACGAGGTAG	ACCGAATCGC	AAGCCAGGCC	CAGTTTAAAG	GCATGAACTT	GCTCACGGGC	14100
CGCTTCTCCC	GcGAGTCTGc	CCTTGGGCCC	aTGcAGCTGc	ACGTCGGTGC	GAACATGGAC	14160
CAGAATGAGA	AAATATTTCAT	TAACACCATG	ACGGCAAGTG	CTCTGGGCTT	TTTCTCCGAT	14220
GAAGGGACAG	ACGGCAGTCG	TTCCATCAGC	ATTGCGACCG	TCGACGGGGC	GAACAAGGTC	14280
ATCGGTACGC	TTGATAGCGC	GCTCAAGGAG	ATTAACAAGC	AACGTGCGGA	TTTGGGTGCC	14340
TACCAGAATC	GATTTGAAAC	CGCGTATCaG	GGAnATCcTA	TCGCGGCGGA	AAATCTGCAG	14400
GCAGCCGAGT	CTCGCATCAG	GGACGCGGAC	CTTGCGCAgC	AGATGGTCGA	TTACACGAAG	14460
AACCAGATTC	TCGAGCAGTC	GACTATGGCA	ATGCTCGCTC	AAGCAAATAC	ACAGCCACAG	14520
GCAGTGcTCC	GCTTGATGCA	GTAAGCGCAT	ATCGCGACGG	TATATTTTTA	AACGTTCAGC	14580
GTCTTCATTA	GAGAGTTTCG	GATGTCATCT	CTTGTAAGC	CCCATGAGGG	AAAGAGGAGC	14640
CGCATGCCTC	TTTCCCTTTT	CTTTCTCTT	TATCTTTCTG	TCATCACACC	cTGCGGTTGC	14700
CATTACGGCG	TAAACGCTGG	GGATGTACTT	TGTATTTGTT	AAGTTTGCGT	ATCTGTAAGC	14760
CGACAAGCCG	CGCGTGGGGT	TTTTTTGAAG	GGAACTCGGC	TGGAGTCTTG	ATCCACTCTC	14820
CGCAGCTTTC	GAGGAGTCAT	TGTGTCTGAT	GTCCGCATCC	CCGGAGTAGG	GGCCGGTAAG	14880
TACGATAACC	TCATCCAGTC	GCTTATGAAA	AAGGAGCGCA	TTCTCGGGA	CAACGCTGCG	14940
GCAAAGGTGA	AGGTTTcGAG	GTTCAGAACA	ACGCGCTCAA	GGACGTGGAG	CGGTATGCGC	15000
GCGATTTGCG	TGACGCCGTC	AAAGGACTCT	wTTCCTTCAA	cAACCCTTTC	GCAGaGAAGG	15060
AAGCyCATTC	TAGCAACGAG	CGTGCGTTCA	CCGTTCGATG	TACTCGAGAC	GCTGCCGAGC	15120
AGAAATCATAC	AcTGCGCGTC	AAAGACATCG	CACAAGGGGA	TGCGTTTCTC	TCAGACCCCC	15180
TCCCTGAGGA	TTTTCGCGTT	CCAGCGGGA	CGTATACGTT	CTGTATTGGA	GAAAAAAAAA	15240
TATGCGTGTC	GTGGAAAGGC	GGGCaTATC	GTGATTTTAT	AsTGCCGTCA	ACAAGCAGGG	15300
CAAAGACTCA	CTCACCCTCT	CAGAGATAAA	AACGAGCGGT	GCGAGCCGTG	CGCTCCTGTT	15360
TCGCTCAGAA	TTAACGGGAA	AGAGCAGTCG	TC'TTTCCTTT	GAAnGcaCTG	CGCTGGACCT	15420
TGCACTGCGC	cTGCGCGTCG	TGCAGGAAGC	ACGTTCAGAC	GTTTTTACAC	AGGATGTACT	15480
CAGTGTGGA	CTTGAAAAC	ACGCGCGTTT	GGATTTTCCC	CACCTCTGTC	GCGCGCAGcA	15540
GGGcTTACGC	TGGAGTTTGT	CGCGTCTCTG	GAAGGGGCAT	CTATTGCAAA	CGAAGAGTcG	15600

cGTGCGCACA	CGCCCGCACA	GGGAGGCGCT	CCCACGTCTT	CCCACGGAAA	TACGGCGTCC	15660
GCTGCACATA	ATCAGGACGG	AGCAGCTGCT	GTGCGCCCTA	CTGAACCGGC	AAACGGCGCT	15720
CCTGTACAGG	AAGAAACCAG	TTCAGTGTTC	TTTGAGGGGG	TCACAGTAAA	GAACGAGGCT	15780
TCCCAGGGAG	ATCTGCCTAC	CACGGACGGC	TTGGA AAAAT	ACCCAGCTGT	CGACGACAAA	15840
GGAGAcAATC	CGCGCGCaCC	TGGAGAGTCG	CAGGGCACGG	CCACCCACGA	AGGTTCAGGG	15900
TCGTCCACAG	ACAACGCGGA	TGACACACGC	TCAACTGGTG	CCTTGGCAGG	ATCGGGTAAG	15960
CTTGCACTTG	AGTCTCTGCA	GGGCCACGCG	CTTCCTTTAC	CACCGCTGGT	GCTTACACAG	16020
AACGCACCGC	AGATGGTATC	CATTCTTTTG	CGCGAGTACG	GGGATGTTTCG	CGCGCTCATA	16080
CTGGATAACG	CGCAGGCGCG	AGGCGCACTG	ACACTGCGCG	CTATCCGTGT	GCGTGCCGAG	16140
GATGCACCAG	GTGGTTATGT	CCCCGTGAAC	CCTGCCTCTC	AAGCACAGGA	TGCAGCGTTT	16200
GATTTTCGATG	GGGTGCACGT	TACGCGCGGA	ACTAATTCTA	TCACCGACCT	TATCCCCGGC	16260
GTTACGCTTT	CGCTGCACGA	ACGTACAGAA	AAAACCGAAA	CGCTCTCTGT	CACCCCCGAC	16320
GTGAACGCCA	TGAAGAACGC	TATTATAGAA	TTCGTTGCTA	AGTACAATCG	ACTCATGGCA	16380
GAAATTAACA	TTGTCACCAG	TAACAAGTCA	GCCATTATCG	ACGAGCTTGC	GTATCTTACC	16440
CCCAGGAGAG	AAAAGAAAGA	GACAGAACAA	CTCGGCAGCC	TCCACGGGGA	TTCCACGCTT	16500
CTTATGCTGA	AAGACAGACT	GAGACGCAAT	ACCAGCAATG	CGTACCGCGC	CGGCGATGAC	16560
GGTGCATCGC	GGACACTTGC	ACACATCGGC	ATTTCCACAA	AAGCGCACGC	TTCGTCTGGC	16620
ATTAACACGG	CACAGcTACG	CGGTTATCTT	GAAATTGATG	AAGAAAAATT	ACATTCCAGT	16680
TTGAACGCAC	AAAAGGATCA	GGTGCGTGCT	CTTTTTGGGC	ACGATTTCAGA	TGGTGACCTC	16740
CTTGTGGACA	ATGGCGTTGC	ATTCACCCTA	ACAGAACTGC	TCAACCCTTA	TTTGGGACGA	16800
TCGGGTATTT	TTGCCATACG	GTCAAACGGC	GTTGACGAGC	GTATTAAATC	GACAGAAAAA	16860
CGCGTAGAAA	CGTACGACAA	GCAACTGGAA	AAGAAGGAAC	GGGAGCTGCG	ACACAAGTAT	16920
CACACCATGG	ATGGCGCGCT	TCGTTCTCTA	CAAAAGCAGT	CTGACGCAAT	TCAGAACTTC	16980
AACCAGTCTG	TTCGCAACAG	GAATTAGTGG	GAGTCTTAAT	GGACATTACG	ATTAACGGAC	17040
ATACACTGCA	GTATGTCATT	GAACATGAAA	AACTATTGG	GGAGGTTCTA	GGCGCGATAG	17100
AAGCTGCGTG	TAAAAAAGAA	AAACAAACGG	TATCGGCGGT	GACGGTCAAT	GGTAGGGAAC	17160
TGTCTGCTAA	TGAATTGGAT	ACACTTTTTT	GCCAATCCTT	GGATACCGAC	GTCACCCTTA	17220
ATCTTACCAC	TCTTTTCAGG	GGAGACGTGC	GTGCACTCTT	GCGTGAGATT	AGTACCACTC	17280
TCCTTGCACG	CACAGCTGCG	TTACAAGAAA	TCGCAGTAAA	CATGCATAGC	GGTAATCTTG	17340

671

CAGAgAgcTA	CGCTATGGTC	AGTGACTTTT	CTGCTCTCTT	GAAAAGTCCT	TATCACTGCT	17400
TTACTCTCTC	GGACATCGCT	GATTTGGATC	ATGGCCTGAG	AATTAAGGGA	AAAGCCCTGC	17460
ACGATTACCA	GCGCGAGATT	TCTCCCCTGC	TTAAGGGCTT	ACTAGAAGCA	ATGGAAGAAG	17520
GGGACAGCGT	TGCTGTCCGT	GATATTGCCG	AGTACGAGTT	GGCACCGGTT	GTTCCGGATT	17580
TAAGTGACGG	TATCTTGCAT	ATGGACATGG	GTGTACAATG	AAGTTTGACG	GA CTGATTCTG	17640
CAATCTCGAC	CACATTACGC	GAAAGGATAC	GTATCTCTAC	TACCGGGAGG	AGTTTTCTGC	17700
TGTTGCATGT	TACTCTCTCT	TCGGTCGAAT	TCATTCAAGG	AGGGTTGAGT	TTTCGGTAGA	17760
GACCaCTCCC	GTTGGGGAAA	AGAGCGTGCA	GGTAAAATTA	GTTGATGCAA	TTGATTATCC	17820
GCTCTTACCG	CTTGTAACAAG	CACTCAAGCG	TGTAGTGAGA	CTGTTGATCG	AGAAGAATCA	17880
GTTGCCGCGT	TAGATCTTGT	CCAGTTTTTT	TAAAAACGGT	AGACTCGCCG	CGGTGAGGTG	17940
CGTCAGTCGC	TCAGCGCAGG	ATACTGCgCG	GtGGGGCACG	GTAGTCGGAA	GGCTGCTTGA	18000
GGAAGGTTCC	GTAGTAGTCT	TGCAGGGGGC	GTTAGCGGCA	GGGAAAACCT	GTTTTGTAAA	18060
GGGGCTCGCT	CTGGGACTCG	GTATCCAAGA	GGAGATTACG	AGTCCTACCT	TCACACTGCT	18120
GGCAGTCTAC	CACGGcAGGc	tGACGCTCTA	TCATATGGAC	GTGTACCGGC	TCGCTTCCCT	18180
GGAAGACTTC	TTTGATATCG	GTGCGCAGGA	GTGCGTATAC	GGCACGGGAG	TCTGTGTCAT	18240
TGAATGGGGA	GAACGGGTCTG	CGTCAGAACT	GCCGGAGTAC	ACTGTTACCA	TCTCGTTGCG	18300
TGTGCTCGCA	GATGGTAACC	GAGAGATTAC	CGTAGCGTAs	CgCAGAGTGC	TTCTGTCTT	18360
GCAAAAAGGC	AAAGAGGGCG	GGGTGTATGA	ATATACTTGC	CATCAACACC	GTTGCGCATG	18420
CCCTCAACGT	TGCAGCTGAA	GGAGCACAAG	GCACCGCTGT	TGTGAGCATC	GAAGGTGCGC	18480
ATTGTTGCAT	ACAGCAACAG	CTCGTGCGTG	CGCTTGACGT	TGTCGTAAAA	CGCGCAGGAT	18540
TTCTGTACA	GGAAACACAA	ATCGTTGCCT	GTCTCGGGG	GCCTGGTTCA	TTTACCGGCT	18600
TGCGTACCGG	TTTTGCAGTT	GCAAAAGCCC	TACAGCTGGG	TGTCGGAGCC	CGTTTTATTG	18660
CCGTGCCTAC	GCTGCGCcTT	GCGGCACATC	CGTTCCGCGC	GTTACAGGA	CGGGTGTGT	18720
CCATAcTAGa	TGCAAAACGT	GGTCGTTTTT	TTTGGAAC TG	CTTTAAGTCA	GGAGAGCCGC	18780
TCTTTGAAGA	CTCTCACAAC	CACGCACAAG	AAATCGTAAA	AAAAGTGAC	ACACGGGTTC	18840
CATGCCTGGT	GTGCGGCACG	GGAACAGCAC	TTTTTAAAAG	TGTAATGGAA	AGCCAGGACA	18900
ACACGGTTCC	TTTCATGTAC	GTAGAAACTG	ACGCTCATGA	AGGAGCAAAG	ACACTCCTTG	18960
CTTTGGTAAA	AGTGCTCAAT	CACAGCGCCG	CCACTCCGGG	GGAGCGCGGA	GCGCCGAGT	19020
ACACAACACG	AACTTACGCA	AAAGGAAGCT	AATACTATGG	GCAATTCAGA	TATCTGTTCT	19080

GACATTAATG ATATCGAAGA ACTTCAATCT GAAGAAGGTG ATGCACCTAT ACGAGAAAAT	19140
GCCAATCCAA TCAGAGAGGA TTACAATTTT ATACGTGAAC AAAACCCCAT TCTCGGCTCA	19200
GGACTTGATC TTATCGGAAG TGCAAAACTG CCCATGCTCT TTTTAGACAG CAATCTGCTG	19260
ATTGAATATA TCAGCGCCGA AGCGAATTCT CTTTTTAGAG GTTATTACCA TCTGGAGAGA	19320
AAGCCGTTCT TTAATGTGTT TGGGAATATC CTCAGCCGTA AGGAACTTGA AGACTTTTTC	19380
TCTTGTGTCC GATCTCACTC TAAAGGATTT ACCTGGAGAG GCACGATGGC CCATAAAATT	19440
CGTGCAAAAA GAGCGCTATA CACGCGCACA AGTTTTATCC CGCTTTCCAT CAGCGACGCC	19500
CAACCTTCTG GATATATCGT TCTTTTCGAA GACATTTTCTG ATATGTACTC GCAGCAGATC	19560
AGTAATATGC TGAGTAGTTT GCTACAAGCG TCAAAGCTTA AAGACAATGA AACAGGGTTG	19620
CACTGCGAGC GCGTTAATCA CTATTGCAGA CTCATTGCAG AATACCTGTA TGACATCAAC	19680
TTATACCCCC AAGTCGATAC GGACTTTGTA GAGAATATCG CCTTCTTGC AGCTATGCAC	19740
GACGTGGGGA AAATTGGTAT TCCCGACTAC GTTTTGAAAA AACGTGGTGG ATTAAACGAA	19800
TTAGAGTGGG AGCTCATGAA GGAGCATACT ATCAACGGTG CGCTCATTCT TTCTTCTTAC	19860
CCTGACCCTA TGGCGAAGGA AATAGCGCTC AGTCATCAG AGCGCTGGGA CGGCACAGGA	19920
TACCCCTTCA AATTGGAAGG AGAGATGATA CCGCTTTCTG CACGTATTAC GAGCATCGCC	19980
GATGTATATG ATGCATTGCG TATGGAACGC TCTTACAAAA AGGGATTTTC TCATGAACAA	20040
ACTACACACA TGATTTTAGA ACAGTCTGGA CAAAGCTTTG aCCCCATTTT GGCACGTGTA	20100
TTTCAGAAAA TACATACAAA GTTCAACGAC GTGTGGGACA gCTACAGGAC TGAGCATCCT	20160
CAATCCTAGT CAGAGATAAG GTTTTCTTCG GTGTCAAATT GCTGCAAGGA GCTCATAACCA	20220
GTCTCTGTCT GCATGCGGGA AATGAGAGCA AACAGGTACC GTGCGGTGTA AGCGCTCAGG	20280
GTGTATGCGT GCACGCTCTG TGCATCCCAC AGAGTCCACT CTTGGTGAGC AGCAGGCTGA	20340
AGACGAAACC GTATAATCTT TCCGTCTCCC CGGTGAATGA CAATTGATTC TTTCCATTGA	20400
GTCCGTGTAG GTCCAACATC AACATAAGAG AAACGTGCGA AAAACTGCTC GACCTCTTTA	20460
AACACTACAG ACGTCCGACT CCTCACGATG TATTTCCCTG AAACCTCCAT CATTTGTATC	20520
TGCGATTGTG TGAAGAGTTC ATGGAAGTGC CGCGTATCAC ACCAAAACCG CTTTTCATCT	20580
CTGAAAAAAG GGGTAAAATC ATCCTCTGTC AAAAAACAG CTGCGTTATC TCCAATTCTGA	20640
ATATAACGCC CAAGTCCTGT ACCGTTCAAC GCACCAAAGT ATATGTCGCC TATAGCAGCG	20700
CCATTTTTTT TTGTAACTT CATCTGCACT GCAGGTTGTT TTCCGAGAGC ATAGTCT	20757

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22191 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

AGGAAGGAGA GGATTTTATC GTACGCGGTT TTCTCGATAG CGGATAGATT ACGATAATCT	60
TGCACGTCAC TGCTCATGTT GATTTCTTCG GGGATCCAGA AGTTGTTcAT TGCctGCCGA	120
TACCACTTGC TGACCCAGGG ATACTTCATA TTGTTaAAGT CGTTGAGATT GGTAGTGTTC	180
CCCCGACCA TCGTCGCTT ATGAAGTTCA ATGTCTCCTG CctCATTAaA CAGCGCGCGT	240
CTTTGCAGTA TCGTTGAAct TTCCATCATG ATGAAACCTC CTCCTGAGTG CGGGCACAGG	300
GTAGTATACT TGATGGACTT TGAATTCTCA ATTGCGGCGG GCGTAAAAAT GTCTGTCTGC	360
AGGGCTCTGT GTCTTGTGTG GTGGTCCCTG TTTTGTGGGT AGGTTTGGGG AAACCTAACA	420
GAGACGTAGG AAATCCGTTA TGCTCGAGCA CATGAAGCGT GAACAAGCAC GAAGTCAGCT	480
ATCACACGAG CCTCCTAAGC GGCGCCGAGC CTCTCTAACC GTCTGCGGCC TGCGTGCTGT	540
GGAAACGCTT GGCAGCATAC ATCCAGAGAA AATTCATCGG TTC'TTTTTTA CCCCTGTGCG	600
TGCGAAACGC TTCGGACCCC TGTGTGCATA CCTTGCTGCA CGAAAGAGGC TCTACCGTAG	660
CGCTAATACG CAGGAACCTG AGCGATTGAC GCAATCCGTT CACCATCAGG GGGTTGCTGC	720
TACCATAGAC GAGCCGCGCT TTCCAGCCGT GACTCATTCT CAGGTTGAAT TTTGGGTACA	780
ACGGCGTGAG TTTGTTGTGT TACTCGATCG CGTAGGAGAT GCCACAATC TGGGGGCGAT	840
TATACGTAGT GCTGCTTTTT TTGGAGTGCA CTCACTGGTG GTGAGTGAAct GTCGACAGCA	900
GGCGCAGTTA CAAGCGCAAC ATATCGGGTT GCGCAGGGAG GAATGGAGTT TGTGCAATTG	960
TTGCGCTGTA CAAATGCGCA GGAAGTATTG GAAATGTGTG CAGGTAAAAT GACCCGTGTG	1020
GGAGCCTCCC CTCATGCGTT CAGATCGCTT ACACGGCTTT CAAACATACT CTCGCCTGAA	1080
GAAGCGGTAA TATTAGTACT GGGAAACGAG GAGACAGGGC TTTCTGAGCA TTTGACTGCG	1140
CATTGCGATC ATCTCTGTG GATTGCAGGC AGTGGTCAGG TGGAAAGTCT AAATGTTGCG	1200
CAAGCGGGTG CGCTTTTTTT GTCCACTATC GTACAGTTGC GTCAATCTCC TCAGGACTAC	1260
ACGCAGGgAC ATCGGGCCAC GCCACGTGCA CAAGAGCGTG TGCACCGCTG TGGGCAATTA	1320
GAGGAAAAGG GGCAGAAAAA TGGAGCACGT GTTCTTATTC CCCGCTCGGG GgCGGTGCC	1380
AATTCccGTG AAAGTTGAGA GTAGGGAAAG TAGACGGGTG TGAGGTATGG AACCTACAGC	1440

674

GCAATTGGTT TTGCAGTCCG TGTGACGTG CGTCCGCGTG TGCCTCTGAG AACGCAGCCT	1500
GCTCTGTTGT CGCGTAGGAA AACTTGTAAG GAGCTTGCAC AAAGCGTCTT TTTTMTTTTAC	1560
CCTCGACCCC GTTCGCCTGA ATTCATCACG TAGGAGTTGC CCGCATGAAT CAGATCCGCC	1620
TGTTTGCCCA GAGTGCCTT GTGAGCGTCA TGGGTATGGG GATGGTTTTT GCCTTCCTCC	1680
TTTGTCTCAT ATGCGTTGTG CGCTGTGTGG GCGCGCTTGT CTCTTCTTTC GGCTGGGATC	1740
GCGGTCTGA CGAAGGTGTC GCGCTGCAG TCCCTGCAGG AGGAGCACTC GCCGCGGCTA	1800
TCGCAGTCGC CGTTCATGAG AAGGCAAGGA GTACTTCATG AGTACCCCGG TTCGCATTAG	1860
CGAAATGGTC CTACGTGATG CGCATCAGTC TTTGcAcgt ACGCGCATGA CTACCGAAGA	1920
CATGCTCCCT ATTTGTGACA AGCTAGATCG CGTTGGGTAT TGGAGTTTGG AGGCGTGGGG	1980
AGGCGCCACG TACGACGCCT GCATTCGCTT TCTAAATGAG GATCCCTGGG AGCGTTTGCG	2040
TGCTCTCAAA TCTCGGTTAC CTAAGACCCC TATTATGATG CTTTTCGCTG GGCAAAACTT	2100
GCTAGGCTAC CGGCATTACG CGGATGACGT TGTAGATGCG TTCGTAGAGG CCGCTGCACG	2160
CAACGGCGTT GATGTGTTCC sCATCTTCGA TGCACCTAAT GACCCACGTA ACCTCAGTCC	2220
AGsTGCGCGT GCTGCAAAGA AAACAGGCAA GCATGTGCAG ATGGCTATCT CTTACGCTAC	2280
CACACCCTAT CATAACGCAG AGAAGTACGT AGAGTTAGCA AAGGAGTATG CGCGCTTCGG	2340
TGCGGATTCT ATTTGCATTA AGGATATGTC GGGGTGTGCTG AcCCCGTACG GGGCGTACGA	2400
TCTGTTTCTT GCCATTAAAA AGAGTGTCGA TTTGCCCGTT GAGTTGCACA CCCACGCCAC	2460
TACTGGTATG TCTGTTGCAA CCCTGGTGAA GCGGCGAGAA GCAGGTGTTG ATGTAATTGA	2520
CACTGCCATT GCTTCTATGT CCATGGGTAC TTCCACACAG CCTACAGAGA CTTTAGTGGA	2580
AATCcTACGG CACACGGGCC GTGACTCAGG GCTCGACATA AATCTCCTGC TAGAAATAGC	2640
AGCCTACTTC CGTCAGtACG GAAGTGCTAT GCCCAGTTTG AGTCTAGTTT TCTGGGTGCA	2700
GACACGCGTA TCCTCGTGTC CCaGGTGCCT GGGGGTATGC TTTCCAATTT AGAAAACCAG	2760
TTGCGTGAGC aGGGAGCCCT GGATAAGATG GACCAGGTTT TTAAGGAAAT TCCCCTGGTA	2820
CAGAAGGACT GCGGTTATAT CCCGCTTGTG ACTCCTACGA GTCAGATTGT AGGTACGCAG	2880
TCAGTATTGA ACGTGCTGTT TGGCCGGTAC CACCGGCTTA CTGCTGAGAC AAGGCGTCTG	2940
CTCACGGGTC AGTATGGCCG GACTCCCGCC TCCTGTGATG CAGGTTTGGT GGAGCGGGCC	3000
TTGAAGGAAG AAAAGTTATC GCAGTCGCTT GTCTGCCGCC CAGCGGATGC CTTGCCTCAT	3060
GAGCTTGATC GCATGAGGTC TGAGGCcgCs CCGCAGGCCG ACAGGATACC ATTGAGGATG	3120
TGCTCACGTA TGCTATGTTT CCCAAGATCG CTCCACATT CTTTGCTTCC CGTGCGCAAG	3180

675

GGCCTATTTC GTTCAGAGGA AAGGGGCAGG GGCAAAAACA GAAGGGTGAG AGTGCAGGGT	3240
CGGTAGCTTC TTATGTGGCT ACCGTAAATG GTAcTGCgTA CACAGTTGTG CAGGAAGGCG	3300
CTGTTCTCCG GGTAATGGT ACTCCCTACA CCGTTAGGgT TGAGGCAGGC CCGTCCGTTG	3360
CTTCGGGTAC GTCGCAGGGT ACCGTGACTA CGGCAAAGGT TGGGGCGTGT ACTACGCTAC	3420
CCGCGCCGGT CGCAGGTAGC GTAtTAAACA CACCGTGCAA GATGGAGCTA CGGTAAATTC	3480
GGGGGAGACG GTGCTCATGG TGGAGTCCAT GAAGATGGAA CTTGAAGTGA AGGCCACCGC	3540
TGCTGGTACT ATCCATTTCC TAATAGCGCC TGGCGCGCAT GTCAGTGCGG GGCAAGTCTT	3600
AGCAGAGATT CGCTAGAGGA TGTGACCATG AATACGCGTT TACCCCTTCG AGTACTCCAG	3660
TGCGTGTGG TGGGATTGCT TGTGTGCGGG CCCCTGTGTG CAGcTACGCG CCGCCCGGTa	3720
CGTGCTTCTG CGCCGGTGCC TATGGTACAG AGTTGTAAAG ACACGGGGGC ACGATGTGCG	3780
CCGGCGTCGT CCATGCGTGA GGACATGCGT GCGTcACACG GAGcTGCGCC GCTTCTCTCT	3840
GTAAGGAAAT TTTTACTCAA TACGTGGCAT AGTACCGGTC TCTACGCTTT CTTTCATGGC	3900
GTAACACAGG TGCCGGATCT TGCAAATCCG CaGCGAACAC ACAGCGTGT CCGTTATCAA	3960
CAGcGTTGCT GCTCGTGgTT GGTCTGCTCc ATCATTTATC TCGGTGCTGC TAAGGGCTTT	4020
GAGCCGCTGC TGCTCATTTCC TATTGGCTTT GGTACTGTCT TCGTCAACAT CCCTGGTGCG	4080
GGCATGTATA GTGAGCATGG TATGCTCAAA CTCATTTACG ATGCTGGGGT GGGGAATGAG	4140
TTTTTCCCTA TGCTCATTTT TATGGGTATC GGTGCACTTA CCGATTTTGG ACCACTGATT	4200
GCGAATCCTA AAATGGCAGT CCTTGGTGCC GCTGCCCAGT TAGGGGTGTT CCTTACTCTC	4260
TTTGGGGTTG CAGCGTTGAA CTTTGTACCC GGGATCCGCT ACTCCATCCT GGATGCCTGC	4320
GCCATTGCCA TTATCGGTGG GCGGACGGG CCAACTTCCA TCTACGTATC TCGGAAgcTT	4380
GcTCCCGAAC TCATGGCCGT TATCGCGGTG GCGGCATATT CGTATATGGC TCTTGTACCT	4440
ATTATTCAGC CTCCGCTTAT GCGCCTGTTA ACTACCAGAA AAGAACGTCT TATTAGGATG	4500
AAACAGCTGC GTCCTGTTTC GCGGATAGAG AGAGTACTCT TTCCGCTTGT CTTGCTCTTG	4560
CTCTCGGTGC TGCTCATTTc GCGGCTTCCC CACTCATCGG TATGATCGCt TCGGGAACCTT	4620
TGTTAAGGAA TGCGGTGTTG TGGAGCGGTT GTCTAAGACG ATGGCTAACG AGCTTTTGAA	4680
CATCGTGTCG ATCTTGCTGT CTTTGGGTGT TGGTTCTCAG ATGACACCCG ATAAGATTAT	4740
GAACCCCAAT GCCTTGGGCA TTATCGTGTT GGGACTCGTT GCCTTTTCTG TCGCAACCGC	4800
AGGGGGAGTA TTCATGGCAA AGTTAATGAA TTTGTTTTTG AGCGAGAAAA TTAATCCACT	4860
TATCGGTTCC GCAGGGTGAG TGCTGTTcCT ATGGCCGCGC GTGTTTCTAA TAAGGTGGGG	4920

CTAGAGGAGG ATCCTTCTAA CTTCTTGCTT ATGCACGCGA TGGGTCCTAA CGTGGCTGGT	4980
GTCATTGGGA CCGCGATACC GCAGGGtGTT CATCTCGGCC TACGGAGGGT AGGGAGGAAG	5040
AGTAACCGCG GGGTTTtTGCC GCTTAGGTAC CCTTTCCTCC GTGCGCGGGC ACACCCTCTC	5100
AGGTGGCTAG GGGCTTTTtGC AGACGAAGCG GGTAAAGCTC GCTTGAATT CGAGCTCAAC	5160
TGTCCCAATG GGGCCGTTGC GTTGctTCGC TAAATGAGT TGAGTCTCGG TTTCGTTGCG	5220
GTGCGGGTGT AGAAACATGA CCACGTGCGC GTCTTGCTCA ATTGCCCCCG AACCACGAAT	5280
GTCCGCCAGG TTTGGCGCAG AGCCCTCTGC CGGTCGACCG ACTTGCGAAA GTGCTACGAT	5340
GGGATGTCT AGCTCGCGCG CGAGGCTTTT TAGTGATTGG GAGATCGCTG CAAATTGTTC	5400
GTAGCGGGGC GCAAAGGGAT TGTCTGCTAC GATAAGTCCC AAGTAGTCGA CAAAAATAAT	5460
CTGGATCTTT TCTTGACGC ATAATCGACG AGCCACGGCA CGGAGATCCA GTAGCTTCAT	5520
GTTTGGCAGC TCCACGATGT AAAGTGGGGC GTCGTACATC TCTCtGCGGC GTTTTGGATG	5580
CGCCCGAAAT CGGAAAGTTG TAAAAGCCCT TTGCGCAGGT TCGTCGCGGA TACTCCTGAC	5640
TCTGCAGCGA TAAGTCGCTG CATCAGAAGC AAATTAGACA TTTCCAGAGA AAAAAAGGCG	5700
GTTGGAATAC GTTGCCTTAT GGCAATGTTC GAGGCCATAG TCATGGCGAG CGCAGTTTTC	5760
CCCATGGAAG GACGCGCACC TATGACAATA AGCTCGGAGT TCTGGAATCC ACCGGTAAGA	5820
TTATCCAGAG CCGTTAGcCG GTGGCAATTC CGACCAGATC GCTTTGATTT CGGTAACGAG	5880
TCTCAATAGT ATTGACCAA TCAGGAATGA GGTTTTTCAG CAATTTGAAG GTTGCTACTC	5940
TCCTTGcATT TGTTAGGTCA TAGATTTCCC TTTGTGCTGT TTCGAGTACG ATGTTGCCCC	6000
ACACGGTGTC ATTGAATGCC TCTGCGGTGA TAATGCGGGC TACTTTTtAGT AGCGACCGGC	6060
GCATGGCAGC GTCGCAAACG ATGCGTGTGT AGTATTCAAC ATtCGCGGCG CTTGGGACCG	6120
CATCGgTGAG AGAGGCAACA TACGCGCTGC CACCGACGAA ATCGAGCGCC TCACAGGAGC	6180
GCAGtGCTCG CTGAGCACGA GGATATCAGG GCGTTGACCT AAATCCGATA AcTCTACGAG	6240
TGCTTGAAAG ATGCGCTGGT GCGCagcGGA ATAAAAAGAG CTCGCAGACA ACTGCTCTGT	6300
TGCCGTGCTC AGAGCAGAGT CATCCAGTAG AACAGCGCCG AGCACAGCCC GCTCGGCCTC	6360
TAGGTtATGA GGGGGAATTT TTCCCTTGAG TTCTTGAGTG GGATTAGGCA TGCCCGGCAC	6420
AGAACCCTCCT CCGAGGAATA CTCAGAGGAG GGAAGGTGGT GAAAAGACAG TCCCCCCCCT	6480
CTCCGTGGAA ACCcTCTAAC GAGGCAAAGG GTTGAGGCCC AACTGCCAAG AACTGTCTCC	6540
CTTCCGTGGA ATCCAGCCCC AAAGTGGCAC AGTTCTTTtGC ACAACTAAAA AACGAACAGC	6600
ACATACTCCG TGCAGAGAGA TACTTCCGCA AACGGTCTAC TCACTCACAC TGTCCgCTTC	6660

677

GCTTTGGTTT TTGATGGTGA CAGGAACAAC AGCACATATT TCCTCGTATA GTCTTATAGT	6720
GACGTGATAG TTCCCCACAC ATTTTCAGAGT AAGACCAGGG ACCTCCACAC GcTTGCGCTC	6780
AACCTCAAAT CCCATGCACG CAAGTTGTTC TGCAACGGTA TGA CTCTGTGA CAGCGCCGTA	6840
CAACTTACCG TTGGTACCGG CGGGCATGGC AATAACCACA GGCTGAGCCT CTAAACGAGC	6900
CTTAAGATTT GCGGCATCTT GTCGCTTGAG AGACTTTCGC ATCTCTATGT CCTGTTGTCTG	6960
CTGTTTGAAG CGAGCCACGG TAAAACGATT ATGAGGAACA GCAAGGTTTC GAGGGTAGAG	7020
GTAATTACGA AAATAgcTGC GCGGACCTCT TTCACATCAC CTTCTTCACC AAGGATCTTT	7080
ACGTCTTGAT TGAGAATAAT CTTCATACGT TTTGTCCCCT CCTACGCAGG AATAAAAAGTC	7140
CACGCAGAGC CACTCTGCCT ATGCACAGCA ACTTCTACTG AACTAGGAAA AACAACCGCT	7200
GTATACCAGC GCTACTCGGT CAGAACGAAA GG TAGGAGCG CAACGGCGCG GGAACGCTTG	7260
ACTTCGAGAG CAACACGGCG CTGGTGT TTG GCACACGTAC CGGTGATGCG TCTCGGCAGA	7320
ATCTTACCCC GCTCTGTGAT AAAGCGACGA AGCGTGTCCG GATCCTTATA ATCAGCTAAA	7380
AGCTTCTGCG TGCAAAAACG GCATACTTTC TTTGATAGA ATTGTCTGTT TTTCTTGGGT	7440
GCGCTCTCTT CACTTTCACG AGGAGAACTG AGATGCGTAT CCAGGTCAAC ACTCGGATGA	7500
TCTTCTGCCA TGATATGCTC CTAGAAGTGG AAAAATTAGC ACGCCCAATT CCTTCTGAG	7560
GTCCAGGCGA ACGCCAGGTT CGGTCATACT TTTATTCATT ATGCATGCTC CTTGTGGGGA	7620
AAGAGACCTA AAATGGAACG GTGTCCAGAT CTGAACTTGA AAAATCAGCC TCATCAAGGg	7680
ACGAGGTTGC GTCCAGTCCT CTTTCTCAC CCAAGATATC GCCTGTGGGT GACcTAGAAT	7740
CTGAGGATGT GCCGCGGACA GACCAGCGGT CGACTCGGCG GCAACGCGCG AGGAAGAAAA	7800
CTCACCGTCC TCGGCACGAG CAGCGCCACC GAGGACAGAA CCGAGGAGTT GAACGTTAGT	7860
CGCAGAGATC TCTACCTTGC tGCGTGACTG CCCCTCTTGC TCCCAACGGC TTTGACGCAA	7920
TTCCCCCTCG ACGGCTACCT GCTTGCCTTT GATAAGATAC TGGCTGATGA CTTCGCCCTG	7980
GCGTCCCCAT AGAACGATAT CGAAGAAATT AACTTCCTCA ACCCAATCAT CACCACTTTT	8040
CCTGCGCCGA TTGATAGCAA CAGAAAAACG ACACAGAGCA CCACCTGCAG AAGTGTA CTT	8100
GAGTCCGCAT CACGCGTAAG CCGACCAACG AGCACTACAT GATTGACGTC TGCCATATCT	8160
TCTCTCAGGA ATCGACACGC ACAAACAAGT GCGTGAGTAA GTCGTGTCTGC AATCTGAGCT	8220
TATGATCGAG TTCGCGCACC TTCCCCGGCT CACACTGAAC AATGAAGAGC AGGTAACGGC	8280
CCCTCTTTTG CTTCTTCAGA GGATACGCAA GTTCCCCTC TCCAATATGG TCTTCGCGGG	8340
CGATGAcTGC GTCGTTTTCC TGTAGGAGGG CACGAACGGC GGTGGAACCC TGAAGAAAGA	8400

GATCCTCGTG	TGCACTGAAA	ACGGCCATTA	GCTCGTAGGT	CCTCATAATA	ACTCCTATGG	8460
ACGGCTCACC	TTATCAGGCT	GCACTAGACT	CACCCGACAA	GGAGGAGTAG	CGTGCGCAGA	8520
ACGCGCGGCG	AGaCGCCAGC	GTAATAAaAA	TCTGTGTGCC	GCATCAAGTC	TTTTGTCTCT	8580
TTATCCGATG	CTGCCGACGG	CGCACGTCGT	cTGAGGGGGT	ACATTCGTGC	GTGTGCTCCT	8640
TACGGCAGAC	GaGGTGAGGA	ACCTGTTCGC	AGAAGGTGCG	CTTTCCTGTG	TGCCCCGCTC	8700
GGTCACGTAT	GTGTGGGGAG	GTcGTGGTG	CAGAAtTTTG	TGTTTCAAGA	CAATATTTAT	8760
CACCTAGCAC	GTTCTATTGA	TGTCCTGTAT	GAGGGGCTTC	AGCTTAACTT	AGATGAGTGC	8820
CTTTATGCGG	AGAAAGTTGT	GTATGACGTG	CGTTTTTTTTG	ACCATGCGTT	GCAAAAGTTG	8880
TGCGCGCATA	TCGATCGCCA	GTCTCACTTC	CCCGATTACT	TACCAATTCT	TCATTGCCTA	8940
TTCTCCTGCG	GTGCACGATT	CTtGAACTTA	TTGAATTTTC	TTATTCATCG	TGCCTCTCCT	9000
GTGACTGCGC	AGGTTGAGTT	TACCCGGATG	CTCCCGTTTA	TTGAGAAAAG	ACACAGCGCA	9060
TTGCATGAGA	ACCTCGCACG	CTCCATTCAA	GAGGTGGACA	CGAGCGCAGA	TGCGAGTCAC	9120
GTGGTTTCTC	AAGATGAGAT	AGATGAGTTG	CTTGAGCATT	AGGTAATCCG	CTTGCTTGTT	9180
ACAAGGCGCG	ACGT'TTTGTG	TACGGAGGTT	GGCACGGGTG	AGGATTACGG	GGGGGATGCT	9240
AAAAAACCAC	GTATTACGTT	GTCCGGATGG	TCCTATCCGT	CCTGCAATGG	ATCGCATGCG	9300
TGAGTCGTTA	TTTGCGATTT	TGGGTGATAT	GCGCGGCTGT	TCCTTTTGG	ATCTTTTCGC	9360
CGGATCGGGA	GTGTGCGGCT	TGGAGGCTTA	TTCACGCGGG	GCGTATCCGG	TAGTGT'TTGT	9420
AGAGTGGAAT	GTGCGT'TCTT	TTTCTGTTTT	GTGTCAGAAC	GTGCAAGTGG	CGCTGTGTGCG	9480
TTTGGAATGT	AGATGTATGG	CAGTGGAGCG	GTATATTGCG	CGTGACGTA	CGCTGTTTCA	9540
TTTTGTTTAT	CTTGATCCAC	CTTTTCCCTA	TCGCTTTCAC	GCTGAGCTGT	TGCAGCGGCT	9600
TTCTCGTGCG	TCATTGTGTA	GAGAAGGAAG	CGTGGTGATG	GTGCACCGAC	CAAGAGAGAA	9660
AAAAC'TGCG	GATAAAATCG	ATTCACTTGT	GCGGACCGAT	CAGCGTGTGT	ACGGGCGCTC	9720
GGTAGTTGAT	TTTTACCACA	GGATAAAGCC	GGTCTTGCGT	AGAACTGAAA	CCCGTTGTAG	9780
GATCTTGCGt	TTTTTGTGCG	AGGGGATGCA	GAGGGTGCTg	AGAGCGACAC	GCCGTACTTC	9840
GTTaAAGGTA	TACAGCGCCC	TGTTTcCACT	CTCTCCGATC	GCGACCGGGg	CGCTGCTAAA	9900
CAGGCGGGGC	AATGCATACC	TGAATGAgGG	GAAGCTGCAG	GAAGCGGCAC	GCGT'TTTCAT	9960
TACCACTGGT	TACCACGATG	GATTGACCAG	GATTGGCGAT	GTGTATATGC	GCAAGGCGGA	10020
CGTGTGgACC	GCACTGCGgT	TTTATTATTT	TGCTCGCAAT	GAGCAGAAAA	TGAGGCCCAT	10080
CGTTTCAGCG	CTCTCAGTGT	TGATTGATG	TCTTATATAA	TTTTGACGCC	GGGGGGGGGT	10140

ATGGGGCTTA	TGGGGTGCGA	GTGTAGTGTT	CCGCCTTTTG	AAACGGTTGA	AACGGGCAAA	10200
CGGTCAGTGG	ATGCGGACAG	GATTATGCGT	CTGTCCCGGG	ATGGcTACGC	GTTCTTAAAG	10260
GTCAATGACC	TTGAGAGGGC	AGAGAGCGAG	TTCGGTAAAA	TTCTCCAAAT	TGAAGCGGAT	10320
AACAACATATG	CCCTCGTGGG	GCTCGGGGAT	GCGGCGCGCA	AGAGACGCGC	GTACCAAGAG	10380
GCATCTGACT	ATTACACGAG	GTGCTTACAG	CATTACCCTC	GCAACAGCTA	TGCGCTCTTT	10440
GGTCTTGCGG	ACTGTTATAA	AAACATGCGT	CGGTACGTGA	AGGCAGTGA	AGTGTGGCAG	10500
CAGTACCTGG	AGCAGGATAG	CCACAACATT	GCGGTGCTTA	CGCGCATGGC	CGATGCTTAC	10560
CGTAAAATAC	ATGATTTTCA	AAACTCGAGA	AACCTTTACT	CCCAGGTTAT	CGCCCTGGAT	10620
GAACATAATT	CCTACGCGCT	AATTGGGCTT	GCTCACTTGC	ACTACGACTT	CAAGAAGTAC	10680
CGTGAAGCAC	TCATCTACTG	GA AAAAGCTC	CTGGAGTGTG	CAGAACACAG	TGTGGATATC	10740
CGTGACTCA	CCTCTATCGG	GAATTGTTAT	CGTAAAATGA	AACCTTTTAG	TCAGGGATTG	10800
CCCTATTTTC	AGGAAGCGCT	GAAGCGTGAC	CCAGGTAATT	TTTATGGATT	TTTGGGATG	10860
GCTGACTGCT	ACCGCGGCAT	GAACATGCAG	GAGCGTTCCA	TCCAGTACTG	GGAGAAGATT	10920
CTGGAGAAGG	ACACGCAGAA	TCGTGTCATC	CTCACCCGTA	TTGCCGACGC	ATATCGGCAC	10980
ATTGGGGAAT	ACGAAAAGGC	CCATCAAACG	TATAAAAGGG	CGTTGGATAT	CGATTACGAT	11040
GCCTATGCCA	CGCTCGGGCT	CGCAGTCCTT	TGTAAACTCC	AGGGGAGATA	CGAAGAGGCG	11100
GTTGTGAGTC	TTGATCGACT	CGTGCACTT	GATCGGAAAA	ACTATCGCGT	ATATGTGGAG	11160
CTTGCAGACT	GCTACCGCAA	GCTCGGGCAG	AAGCAAAAGG	CGCTTGAGAC	ACTTCGTCCC	11220
TTTCAGCAGT	TTGGGGTTAA	GAACCGTGTT	GTTTCTGAGC	TTATGAGTGA	GTTGGAGGGT	11280
GCATCGTAGT	TTCCCCCTT	TTTCTTCCTG	GTAAGCTTGG	GTATGGGTGG	CGTTTGCCAA	11340
GTGTGAACGG	cTCGTTGCGC	AGGTGTGGCT	GCGCGATGCC	TGTCGATTTCG	GCGCTTTTTCG	11400
TGTGGTGGTC	GGGGTCCTCC	TC'TTCGTCCG	AGGTGGTGCA	GGACTTTGCG	ACGAGGGGGT	11460
GGAGCGTATA	TGGAGTGGTG	CTGCGCCCTT	TCGGGGCTTT	TGCCAGAAGA	AATCCAGAAG	11520
GTGTGTGCGT	TTGCTGAGCG	CTTTCGTGGG	GTGCAGGTGT	TCAGATGGAT	TGCCGCAGGG	11580
TGCACTGACT	TCCATGCGAT	GAGTGATCTC	TCTTCTGAGA	CGCGTGCACG	CCTGGCGAGG	11640
GCGTGCGTCA	TCTCGGACAC	TCGTGTCTAT	ACCACGCTGC	GTGATGTGGA	TGGTACGCTC	11700
AAGCTGGGTA	TTGAACTGAA	AGATAAACGG	GCGGTAGAGG	CAGTCTTACT	CGTCGATCAA	11760
GTCTCGCGTA	AGACTGCTTG	TCTATCCTGT	CAAGTCGGCT	GCCCTATGGC	GTGCGCGTTT	11820
TGTCAAACAG	GCCAGTTGGG	TTTCGCGCGA	AACCTTTCTG	CCTCAGAGAT	CGTCGAGCAG	11880

680

TTCCTTCATC	TGGAACGATG	TGTCGGTACA	TTGGATAATG	TTGTGTTTAT	GGGAATGGGT	11940
GAGCCCATGC	TCAATCTGGA	TGCGGTGTGT	AGAGCTATTG	AGATACTGTC	TCATCCACAG	12000
GGTCGTGACC	TATCTGAAAA	ACGTATTACT	ATTTCTACGT	CTGGACATTG	CCGTGGTATT	12060
TATTCGCTTG	CTGACCGCGC	ACTGCAGGTT	CGCTTGGCGG	TGTCTTTAAC	CACCGCGAAT	12120
GCACCGTTGC	GCGCACGCCT	CATGyckCnt	GCGCACGACA	GTTTAGCAAA	ACTGAAAAGC	12180
GCTATTCGCT	ATTTTAACGA	GAAGAGTGGA	AAGCGTGTGA	CACTCGAGCT	CGCCCTCATG	12240
CGGGGAGTGA	ATACTTCTGA	ACGGCATGCG	CAAGAAGTTA	TCGATTTTGC	ACATGGGCTT	12300
AACGTGCACG	TGAACTTAAT	TCCCTGGAAT	CCGGTAGCAT	CAATCCACTT	TGAAACACCT	12360
CGGGAAGTGG	AGGTTCGCGA	TTTTCAGGCG	CTTCTCATGC	GCGCCCGCAT	CCCCGTGACA	12420
CGCCGCTATC	AGCGTGGGAA	TGGCATTGGA	GGCGCATGCG	GACAACTAGG	TAAAACAGCC	12480
GGCGTGTAAC	TCTTTCGCTC	CGTTTGTAGA	TGTTTGTACG	TGTGGCCATG	CTCGTTCCTG	12540
TTTTTCAGGA	AAGTTTCTTT	GAGGCAGCCA	GCGCTTTTGC	CTTGCTCGAG	TAGAGCTGTA	12600
CGCAGTCCCA	GGGTAACCAA	CCTCTTTCTA	CGTTCACCCA	CAGCGCTGAC	TCTTTATCCT	12660
TTGAAAGCAA	ATCAATGCCG	AGCACTGGAA	ATATGTCTTT	GCGCCGTGCG	TACGCAATGA	12720
CGATCCCCGT	GACACCTGGT	TTGTCACGAA	GCAAAACATA	AGCCTTGGTG	ATTACTGCGA	12780
AGCGACGCGC	TTCTCCAATT	GGAGAGCTCG	AGGGGAACCG	TACATCTTCC	AGTGAATTTT	12840
TCCGCACACA	GGCGGAAGTG	CTGCTGAGTA	CGAGCAGTAC	CAACGCCCAT	GTGCGGCGCT	12900
GCAGCACGGG	GATACCGCGT	ACCTTCATAG	AAAAAGCGTC	GGCGCAAACA	GAAGGTGTAG	12960
AATGCTCGCT	GCGAGAGAAA	ACAATCCCCa	AGGGTTTGGC	ATACTGCACC	AGCGTGCGCG	13020
GAATAGGTGA	CGGCTTGGA	AGGGCCACAC	AATACCGATG	TAGAAAAGA	GCACATCCTG	13080
TACCGCCGGC	AAGGGTGGGT	ATGAGATCCC	CAAGCACGGG	AAGTTGGGCA	CCGATAGGAT	13140
TAACGCACTT	GCACACTGCG	GCAATTCCCG	AGAGAAGCGC	CACACTAGAG	AGAAAGTCGC	13200
GTCATACAGA	AAGGGACAGT	CGTGCGCACT	CTCCTCTTGG	GAGTCGAGCA	CCGTGAGGAT	13260
AAAGCCTATC	GCAGCGTTGG	TCGCCACAGA	TAAAAAGTAA	AACGGTAACA	TGATGGTCTC	13320
CTCTTACATG	TGGCATGACA	TTGCCATATT	TGAATATGCA	CTCAGGATGT	TTGTTTCAGTG	13380
AAACACAGAG	CATCTTTACA	CATATCCACC	ACGATAGTTG	AGCCGCCTCT	GAATCGGCCA	13440
CTGAGAATCT	CACGCGCTAG	GGCATTTCCT	AATTCCGTTT	GGATTGCACG	CTTCAGTGGT	13500
CGTGCTCCGA	AAGTGTCGTC	GATCCGCGC	TCCGCAAGAT	AGGCTTTTCGC	CGCGTCACGC	13560
ACACGAAGTT	TTATATGTCG	ACTTTCAAA	CGCTCCACTA	CCATCTGCAG	TTGGATGTCT	13620

681

GTGATGAGGC	GAATATGTTT	CCGTGTGAGA	CGCTTAAAAA	TTAACACTTC	GTCAATCCGG	13680
TTTAAGAAAT	CTGGGCGAAA	GTATGTGTGC	AGTAATCCCC	GTATCTGCTC	TGGTAGAGTT	13740
TGTTCTTCTG	TAGATTGTGT	CTCGGGTACA	GGCAAGTCCG	ACGTGTGTGT	GCGCGACTCG	13800
CGTGCAGAAA	GAATATGCTC	TGATCCGATA	TTGCTGGTCA	TGATGATGAT	CGTGTGCGG	13860
AAATCCACCA	CCCTTCCTTG	GCCGTCAGTC	AAGCGCCCAT	CGTCGAGTAT	TTGCAGGAAT	13920
ATATTAAACA	CATCCTGGTG	CGCTTTCTCT	ACTTCATCAA	AAAGAAGTAC	GCTGTAGGGT	13980
CTACGTCGTA	CCGCTTCTGT	CAATTGTCCC	CCCTCGTCAT	AGCCACATA	CCCCGGGGGC	14040
GCGCCAATGA	GTCGGCTGAT	CGCGTGTTT	TCCATGTATT	CACTCATATC	GATACGCGTC	14100
AGTGCACGCT	CATCGTTGAA	AAGAAAATCA	GCTAACGTAC	GTGCAAGTTC	TGTCTTTCTT	14160
ACCCCCGTGG	GACCGACACA	TAAGAACTG	CCAAGAGGAC	GGCGCGTATC	AGAAAGTCCT	14220
GCCTTATTAC	GACGAATCGC	GTCGGAAATT	ACCCGCACTG	CTTCGTCCTG	CCCTACCACA	14280
CGTTGCATGA	GTA CTGACTC	AAGCTGCAGA	TATTTCTGTT	GCTCGCTTGC	CATCATTTTG	14340
GaTACCGGAA	TTCCGGTCCA	CATAGAAATA	ATTTTCGCAA	TGTCTCTTTC	ACACACTTCC	14400
TCGCGCAAGA	GCTGTCTTTC	TAGACCGGAT	TTTTTCTCTA	CTTCTGCAGT	AAGAAGCATG	14460
ATTTTTTTTT	CAAGTTCTGG	AATTTTGCCA	TACCGAAGTT	CTGCAGCCTT	GTTCAGGTCC	14520
CCTTCACGTG	AAAACATGGT	TTCTCAATG	CGGAGACGCT	CAAGCTCCTC	TTGTAGCGG	14580
CGTGACTCTT	CTATCCTCCC	TTTCTCATTT	TGCCATTGGA	CCTGCATTGC	AGCACGGCGC	14640
TCTAGGAAGC	CTGCGAGCTC	TTTTTCTAAC	TTTTCCAAAC	GTTCTTTTGA	AGCCGGATCA	14700
CTTTCTTTAA	GGAGAGAGGC	CTTTTCGATA	TTCAGCTGTA	ATATCTTGCG	CTCCACCTGG	14760
TCTAGCTCAA	CAGGCTGACT	TTCAATTTC	ATTTTCAGGC	GGCTTGCTGC	TTCATCCACC	14820
AGATCAATCG	CCTTATCTGG	TAAAAAGCGG	TTGGTGATGT	AACGGTCAGA	CAAAACGGTT	14880
GCTGCAACAA	GCGCTTCATC	TTTGATACGT	ACCCCGTGAT	GCAATCGTAC	TTTCTTGCA	14940
AACCGCGCAG	GATAGCAATG	GTGTCTTCCA	CCGTAGGCTG	TACGCAGTAC	ACTTGCTGAA	15000
AGCGGCGTTC	GAGCGCTGCG	TCCTTTTCGA	TATATTGCG	ATATTCGTTG	AGCGTGGTTG	15060
CGCCGATTGA	ACGCAATTCA	CCGCGCGCAA	gcgCAGGTTT	CAGAAGGTTT	GACGCATCCA	15120
TAGATCCCTC	ACTTGCGCCG	GCGCCTACGA	GCGTGTGTAG	TTCATCAATG	AATAAAATAA	15180
CGCCACCGTC	GCTTTTCTGT	ACCGCTTCAA	TTACCGCTTT	TAGTCGTTCT	TCAAATTCCC	15240
CGCGGAACCT	TGCACCGGCA	ACCAATGCGC	CGAGGtCAAG	GGAAAGCAA	CGCTTTCCCT	15300
TGAGGCTTTC	TGGTACGTCT	CCTGAAACGA	TACGGCGTGC	AAGTCCCTCG	ACAATAGCGG	15360

TTTTCCCTAC	GCCGGGTCT	CCAATAAGCA	CTGGGTATT	TTTTGTACGA	CGTGAGAGTA	15420
CCTGCATAAC	GCGCCGGATC	TCTTCATCAC	GTCCAATAAC	CGGATCTATT	TTTTCTTCTC	15480
GGGCGAGGGT	AGTAAGATCT	CGGCAGTATT	TCTCCAAGCA	CTGGAATGTT	GATTCTGGAT	15540
CCTGGCTCGT	AACGCGCTTG	CTGCCGCGTA	TATCTTTGAG	GGCGGCACTG	ATAGTTTTAC	15600
TGGTAATGCC	CTGACTGTGA	AGGAGACGTG	CAGTGTGCT	ATCTGTCTCA	CTTATGGCAA	15660
GCAGGAGATG	TTCGAGGAG	ACATATTCAT	CTTGGTTCTT	GAGCGGAGG	CGTTCGAC	15720
GTGcACAGGC	TTTGCTCAGC	GTTGGTGAC	AGCGCGTTG	GGCGGAGGA	CCGGTAACAC	15780
GTGGTTTGCG	GCGCAGGCAT	TGGAGTAATT	CATCGTACAG	GAAGTCCGGT	TTTGCCCCAA	15840
TTTTTTCAAT	GAGCGGAGAG	ATAATCCCGT	CTTTCGGA	AAGTAGGGCG	TGGAGTAGAT	15900
GTTCCCTCCTC	AACTTGACCG	TGGTCTCCG	CTTCTGCCAG	AGATATGGCG	TCATTGAGCG	15960
CTTCGCTTGC	TTTGACTGTG	TACCTGTCTG	TGTTTCATGC	GTGATTATAG	GTCTTTTGAA	16020
CGCTTTTTtC	TCGTCACTCG	TATGTTTTTT	CTACCGCTTG	CAGGGGACTT	ACGGGAGTAG	16080
TCGCGGTGGA	GAACArGGGT	GTACATGGTA	TGCGGTGCGC	TTtGGCAGGC	CGCGGTAAGg	16140
CGTAgCcTTT	TATATTTTCT	tGTTTTGAAG	TAGGCTCCTG	CGAGTTGGGA	GGTTGGGAAT	16200
ATGGAAAAAA	CGTTAACGCT	TTTTGGGAGC	AACCATGTG	GACAATGCGC	TACGGCGCTT	16260
GAGTATTTGC	GGAGCAATCA	CATTAACTTT	GAGTACGTGG	ATATCACCGG	CAGCGGAAG	16320
AACCTCAAGC	GTTTTTTAAA	GATGCGTGAT	TCAATGCCAC	TCTTTGATGA	CGTGAAGAAG	16380
GAAGGGCGCA	TTGGTATCCC	GTGTCTTTCG	GTGAACGACG	GAGAACAGGT	CTTCCTTGGT	16440
GTGGAAGGTT	TGGACCTCTC	GGCGTTTCGC	TAGGGGTTAG	TGGGCCGGTG	TGTTCGGGGG	16500
CGTGATGTCG	TCCCCCTCTT	TGCGCTCTTT	TCGGGCGACC	AGCTAGGCGG	TTTGCTCTGC	16560
TTCAAAGCTG	CTCTGGAGCG	TCTGTGCGGT	TGTGCGCagC	TGCTGTTCAG	ATTGAATGCG	16620
GAAGAAGGAG	AGGAGGCTGC	GTGGGATCTG	CTCGTAAGGA	GTTTCGCCGT	CGAGAAAGCG	16680
GATGGTCATG	TTTGCAAACG	CCACGGTGGA	GATGAGCGGC	TTATATTCCT	CAGGAGCGTG	16740
TGGCAGATTG	TGGTGAAAGC	GAATGGTGTT	GATAACCGGT	TCAGGTAGAT	TCCAGCGCTG	16800
TGCGAGCGCC	GCGCCAATTT	CCGCGTGGCC	TACGTCCGAC	ATGATGGTGT	CGAGCACATG	16860
CGGGGGTATG	TTACGctCCG	CTGAATTTT	TGTGAGTTTG	ATGAGCATCT	CAGGGTATGC	16920
GGAGGTGAAA	ACGACTTCCC	CCAGGTTGTG	CAGGAGGCCG	CAGATGTAAG	AGTCTGCGAT	16980
GAGCGCCTGG	TCGCCAGTGG	CTTTGGCAAG	ACCGAGCGCA	AAGTAGCCGG	TGCGGTATGC	17040
TTGGTTCCAC	AGCTGCTTTT	GCTCATCGTC	GGTAGACTGC	AGCACGCGCC	CGGCGCCGAC	17100

683

TGAGTACAAC	AGATTCTGTA	ATCCGCGCAG	CCCAGCGCGC	TTCnAcCgcT	TCGCTGATAT	17160
CCAAACAACG	TTTGTTCATA	CCGAAGCGCG	CGGAGTTGAC	GAGTTTGAGA	AGGTTCGGTTA	17220
CGAGCGCTAC	GTCTTGGCTA	ATGAGAGCTA	CAATGTCTGA	GAGTTGGACG	TCAGGATTTT	17280
CAATGGCGCG	TTGAATTTCC	AGTAGTTTGC	TTGGCAGCTG	GGGTATGTCG	TCGATGCGGT	17340
CGGCGATAGA	CGCGGCAAGC	TTTGTGGTTT	GAGTTTGGAT	CTCAATGTTG	CGGGGAACATA	17400
CCATGCGCGA	AATGGTTCTGA	TCCTCTTCCA	CTACGAGGCG	GTACACGTCT	TCCTCAAGTC	17460
CGAGCTTTTT	GAGCATGAGC	ATCATAATTA	CGAGCCCGAG	GCCGGCCCCC	TCGGAATTGT	17520
CCAGGATGTG	CGCGAGTGCC	TCTTCCAAAC	CAGAATAACG	GCGCGCACGA	ACGCGCTTGT	17580
CAAAAACGCG	CTTAAATTCC	ATGGGAGTCA	TTTTCAGTT	ATTGATCACC	TCGATGACAA	17640
GCGCATGTGA	GAGCACCTGC	ATGGTCACCT	TTACGTACAA	CCCCTCCTGT	TGTTGGAGCT	17700
TGAGGTAATG	ATTGATGTTC	TCAAGGCTTT	CTTCCTTGAA	GCTTTTCATA	CCGCGCTTGT	17760
AGTCCTGTGG	ATCAAAGATG	TCCAGTCCTT	TTTCGCGGAA	GTAAATACGC	TTGGTGTGG	17820
CCTTTTTTCGC	GTTTGTGGTG	AGTTCACTAA	TGCAGTACGT	TAAATAATCC	TTACCGTGCG	17880
GCTGGCCAAT	GAGATCTAGG	ATTGTTTTTG	CCACCTGTCC	AATATAGATG	TCCATATCAC	17940
GGGGGAGCGT	ATAGGTGGTG	ATGGCAATCG	GGAGCTGCAG	TTCAATTGCC	TTACGAATTT	18000
TTTCAGTGTC	AACAACATTT	TGTGTATCAC	ACATGGGCAG	ACTGTACACG	CTGTGTATGC	18060
TTTTGACAAC	ACGCGCGAAA	TGCACAGCTT	TCCCTGTGCC	AGAATGCAAA	CGCGTGTGGG	18120
TGCGGTGTAT	GTCTTTGTTG	ACAACGGGGA	GAAAAGCGTA	CGAGAATCTG	CCCCGTTAGG	18180
TTGAAGGGGG	AGCAAACGTG	ACGTGCTCAT	GTAATCTTTG	TTTCCCGTA	TCGATATGGG	18240
GTGCGATGCG	CGCGGTGGAT	ACGCTCCTTC	TCGACTGAGG	TCGCAAGATT	TTGTAGGAtG	18300
CGTAGGGGCG	TGCGTCGATT	GGTGTGGTGC	TATGTGTCGT	GCTGGTTTGA	TGTATCAGGA	18360
CTGGGGTGTG	AGGGGAAAAA	CGGACAGGAT	GTGCTTTGCG	CGGAGTCGGT	TGTTTTCCCG	18420
TGGTGCGGTG	GGCACGGTGT	GCTGCACTGT	GTTGTTTCTC	GCGTGTCGTG	TGCGCACTCC	18480
TTCTTCCGTG	CCTCTGCGTT	CTGGATCGGT	CCGTGCCGCA	GTACCCGAGG	CCACATCCTT	18540
TCACTGGCGG	CGCTATGCGG	gTACGCGCcT	GCGCGTGTGT	TTTCCGTACC	ATGCTTCTTA	18600
TCGCGCACTC	AAAGCGATTG	TTCCGGAATT	CGAGTCACTG	ACGGGTATCG	CTGTTGAAAT	18660
TGACTGGCTT	CAGTATGCGC	GCATGCACGA	TAAGCAGGTA	CTCGAACTGA	GTAAACCGCG	18720
TGGTGACTAT	GACCTTATCG	CTATGCTGTG	TACGTGGAAG	ACGGAGTACG	CGTCGCGCGG	18780
GgCTACTCCG	GTACTCGAT	TCGTTTTTTC	AAAATCCTTC	CCTGTGTATG	CCGCATTACG	18840

ATTTTGAAGA TCTCATTCCT GTGTACGTAG AGACAATCGG GTATGTAGGT GGACGCAAAC	18900
CCTGGCTTGG GGGTCCGGGT GCGTTTTTGT GCGCCGTGCC CTTTGGAGCG GAGACGAGTA	18960
TACTTGCCTA CCGCAAAGAT ATCTTCCACA AGTACCGCAT CAAGGTACCA GAAAATTATG	19020
ATGAGCTTTT GGATGCCTGT AAGAGACTGC GTGAACGCGC GCAACTATAC GGTCTTGCAA	19080
GCCGCGGCGC TTCAGGACAG CAGGCTTGCA CGCATATTTA CTACACGCCg CACCCTTTGG	19140
TGCTAAGGTG TTGGACGATT CTTTAGTTCC TGCATTCCAT CGTTCGCGTT CTATCGCCAC	19200
ATTACGGTGG ATGCAAGAAA TGTTGCGTA CCGTCCACCG GGTATGGCGA GTTTTGCCCA	19260
AAACGAAGCA TTGCAGGCCT TTTTGCAAGG GCAGACGGGG ATGTACTTGG ATACCAATAT	19320
GATTGGACCG TTAGTTCGTG ATCCGACACG CTCAGCCATA CGCCCGCACC ATGTGGGATT	19380
TGCgTTGCAC CCGATGGCGC AGGTGCGTGC AGGAGAAGTT GGCGGCTTCG GGCTTGCAAT	19440
TCCACACAAT AGTGctGCGC CCGAAGCAGC GTTCTTGCTT TTGCAGTGGA TTACGGCGCC	19500
GCAAACAGGA CGGCGAGTGG TGGAACAGGG TGCCTACCA TTCCGCCAGT CGCAGCTTGC	19560
GGACCGCGCA TTGCGTGcAC GTTTTGCTGA GTTTGAGGTA TTAGAGCGTC AgcTTGcACA	19620
TTGCGATCCA GATTGGCGTC CTATCGTGCC TACCTGGGGG GAGTTGGGAA CCCTTTTGGG	19680
AATTGGGATA AATGAGGTGC TCACCGGTGT GAGTGAGCCA GAGGAAGCGA TGAGCGCATT	19740
AGTGCTGCCG GCACGTCGTA TTCTCCGTCG TCACGCGCAC GCACGTTATG TGCCGTAAAA	19800
AGTCTCTTCT TcTTGGGGGa AGAGAGGGCA GAAAAGATGC TGGATATGAG CGGAAACAGA	19860
ATGACGTGTT CTATCTGTGG AGCGCGTTAC GTTGGGTAGC GTAAGAGGGG GAGTGCCGTG	19920
GGGAAGAGTA TGAGCAAACC ACGTGATACC GTAAGCGCGT ATTGTTTTTA GCGCTCCAGC	19980
GCTTGATTG CTGATGTTG TGCTGGTGT GCGGCCCTTT TTGGGGCTCC GTATGArTTT	20040
TTTTCAGTGG CAACTGaACG CGTTGCCGAC GCAACCTGTA TTTGTGGGTT TTGAAAATTA	20100
CCGGGAGCTT TTCTCCAGTA TTCACTTTG GGCCAGTGTA AGAACGACGC TTGTCTTTAC	20160
GCTCTCAGTG GTGGTGCTTG AGGTTGTACT TGGACTTGCA CTCGCGCTGG TGTTGGAACA	20220
CGGAGTACCC GGGTTGCGTT TTTTTCGTAC AGTGTTTGTG TTGCCGATGA TGATCGCTCC	20280
CGTGGTGGTG GGAGTGCTCT GGGGGTTTTT GTATCACCCA CAGTTTGGTA AAATCAACTT	20340
ACGCTTGCAG GCTTTTGAGC TTGGACCGGT ATTGTGGCTT GCGAATCCGC GTCTTGCGCT	20400
TTTGTCTGTG ATACTCACTG ATGTGTGGCA ATGGACGCCT TTCGTATTCC TTGTGTTGCT	20460
TGCAGGTTT CAGGGTATTC CGCAACATCT TTTGTATGCG GCGAAAGTGG ACGGAGCAAA	20520
TTATATGCAA ACACTCCTGC ATATAAAGAT TCCACATATT GCGCCTGTGC TTGGCATTGC	20580

685

GACCGTCCTC	CGTTTGATAG	ATTCTTTCCG	TGGTTTGGTA	GTGATTATGA	CACTGACAAA	20640
TGGTGGTCCG	GGAGTTGCAA	CAGAAATCCT	GnCCGCTTCA	CTTGACGCGT	ATTGCCTTTG	20700
AGGATCACCG	TCTGGGTAAA	GCATCGGCAG	TTGCTGTGCT	TCTGTTTCTC	CTGACAAGTC	20760
TTTGTACTTG	TATTTTCATT	CTCCTTACGA	TGAGGAGACA	GGCGCGGTGA	GGGTTGCGTA	20820
CGGGTTAGAT	AAGAGCAGGA	GCAGATAGCA	TGAACATGAT	TTTTTTGAAG	TGGCGTACCG	20880
CGTTGGTGTT	GTGTCTGTTA	AGCTGTATTG	CGTTGGTGAG	TATGTTCCCT	CTCTATGAAA	20940
TGGTAGCTAC	TTCTTTGAAG	CGTGATGCGG	ACGCATTTTCG	GTTGCCGCCA	GCATGGTTTT	21000
TTATACCAAC	AATTGAAAAC	TATCGGCAAC	TC TTGCAGGA	ACATCATTTT	GGACGTGCCC	21060
TGTATAACAG	CTTGGTGGTG	ACGTTGAGTT	CCACGGTGGT	GAGTGTCAGT	GCAGGGGCTG	21120
CAGCAGCGTA	TGCAATGCAG	CGCTTTCGGT	ACCGAGGTAA	AAAGGCAATC	ACGGTGGCGT	21180
TGTTGCTCTT	GCGAGTGATT	CCGCCGGTTG	TGCTTGTAAT	TCCTATCTTT	GTGTGGTGGA	21240
CTGCGCTCGG	GTTAGTGAAT	TCTTTAGCAG	GA CTTGCGcT	CGTGATGGT	GCGCTCAATG	21300
TTCCATTTAA	TGTGTGGGTA	ATCACTACCT	TTGTTGCGGA	AATCCCCCT	TCGCTGGATG	21360
AATCTGCAAA	ATTGGATGGA	TGTTCTCACT	GGATGATTTT	TACCCGCATT	GTGATGCCAC	21420
TGATTACACC	CGCACTTGCG	TGGTGAGTAT	TTTTACATTT	CGTTTTCAT	GGAATGAGTA	21480
TATGCTTGGA	TTTGCGCTGA	CCAATCGGAA	AACACGGACA	CTGCCGGTGG	CACTTTCACT	21540
TTTTCTCAG	GATAGTGGTG	TCGAATGGGG	GCGGATTACC	GCAGCAGCAA	CGCgATTGCA	21600
ATTCCTGCAT	GTGTTTTTAC	CTTTGCGGCG	GCGAAGTACT	TGGTGGTGGG	TTTGACCGCA	21660
GKgcGGTAAA	GGGATAAACA	CTCTGCgCGG	GTGAGTACGT	GCAGCAGATA	TGTGcGGCGC	21720
ATCCCTGGGA	gACTGCGTCG	GGTCGTGTGC	GCGTGTC AAT	GCgTTGTATG	TAGGGAGAGA	21780
TGGGGTGGGT	GCaGAAAATG	TATGGGGCTG	TGGTAGGTCT	GCGGTGAGAG	AGAGTGCgCA	21840
CCGGATGGC	aTCTACATCG	TTGGCGCAGG	ATTCGCAGGG	AGTGTCTTTG	CCCGTGAGAT	21900
CCAAACGAAA	AAAGTACTCG	GCACAGTTAT	TGCTTTTTTG	GATGACGATC	CGTGCAAAAT	21960
CGGATCGAAT	CTTCACGGTG	TCCCGGTGCT	TGGTCCCATT	TTTGAAGTTG	CCCGGATTGT	22020
GCGTATTACT	CCGCATGATC	ACGCGCTGAT	TGCAATTCCT	TCTATCTCCA	TTGAGCGTTT	22080
GCGTGACATT	TACCTGnACT	GCGCGCTGCG	GGGTTTACGG	TTATCAAAC	TCTGCCGGCG	22140
CTTGCTCAAA	TCATCGATGG	TACTGCGCAT	TTAGTGCAAA	CACGTGAAAT	T	22191

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5420 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

ATCTTTTCTG CACAAAAGTT ATAAAAAGAT TTGATAAAGC TTTTCGATTTC CTCCATCGGT	60
TTTGAGCnCG CACGCCAAAT GCGAGAAAAG TCCTTCATCC TTAAAAGnTT GCGCnTTCAC	120
ATTGGGGAAA AAACGCGGCC ATACGCGGCC GCACATCGGT AAAACGCCAG GGAAACTCTC	180
CACCAAACAC TTTGGCCAAC TGCCTGCGCA CCACCTGCTC ATCCCATACG AAAACTTCCT	240
GACCTCCAG GAAGGCACCA AGACGCGTAT GAGATGGCAG GAGCATACGT GGGACCACCG	300
TTTCCGAAAG ACGGTCCACC ACCTCCATAT TACACATTTT TACAGCCTcA ATCGTATACG	360
CCCCaGTCAC CGGACGAACG TGTAAGCA CCACAGGCCG CTGATACCAG CCGCTGGTAC	420
TGAAACGGAG CGCCGTtACC ACCTTCCACG CAGTTGCACA GCCTGAGAGA AACTCGTGCG	480
GATACCCTGC ACCTGGCACT TTTGCATTAA TGATAATTGC ATCAGGGAGT GTCTCAGGGG	540
CCGCATGGTG ATCAATAACC AGTACGTCAA TACCTCTGTG ACGCGCATAC GCAATTTCTG	600
CGCGATTAGA AATACCGCAG TCAACGGTCA CAATGAGAGT ACCCCCTGCG GCCGCATGCT	660
CATCTACTGC ATTGCACGAG AGCCCATAGG GCTCATCGGC AACCAGGCAG CGCCAGCACA	720
CCGTCAAGCC AAATGCACAG AGAGCCTCAA AAAGAAGGGT GGTGGCGCTA ATACCGTCTG	780
CATCACGATC ACCAAAGATG AGCACCTTTT CTTTCCGCTC ATGCGCAAGA CGCAAACGGT	840
CAACTGCAGC GCTCATCGCA TGGAAACGGA AcGGTcCTGG CAGATAGCGT AGATCACGCT	900
CAAAATGAAA AAGGAGTGCG TCAGcATnCC ACTACCTTGC GACGCACAAG GATGGCCGCC	960
TCAAGCGCCG AGCAGCTATA CCGCGCGGTA AGCTCGCGGA CACGCCCTTC GTCAAGTGCC	1020
TTTGCACGCC ACCGTTTCAT GCGTA _s CCTT CCTCCGAGAG AGTACCACCC GACGCAAGAG	1080
GACCCGCCAG AACGGCCACA CGCACCACAC ACGCGCCCCG GTGcCGGAC GCTTTCCGTC	1140
GGCGAAgcaT CtTCTCTAA AGAGACTGCC CAATCTTTCT TACGGACCGG TATCCAGACT	1200
CTGCACACCA CGAGCAGGAT CGTCCTGCAC GTCTTCTGAC TCCTCCTCTG GAGCGTCACG	1260
CGACGGGTCTG GATGCAGACG GCACAGGCAC ATGCGGCGCA TCAAAAAGCG GCGCTTCCTG	1320
CGGATGCACC GGCGAAAAG GATTGCTCGG GACAAGCACC TCCCCCTGCA CGCCCGGTGA	1380
ACCCAGTGGC GGATCTTCAA AGACGCGCGG GTCTATATGC AGCCCTTCTT CGsTcACTGC	1440
CGGCCAGAAC CCAgTGCTGT ATCCA _c TTTC CTTCAACCGT TCTTTAGCCA GTTCCTCAAG	1500

687

CATCTTCCCA CTTTCATGGT ACGAACAAAA GCGCTCAGGC AmCGTGcCAr GCAAAAATGA	1560
CAGAGAAACA AGCTCATCCC CACAGTACGG GGTAGGCAGC AATCCTGATT TTGCACACAC	1620
CGCCTGGTAC ATCAACCCTG TTTCAGGACG AACAAATGCC CGGTGCGGCT TATCCTGATG	1680
AATAGCCCGC ATAAAAACGC CCCACGGAGG ACCTGCAAGC GTCGCGCCCG TGCTATGCAA	1740
TCCGAGCGAT CGGTCTCCTT TGTCAAAGCC AAACCACAAC ACTGCAGTGT AATAAGGAGA	1800
GTATCCAACC GCCCACGCAT CAGACCAGTT TTGCGTAGTC CCCGTCTTCC CCGCAACCGG	1860
CATAACAAAC GATCGCcCCG TTGCAGGGTC TTGGTATGTA AATGCGCGCC CCCGCTCAGA	1920
GGCCACCGCC AACGTCCCCA TCGTTACCGT TTTCTCTAGC ATATTCTGTC TGAGCGCCGC	1980
GTTCTCCGCA GAGATCAGTT GCGTTGCCGC ACCcTGCGCG CGCAGgCGGG CCCGCACTTC	2040
CCGTCTTGGA TCCAAAATCA CCCGCCCTAA ACGATCCTCC ACTGAACGCA CTGCAATCGG	2100
TTCTACCGCT TTGCCCCCAT TTCCAAACGC TGCAAATGCA CGCGCAAGCT GAATCGGCCG	2160
GAGGGCAACT ACGCCCAACG CAAGCGGATA GACGCGTGGG AAGGTGCGCT CAATCTCCTG	2220
CCGATCGGTT ATATGCAGGA GCGTCGCCGC ACGCTGGATT ACCGCGTCGA AACCGACCAT	2280
ATCCAGTACA CGAATAGCAG GAATATTGAG CGACTGCGCA AGcGCCTTCC ATGCAAGCAC	2340
TACCCCTGTC CATTTTCCCC CATAGTTGTT GGGAAATATAC GAAACACCAT TGCGGCTGaA	2400
mACCTGCGGT GCATcGTGcA AtGCGTTGCC ATCGTGAGCT TTTTGCTATC CAACGCCGCA	2460
GAATACACCA GAGGCTTAAA TACACTGCCT GGCTGCAACA ATCCTTGCGT TGCACGAATC	2520
ACTTGGTAG AAGCACCAGAA TCTGCTGCCC CCTACGAGAG CTGTAATGTA TCCGGTATCG	2580
TTCTCAAGCG CGATGAGCGC ACCTTCCACC CGCTTACGTG CAATTTCTGTC GCGCACCAGA	2640
GAGGCGCCTT TGTCAGACAA CGTTTTAAGA TTGTCGAGGC CGAACATCAG CGCCATAACA	2700
TTCAACAGGG GACTGAGCGT ACTGCGGTAA TaCGCGCCGC TTTTGCCTT CATGCGCCGG	2760
TCACCGACGT GCAACTGCGG AACGTTGAAC ACCAACCCCA ATAGCTCGCT GATATTGCTG	2820
TACAGTTCTC TGCGCGCAAC GTGTGTGAGA GAAGATTTTT GCACGTGTGC ATTGGCCTGC	2880
TCCAGCGTTT GCTCAACTTG CTGCTCTGCA ACCAACTGAT GACGCAAATC GCACGTGGTA	2940
TGCACGGTAT ACCCGTCTTG GTACAAATTC ATCGTGCCGT ACATCATGCG GTCCAGCTGC	3000
CTCCGCACAT ACTCGGAAAA CCAACGCGCC TTATCCGCAC GGGCATAGAA CGCAGAACTT	3060
GTGGTGCGAG TGTAATCGAA ATGCGCCCAG TAGTGCTCGT AGGACTCATC CCGTTCTTGT	3120
TCACTGAGAT AGCCAAGgCG CGTCATTTCA TGGAGTACGT AACGCTGACG GTCTTGAGCG	3180
CGGTTAGGAT ATTCAAAGGG ATTGTAGTGT GCCGGGTTAG AAAGCAAAAT AACCAAGAGC	3240

GCCGCCTCTG CTGCGCTCAT CTGACGTACC GAATGGCCAA AGTAGAAGCG GGCAGCCGCT	3300
CCTACGCCGT AGTGCCGCCA CCGAAGTAGA CGCGGTTCAT ATACAACTCC ATAATTTCGT	3360
TCTTGGAATA ACGCCGCTCC ATATGGAGTG CCCACCACAA CTCTTTGATC TTACGCCTGA	3420
GACTGCGGTC GCTGCGGTCT GAATAGAGAA GACCTGCTAT CTGCTGGGTC AGCGTACTCC	3480
CGCCCCCTAA GCGCGACCG GTGAGGGTGC CGACAAGGC ACGGAAAATA GCCTTGATGC	3540
TGTAGCCGTG GTGGGTATAG AAGGAGCGGT CTTGCGGGT GAGTAGAGCG TGCACAAGGT	3600
GTGAAGACAA GTCAGCAAAG GAAACGATTT CGCGCTTTTC GTCTGAGGAA AACTCAGTGA	3660
TCAAATCACC CCGAATGTCC AGGATTCTGG TGGGAAGCGC CGGATTAAAG CGGGTGAACC	3720
GTTCGCTCTG CTTAATGTTT TCAATGGAGG CAAGCAAGAA CCCAAAGAGC GCAGcTCCCC	3780
CCACCAACAG ACCGCACAGC AACACCAGAT ACAGGTAACA AACGCGACGC ATGGGCCAAG	3840
AGCGGAACAC AAAAAGGCGA AAACCTCAAG GCAAGAGGCA GAAGACCGTC AACGGCGCAC	3900
ACCGCACGAT GCACTCAGGC AGACACACAA AAAGGCCGGC TTTCTCAAAC CGGCCCCACT	3960
ACGTACCGAC CGCGCGATAG GTGGGAGGGG AACCACGCAG CCGGCGCCCC CAGTATCGGT	4020
TCTACCTGCA AAACCTTGAG CCTGGTGCGA ACCCCACGCC CAACGGTAGT GCCACAGAGA	4080
GGAGGAGCGC GTCGACACCT CACCTGTCGG CGCCCCGACC GTCACGTATC AGCGGAACCT	4140
TTCCATGAAT CGCTCAGGAT TTTGGGGTAC CCCCCTTCC CGTACCTCAA AATGCAAGTG	4200
TGGCCCGGTC GATGCGCCTG TCGATCCCAC ATTGCCGATC ACCGCTCCCA CACTCAGTTT	4260
TTGCTGTACA CGGACGCGCA CTGCACTCAA ATGTCCGTAT AAGCTGTGCC TTCCGTCTGT	4320
GTGCTGCAAA ATCAGTACT TGCCATACAG ACGATTGTAC GCAATCGTCG CCACCTGTCC	4380
GCTCGCACAC GCATACACCA GCGCGCCCAT GGGAGCGGCA AGATCTATAC CTGGATGATA	4440
ACTCAGCCgC CCGGTGAACG GGCTTTTGCG TGCGCCAAAC CCTGAGGTGA GTCTTCCGGA	4500
TGCCAACGGA AAACGATAAA ACGGCTTAAG AAAGAAGGCA CGCACCCTTC CGTCAAACAA	4560
GGCCTGAGGC GCGCACACTA CCTCCCGCTT TTCTCGCGTA TGcgTTGTCT GCGCAGTCCC	4620
CGGAAGGGAA AGAAAAAAG ACGGCCCTTG ACCCTTTTTT ATCAGTGCGT AAATGAGCCG	4680
CTCAAAGGGA AGGTGCGGAT CCGCAGAAAC GTACAGTCCC GGAACGnTTG GCAAAAGCAA	4740
CGTACGCCCC TCAAGGGGGG TATGCAGCGT CTCAATACGG TTCAAACCTAG CCACCGCGTC	4800
ATAGGGAATA CCGCAGCGCG CGGCGATACG GATGATGGTG TCTGCCTTTT TTACGCGATA	4860
TGCATAAAAA CGCAAGGGTA AATCGTTTCC CCGCTTGCCCT TGCGCCAATG CCaCGCgCGC	4920
aGCAcGtCAT CGCTATACTG ACGAAAGAGC GCATCCTGCC CTTGCAGcTG CGCTATCAAC	4980

689

GGATAGGGAC CGCACACCGC AGGATGTGCC ACACACACAC ATAGGCAGGA GCACACgcTG	5040
CGCGCACCAT CCGCACGCGC AGGAGAAAGG AGAACGGAGA AAATGGGCAC AGACGCATCA	5100
CACGCAGCCG CTTAGCACTC CTGCGCGGGG CGAACTTCCG CGGAGGAAGA GAGCCCCATA	5160
GCACCGACTT CCCCTGCTTG CACTAAAACG CATGGCTCCT GCGCGGCGGC CCTACGcCCT	5220
GCACGTGCGA CCCGTGCATA AGAAAGArCG TTGCACACGC GTcTCAGTCC CCACAGGACC	5280
GCACCGCCGC CATAGAGCAA ACCGCTCAAC ACCGAGAAAA CACGCGGACG ATGCACCGCC	5340
AACGCCCAGA GAGGGTAGAC GAGCGCGCAG CCGAGCGCAA ACGAAAGTAT CAGCAAGCAT	5400
CGCAGCGAGT GCTCCAATGC	5420

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6754 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

GGGATCAGAT TGAAAATGCA GAATATTTTA GCGCACACGG TGCTGCGTGC ATCCTTCGTG	60
CTCAAGATGA AAAGGGACAT CAACTGGTGT CTTTGCTCAC AGAACTGTTC CATCCTTCCT	120
GCGCTAGGAT AGAGGAGATG GCACGTGCGT CTTACACACT TGGAATTGGC AATGCCGCGT	180
ATGATATTGC GCAGCAGTTG CAGACTTTCA TAAAGGAGGG GATGTGACAA TCAGTACCCT	240
GGATCTCATT CTTGGAATCA TCATGGGGAT AGTGACCGTC CGTGCCACCA TGCGCGGGTT	300
TGTCGATGAG TTCTTTTCTA AGGCAAGTAT CCTGTGCGCA gCAGTTGTTG CAATACTGTG	360
TCATAAAAAGG CTCGTGCCCT TGACACGTGT GTTGTTAGGC CACAGTATTC TGCTTCCGTG	420
TATAACGTTC TTGATTACCT TTATGGGCGT CTATTGCGTT ATGCTCTTCC TCCGTTACG	480
TATGCGCACG TaTGctACGC GCGATCTTAT CAGTGGTTTT AATCAGGTGT TTGGCTTTTT	540
TTTCGGGATA ATTGAAGGGA GTGTACTACT CACTGTTATC CTTTTGCTTT TACACGTGCA	600
GCCTTTTGTA TCTGTTTCGC ATATGTTGCA TGAAAGCGTA ATTAACACTG TTCTCTCTCC	660
CCTTGCTCTTA GATGGCGTTC GCTATATGCG CCTGAAGATG TAGGCGCGTT TTCGTGTTG	720
AGAACATTGT CGGACAGCCA GCTACTGACC TTCTGCGCGA TGATGTTATG CACGCGCGTC	780
TTCTGCTGCG GCTCTTATTT GTTGGACCAC CCGCTAGTGG CAAGCTAACT GCTGCACTTG	840
AGcTTGCGCG CGTGCTTTCC TGTACGCAGG GGGGCGTGTG GCAGTGTCTT TGTGCACCCT	900

GTGTGCAGCA TACGGAGTTA CTTTCTCCAG AACTACTCGT GATGGGGATA AAAGATCTGA 960
TCCTCGAAAT ACGCGCGTCG GCACGTGCCT ATATGTCAGT GCACACGCAG GGTACGCGCT 1020
ATCTTTTGT GCGGGCAGTG CGTAAACTCA TTACACGCTT TGACGAACGA CTGTGGGATA 1080
GTGATGATAC TCGTTTCTCT GCCGCGGTTT CGAGCATTCG TGAGCTCGAC CAGGAGCTCG 1140
CATCACTCCC CGcACAGGGA GACCGACGTA CCACTCCAGA GCAAAAAGAA AGAGTGCAAA 1200
GGATATGCGT GATCGCCGAA AGGCTACAGC AGGAGTCACT CTATACCCAA TTACCCGTAC 1260
AGCAAATACG AAACGCAATT CAGTGGGTGC GTCTTACACC CTCAGGAAGA AAGAAAGTGC 1320
TGATCATAGA ACACGCGCAC GCGATGCATG AATCTGCACG AACTGCTTTT CTAAAGATAT 1380
TAGAAGAACC TCCGCGCGAT ACGCTTTTTA TCCTCACTAC CGCTACAAAG TATGCAATCA 1440
TGCCTACTGT CCTTTCGCGT GTGCGCAGTT ATTCTTTCAG AGAAAGAAGT GTTGAAGTCC 1500
AATGTGCAGT AATTACACGC GTATTTTCATG ACAGACCGAC CGATGCAAAA AACACACAGG 1560
GTGTACTCTT GCACTATTTA TATCAGTTTT TGTCGTTTTT TTTAGAAGAG GTGCAAACGT 1620
CCGTGATGTA CTTTTCGCTG TATGTGTGCC AGCACGCTAG GTGTATCGGA CGCATCATTC 1680
CTGATACTTG GGTTCGGTA GGTACTCAAC CTCAAGTATC AGGAATsGAT CTTACCTCAC 1740
TTGATTCTAC GCTGCATTTT TTCCAAGCTC ACAAACAGCA ACACGCCGTG TCCC'TTTT'TT 1800
TCTCCTTACT CGTCAGGCAC ATGCGCACCC TGCAGCGCAC CACCGAGTAC TCCGCACGGA 1860
ATACAGAATG tTCGCACACA TTGCTCACTG TATCGAACAG GCACATCGCA ATGTGCAGTT 1920
GTGGAATCTA ACAATACAAG GGACTCTCGA ACACTTAGCA CACACCATCG CGAATCATCT 1980
ATGAGAGATT TTATTGCACG CGCGCTAAAA AAGTCAGCGA AAATGAATGA CTCTCAACTG 2040
AGAAATATGA TTGAAGTTAT TGCCAACGAG TACACCTTGT TGGATGCACT TATGGATTCT 2100
CTGAATTAcG GACTTATCGT GTTGGACTGT TTACACATTC CATTAAAGAC AAACCGAGCA 2160
ATTGCACGGC TCTTGGGTAA ACCACTGCCT TCAAATCCTC GCAGGCCACT GTGGCATTAT 2220
CTTGATGACG AACACATTGC GCAGTTCATT GTGGCAATTA TTAAAAATGA GGTAGGAAAA 2280
GCACGCGCAG AATTCATTGT ACAAAGACAA GGTGAAACAT TGTATCTGGA AGTATCCTTA 2340
TTCCGCTAA TTTGTGACCA AAAGATCCGC GGAAGTATTA TCGCAATACA TGATATCACA 2400
GAGAAAAAAC AAGAAGAAAT CTATAACCGA AGCTAGAAAG TCTTGCAAAT TTAACGAATC 2460
TTGCAGCAAC CGTTGCGCAC GAAATCAAGA ATCCCTTAGG AGCAATGAGC ATTCATCTGC 2520
AATTACTACG TAAGAATTTT AGTACCTGTA GTTTCGAAAC AAATAAAAGA ATCCAAAAAC 2580
ACCTCCATGT GGTAGAGGAG GAAATCGAAC GGCTCAATAG AATTGTCACC GGCTTCCTTT 2640

CTGCAGTTCG TCCCTTAAAA CTAAATATCA CACGGCTGAG CGTTTTTGAT CTTGTTACAT	2700
CCATACGAGA CACATTTATG AAGCCTTCAC CAAAGCAGAA CTGTCTTTCT CTGTACATAT	2760
GCCACACAAT CTTCCCCACA TACGAGGCGA TGAACACCTG CTAAGACAGG CATTTGGTAAA	2820
CATTATCACT AATGCTAAAG AAGCCATGCA AAGAGGAGGG GCCCTTGAAG TCTTTGTCCA	2880
TAAACAAACT GACCACATCA GTATCAGTAT TTCGGATACA GGAGAGGGAA TTGATGCCCCG	2940
AAATATTCAC AATATTTTTG AGCCGTACTT CACTACTAAA ACTGAAGGTA CGGGGTTAGG	3000
GTTAACCTTA ACGTTTAAAG TGATTAAAGA ACATGGCGGT GACATCAGTG TGTCTCTAC	3060
TGTTGGACGG GGTACGTGTT TTA CTCTCTT TTTACCCATA GATAAATTGG GACGATCGCT	3120
TTTACAAGAA AAAATATCCA CCCACCTAAG ACATACGAGT AAAGAATAAG GAAATGCGAT	3180
GAAATTCAGT ATTCTCGTAC TAGATGATGA AAAAAATATC CGTGAAGGTT TGCAAATGGC	3240
CCTCGAAGAT GAAGGATATG AGGTGTTTAC CGCAGAGGAT GGAAATACAG GGGTAGAGAT	3300
TGCCCTCAAA GGGGATATCG ATCTATTAT CACTGATTTA AAAATGCCtC GTATGAGCGG	3360
GGaATTGGTG CTGCaACATG TGCACGCGGT GTTGCCCGAT ATTCTATCA TTATTCTCAC	3420
CGGGCATGGC ACAGTAGAAA ATGCAGTTGA AGCAATGCAC AAGGGAGCTT ACGATTTTTT	3480
AACTAAACCA TTGGATCTTA ACCGATTGTC TTTGCTTGTG CGCCGGGCGC TACAAAACCG	3540
AGAGTTGATC GTTCAACATC GAGAGTTAAT CAAACAAATA GGAAATCGCA CCTCATTGCA	3600
GAACATTGTA GGAGAAAGTC CTGCAATGAA CAAAGTGTtT GACATGGTAA AAAAGGCAGC	3660
CGCCTCAAAA GCGTCCGTGC TCATTACTGG AGAAAGCGGG GTCGGTAAAG AACTTATCGC	3720
GAATGCAATC CATAATCTTT CGCCGAGGAA GGCAAAACCT TTAATTAAAG TACACTGCGC	3780
TTCTTTTGCA GAAGGAGTGT TGGAAAGTGA GTTATTCGGT CATGAAAGGG GTGCCTTTAC	3840
CGGTGCGGTC AATCGCATGA AAGGTCGTTT TGAACCTGCG CACGAAGGAT CAATGTTTCT	3900
TGATGAAATC GGAGAAGTAA GTATGGCTGT GCAAATAAAA CTACTCCGTG TGTTACAAGA	3960
ACGTTCAATT GAACGTGTAG GTGGAAGAGA AACAATAAAA GTTGATGTAC GCGTAATTTT	4020
TGCAACAAAT CGTAATCTTT TAGAAGAAAT TAAACGCAAT TTGTTTCGAG AGGATCTTTA	4080
TTACCGATTA AATGTTGTGC ACATTCACGT tCCTGnCTGC GCGAGCGcAA GGAGGATTTG	4140
CCATTACTGA TTGCAACATT TCTTAAAGAG ATTGCAGAAG AAAACGGTAA AAAAATTACC	4200
TCTATAGATC CTCAGGCCCA GTCTGCACTG CACGCGTATG ATTGGCCTGG TAATATTCGT	4260
CAGCTGAGAA ACTGCATTGA AAGCGCTGTC ATTATGAGCT CAGGTCCTGT TATCCACATA	4320
GAGGATCTCT CAGAGCCAAT TCGATCTCTC GGTGAAACCT CTTCCATACG CaTTCTTATA	4380

692

GGAGTGAGCa	TGGAGGATGC	aGAAAAaGGAA	aTCATCCTCC	AGACACTGGA	AGCACAAAAA	4440
GGTAATAAGA	GCAAAACCGC	AGACGTGCTT	GGCATTGGGA	GAAAGACGCT	CTATCTAAAA	4500
TTAGATCAAT	ACACGAATAC	AAGCTTTGAA	CCTGATGCCG	CAGCAAAATC	ATGaAACGTG	4560
cTTTGATAAT	CACCGGAGGT	GAATATGCAC	CCTATGAGTT	TGTGCAATAT	TACCTGCCTG	4620
CGTACGATCT	GCTCATTGCC	GCTGATTTCAG	GGCTTGATAC	CGCATTGCAA	TTTGGTCTTG	4680
TGCCCCGATTT	TGTTATTGGA	GATATGGATA	GCGTTAAGGA	CAACCTGTTC	ATACAGGCGT	4740
GTGATAAAAC	GCGCACACAC	CTTTTCCCCC	GAGATAAAGA	TTTTACTGAT	ACTGAGCTTG	4800
CAGTCACCCT	TGcGCACCAA	TTGGGAAGCG	ACGATTTGAG	CATCGTCGGA	GGGGGTGGGG	4860
GAAGGGCAGA	TCACTTTTTA	TATTTTCATGC	GTCTTTTTGC	CGCACCTCTG	TCACCGCGTC	4920
TGTGGCTGTA	CAGACATGGA	CTGGGATATT	GCTTTGGGGA	AGGATGTGTT	ACACAACAGT	4980
TATGTATTGG	AGGAGTGGAT	AATACTTCTT	TTCTTTTCTT	TCCCGTTGGA	GATGCTACAG	5040
ACTATTCGCT	CTCCTCTGAA	GGATTGCATT	GGCCCCTCGA	TGGGgTGCCg	TGGCACACTC	5100
ATGTAAGTAT	GAGTAATCGC	AGCAGCGCAC	CTGTCGTGCG	CGTCGAAGCA	CACCGGGGGA	5160
GATTTTTGCT	TTTCCTTTCT	CCCCTCGGAC	GTTACACCAT	TGATCATCAC	GAGCGGGGTA	5220
TTGCGTGCAC	GCACAGAACG	TAGATATTGC	GCCGGGCAGT	ACCTCGACCG	TTCCATCAT	5280
AGTGGGTATT	GACCCAGGAC	TTGAATCTAC	CGGATACGGC	GTTATAGAAG	CAGGGGGAGG	5340
CAGTCTGCGC	TGTCTTACTA	CGGGGTGATT	GTTACCCAAA	GCAATCAGCC	ATCTGCTGCA	5400
CGACTCAGAC	ACATCTTCGA	TACCCTGCAA	CAGGTAATCT	CAATATATCA	ACCTCAGTAT	5460
TGCGCAGTGG	AGACAATCTA	TTTCGCAAAG	AATGTAACCA	GTGCGTTGTG	TGTTGCGCAA	5520
GCGCGTGGGG	TTGTATTACT	TGCTATGGCA	CAACAGCACA	TTTCAGTAGC	TGAATACGCA	5580
CCGAATGCGA	TTAAAAAAGC	AATAACTGGT	ATTGCCCAAG	CAGAAAAAAG	ACAGGTACAG	5640
CATTTGGTAA	AAATTTTACT	CAATCTTAAG	GATATACCTC	ATCCTGATCA	CGCTGCTGAT	5700
GCCCTAGCGG	TTGCTGTTAC	CCATGTACAC	TGTTGTATGT	CTTCAAACCTA	TGCGGTAGGT	5760
TCAACGCGCT	CTAGGGGAGC	GTACGTTACG	CTGTACAAAA	AAGGTAAGAG	ATGAAAAGCA	5820
AGAGTTCTTT	GTGAAAAGT	GGGTTGCTGC	TTTCTCTTTT	AACACTTGTC	TCTCGTGTAT	5880
TGGGTTTAGC	GCGAGAAGTA	GTGAAGTCTA	CGCTTATGGG	GACCAGTGCG	ACAGCAGATG	5940
CATTTACCGT	TGCATTTATG	ATCCCAAACC	TTTTCCGCCG	ACTGTTTGCA	GAAAACGCCA	6000
TAAGTGTTGC	CTTCATTCCC	GTCTTCACAC	AGCACTACTC	AATGCCGAGT	TCAGCGCAAG	6060
TGCCATGTTT	TTCTAAAACG	AAGGAGTTTC	TTTCAGCTAT	CTTCACACTG	ATGAGTAGTG	6120

693

TCACTGCAAG CATTTCTCTT ATCGGTATAC TCGGTGCTCC GTACATCGTG CGATTATTTG 6180
 ACACTGATCA GTCATTAACC GTTTCATTAA CCCGCTTGAT GTTTCCTAT TTATGGATGA 6240
 TCTCTCTCGC AGCTTTCTTT CAAGGTATGC TGCACAGTAT TAAGGTATTT GTCCCCTCAG 6300
 GATGTACCCC AATATTTTTT AATGTCAGTG TCATTTTTTC GATGTACTTT CTGAATGTGT 6360
 CACATATGAA CGTGGCTATT GCTGCAGCAA TAGGTGTTCT TATAGGAGGA TGTGCGCAAG 6420
 CACTCTTCCA GCTAATATTT GTATATATGC ATGGGTTTCG TTTACGCTC CAGTCTCCTT 6480
 TAAAAGCAAT GCACGATGAA GGTGTGCGAC GAATCATTGC GTTACTTCTA CCGACAACGT 6540
 TTGGCATTGC AACCTATCTT CTAAATGACC TGGTGTGTAC TGCCTTGCA ACCTCTGTTG 6600
 AGATAGGAGT TGCTGCGAGT GTGCAATATT CATTCGTATA CAAGAACTTT TATTAGGrAT 6660
 ATtLATCGkT TCTCyAAGCT CyGtGGkACT TCCTGAtCyT TCyTTCCaTG tTATGAGAAA 6720
 AGATTGGCAA TCGTTTGAGG ACCTCCTGAT AACA 6754

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

GCCAACGCGT TGGCGGCCCT ATGTGCATTT CCGTTCTGCT TGGTGGTAG TGGATTGTGG 60
 AACACGCTC ACCTTTACGG CGGTGGATGG CACGGGGTTG ATTtCAAGGG GTGGCAATTG 120
 CGCCTGGTct GCgcACTGCG GTGCAGTCTC TCCATACAGG AACGGCACAA TTACCACTTG 180
 TTCCTCTTGC CCTGCctGAT TCCGTTCTGG GCAAGGATAC TACGCATGCG GTGcAGGCGG 240
 GTGTGGTGCG GGGCACGCTC TTTGTTATTC GCGCTATGAT TGCACAGTGT CAGAAAGAGT 300
 TAGGGTGmCG CTGTGCAGCG GTGATAACGG GGGGGCTTTC GCGTCTTTTC TCGTCAGAGG 360
 TGGACTTTCC TCCTmTCGAT GCACAGtGAC GCTCTCAGGT CTTGCACATA TTGCGCGGCT 420
 GGTGCCGACA TCTCTCCTGC CACCTGCTAC AGTGyCaGGT TCATCGGGGA ATTGAGGAAA 480
 CTGTTATCCG CGCTCCCCAT CTTCCGATAC TGGATCGGTG TCGGGGGAG TAGGAGTGGG 540
 GAAGCGTCTG TGCTGTATCG CGCTGGTGAT GCGCGCGTTC TGGTACCTCa kTsCGAAGGG 600
 AgTCAGTaTc GCTTACGTGC CCgTTCaTcG CAGTGGGGGC TCTCAAGATT cGAGCATGAG 660
 CACAGCAGTG GCGGATACGC TCyTTAACGC CTTyTTGAC GAGGrAATGG TGGTTACGgC 720

AGTACCGCCG	GGTGACACG	ACGGCCAGAC	TATAGCAGAA	ATTGCTGCAT	GTTTTGAAGT	780
AATGCCCGAT	TACGCGTTGT	TGGTGCAGTT	TCATTCCGCT	CGTCTCCCTG	GTGGGAAAG	840
CCCTACCTCC	CGTGCCCGCG	GCGCTTGGTC	TTCAGAGAGG	CCGTGCTG	TGTGGACATT	900
AGTGGATTTG	CATACGCAGC	GCGCGTGTGT	CTATGCGTGT	GTCGCCCCAT	ACAGGGAGAG	960
TATTCCCGTT	TCTGAGTGTG	TTGACGTCGT	TACCCGTTGT	ATTGCGGA _g C	AGG _c AATTTC	1020
GTACATACGG	GTGGGCACGA	GCACCGATAC	AGCCGGAGTT	CAGTTATAGA	AAATAGGGAA	1080
TACGTAAGGT	GTCTGCAGCG	TCGCTTCAGC	TGGGAGGAGT	CTTATGATTA	AACGCCACAT	1140
GTTCGCAAAA	AGGGGTGTCA	AAGGAAGATC	TTACCTGGTT	AGGGTGAAn _a	mTGCCTTCTT	1200
AGTGCTTTGT	GTGCTTCTG	TCACGCCGCT	TTGGGCTGTG	TGGGAAGGGA	ATGCAGAAAT	1260
TGGCCCCCAG	GGAAGTTTTC	TGCAGGACGG	CATGTTTGTG	CGCAGTGACA	TGTTCCCCAA	1320
AAACACTGCT	GTTGAAATTA	GCAACTTAGA	AAAGAAATGCC	AAGGCTCAGG	CAGTGGTTAT	1380
TGGGCACGCA	GGGATCCCCG	GTCTTCTAGT	TAGCCTTGCA	CCCCTGCTG	CAGCACAGCT	1440
TGGGATTGGC	GTATACCAAG	CTGTGCGTGT	ACGCGTACGT	ACCTTGGGTA	CCGTGCGCGG	1500
TGGGTCTCAA	ACAAGTCAGG	ACGGACTGTC	CCTTGCACT	TTGCCGTCCC	GTGTGCCTGC	1560
GCGCCCCGCC	AG _c gTGATCC	TCTGTCAATC	CCGCCGCGAG	GTCACACTGT	ACCGGAATAT	1620
CGCGATACGG	TTATTTTCGA	TGACCCGCGT	TTGGTTTCCC	CTTTGTCTCG	TGAGGTGGAG	1680
GACGCGCCGA	AGtAGTGAG	CCGGCCTCTG	AGCGTGAGGG	AGGGGAGCGT	GAGGTGGAGG	1740
ACGCGCCGAA	GtAGTGAGC	CGGCCTCTGA	GCGTGAGGGA	GGGGAGCGTG	AGGTGGAGGA	1800
CtGCCGAAG _g	TtAGTGAGC	CGGCCTCTGA	GCGTGAGGGA	GGGGAGCGTG	AAG _g TGGAGG	1860
ACTGCCGAAG	GTAGTGAGC	CGGCCTCTG _c	AGCcGTGAGG	GcAGGGGAGC	cGTGAGGTGG	1920
AGGACGT _g CC	GGGGGTAGTG	GAGCCGGCCT	CTGGGCATGA	AGGAGGGGAG	C _g TGAGGTGG	1980
AGGACGTGCC	GGGGGTAGTG	GAGCCGGCCT	CTGGGCATGA	AGGAGGGGAG	CGTGAGGTGC	2040
CTTCTCAGCA	TACGAAGCAG	CCATCCCCT	CGGTTTCCAA	CTCAGCTCCC	AATCAGTTTC	2100
GGAACCCTGA	GGGGGAACTC	CCCTTTACGC	TCCCTGACCT	ATCCGAGTCA	GAAATTGTGG	2160
TTCCGAGGA	ACAGAAAGGA	CGTGCGCATC	CCCAGGTGAT	ACCCGAGGGT	GCGCCACGTG	2220
GA CTGCAACC	TGGTGAAT _a c	TACGTACAGA	TTGCAGTCTT	TCATGACGCT	ATCCAGGTGC	2280
AGAGCATTGT	CCACCGTTAC	GGGGTAGAAT	ACCCCATCGC	AGTGGAGCAG	GACATCCATG	2340
AAGGTAAGGT	GCGTTTCACC	GTATGCGTCG	GTCTGTCCA	AAAAGACGAA	CGCGGCGCGt	2400
ACTAGAGAAC	TTCCAAAGGT	TTGGATTCAA	GGACGCCTTT	CTGAAAAAGG	CGCGATGATC	2460

AGGTCGGCCC	TCCTCTTCCC	CTCGTGACCG	TGGTGACTCG	CCCCGAAGc	GnCaCAGAGC	2520
CCGAAGaACG	GAAGGGAAGG	GGCAGACTTA	ACTATTTCTT	TGTTTTTTTG	AGCACGTAAA	2580
ACGGCGCCAT	CTCCTTTGAA	GGCTTTCCTG	CGCCGGGAGC	GCCCATGTAG	CGAACGGAgT	2640
TACTGTCTAT	CAGCTCGTAC	AGCTCTTTCT	CGTGCGGTGC	CTTCGATTGC	TCCGAGGACA	2700
CAAGCGAGAG	TTCGACAATT	CCGTCTTCAC	GTACCATCCA	CGTACCGCGA	TACGTAAGAG	2760
GAGAAGGTGC	CGACTTCTTC	TCAAGGGCAA	GCTCTACCTT	TTGCGCAtGC	CATCCGCGTT	2820
GAACGTCACA	GTCGTATCGA	TTCCCGGGCA	ATCGGCCGCA	GTAGCGTACC	CCGAAAGATA	2880
CCTCCCTTCA	ACGCGCACTC	TAsCTTTTCC	GCTTtGGCCT	TCCCGGCGTG	CGGACACAgG	2940
TTGTGCACGA	GACACACAAA	GCGCTAmCGA	GCGCTCCAAC	ACCAAGGAAC	GCGCACAGgs	3000
CGGsACAGAT	CtTTCATCAC	AGAAAACCCC	CTTGTCACGT	CTGTAAGnTC	AGGGGAGAAA	3060
AGCCCAACGA	TGCAAAAGTT	ACGCTCCCTC	TTGCCAAAAG	TGAGAGAAGA	GCGCAGGCCA	3120
CgCGCACGgr	GGCAAAAGTG	GGGTTTAGGA	GCGCACCTGC	GCCCCGGCCG	CGGGTGCACG	3180
CATCTGAGCC	TCAAAGGCAG	CAACAAAGCG	GGGTAACAGT	TCATCAACGG	TGCCCTCGAT	3240
ACGAAGGCCA	GCAGCGCAGC	GATGACCTCC	ACCCCCGAAG	CGAGCGGCGA	TAACGCTTAC	3300
GTCAATCGAT	CCTCGCGATC	GAAACCCAC	CGAACAATGT	GTGGGAGATT	CCTGACGTAC	3360
CACCACAATT	GCCTCGACGC	CCTGGATGCT	CTGGATGAGC	TGATACAGAG	CATCGGAGTC	3420
TGCGACATCA	AGCCCCAACT	GGACCGCGTC	TTCGCAAGTT	TCGTACGAGG	TCATGAGCGC	3480
GCCACCATAA	TACGGCGTCA	GTCGAGAAAG	CACGCGCGCA	ATCAACATGC	GCGAAGCAAG	3540
GGATCTCCCA	CCGTTTCATGG	CAAGAAACGT	GTCTTCGGAT	TGGCGCCTGC	ACGTACAAGA	3600
CGCGCAGCAG	AAGCGAAcGT	GTCCGCACTG	TGCTCGTCTGA	GGTGGCGAAA	AAAACcTGTG	3660
TCCGTAGCCA	ATCCCCAAAA	AAGTGCGCGC	GCCTCGGCTG	CTTCAAGAGA	TCCGGCCATC	3720
GTCTCGATTA	ACGTTTGCAC	CAATGTAGTG	GTGGACGGAG	CTGTTTTAC	GACGAACGAG	3780
TGCGCGCAGT	GGTCGCCGCA	CGTTTCGTGA	TGGTCTATGA	ACGCGCGCGC	AAAGGGGGCA	3840
AGCTGCGAGG	CGAGCTCAGC	GCCAACGCGG	CTGAGCTCAG	AGCAGTCGAC	CACGATGAcG	3900
gCCGTCTGAT	CAGACGGCcG	TnAtCTGCGC	AGAGAGACTT	GGACGGAAGA	GTGTCGCGTA	3960
CGCAGCGATC	TCTCTACGCT	TGAAAGGACC	CGCAGACAAA	AGCTCAACCT	CTTTCCCTAT	4020
GCGTCTTAGG	AACGAGGCAA	GCGCAAGACT	GGAACCTACA	CAGTCCCCAT	CCGGCTTCTC	4080
ATGCCCCACG	ACCGCAAACG	CGCGATGCGT	GcaATGAACT	CGATGAGCCC	GGAAAGACCC	4140
CTCCCCCGAT	CCCCTGTACG	CGCCGCGCAC	GGAGAGGGGG	AGGAAACGGA	CTTAGGAAGA	4200

696

GAACTCGGGG	GACTGGAAGT	GAACATCAAA	CTTATCGTCG	TACTCAGAAG	GACTTTTCAG	4260
CGTTCCCCAC	ACCGGGCTGC	TCAGGCTGCG	AGGGAGTGTG	AGCTTTACGT	AGGTAAGTGT	4320
GTTCCCTTCC	ATAAAAAACG	AAAGGTAGGG	ATCGACGCGC	ACTGGAGcGT	GCCGCAAGAG	4380
CGCCTTACCC	ACCCTGGGCG	AGAACCAGGC	GGACGGCAGA	TAGATCTCGG	CCATTTTCGAA	4440
GTTAGCACGC	CGGTAAATAA	CCCATAGGCC	CAAGCGGTGA	GAGAAGACTT	TCACCACAGG	4500
AAGATTGACG	TAgTACATAC	GAGAAGAGTT	GCTCTCTGTG	AGCCCTGGGG	GAGGGGGCTC	4560
TAACACACGC	CCAGCAGTAT	CAGATGCATC	CTGCGCACTC	AGAGCGACAG	CAGAAGCGCA	4620
CAGCACAAGG	CGTAGACAAC	GAGTTGAAAA	TTTCATAGCA	AAACCTCCGC	GGCGGCAGGA	4680
TTCTAGCCTA	GGTGTGTCCC	TTAATACAAG	CGTCTGTATC	ACGCTCCTTG	CAGGTAAGTG	4740
CGCCGTGAAA	AATGCGCGCG	GTTGATTTCT	TGCGTAGAGC	TACAGTATGC	TGGTACATGC	4800
GCATTTATCT	TGCGTCAAAC	AACGCGCACA	AGCACGCGGA	GTTCTCCTCA	CTTTTCCCCA	4860
TGCACACGAT	TCTCCTGCCG	AAAGACGAGG	GTATCGATTT	TTTCTCGCCT	GAGGACGGGT	4920
CTACTTTCTT	TGCTAATGCA	AGGCAGAAGG	CTGACGCCCT	CTATGACGTG	GTACATGCGC	4980
CTGTGCTCGC	CGATGACTCA	GGTCTCTGTG	TGGATGCTTT	AGACGGGGAC	CCAGGGgTGC	5040
ATTCGGCGCG	TTTTGGTGCA	CAGCATGGGG	TACACACAGA	CAtGCGCGCA	TGCAGCTCCT	5100
TCTGGAACGT	ATGCACGGAC	GGCArgACCG	TGCCTGTTCC	TTTGTGTGTG	TGGCGGTACT	5160
GAAGTTGGGA	TCGGTGCCGT	TGTGCGTTGG	GCGGGGGGTG	TGCCgGGGAG	TGTTGACTAC	5220
AGAAATGTCT	GGGGTAGAAG	GTTTTGGCTA	TGACCCGATT	TTCTGTGTGC	CACACCTGGG	5280
CAGGACGTTC	GCTCAGCTCA	GCATTGAGGA	GAAGAACCGC	GTCTCTCACC	GGGCACTTGC	5340
GGCGctGCGC	CTCGCACAGG	TGTTGGCCAT	GATGCAGCTA	CCCCGTkgsT	GCGCTACGAG	5400
TTAAAGCTTT	TGCGTGGTGC	TCGTCGTATG	AaCGCGCGGC	GGCGTGCTGC	GGCCTGGCGC	5460
CCCCTGTGCG	CAACGTAAGG	GACAGACCGC	GCAGACTGCC	CGAAGACACA	AATTTTATGC	5520
ACGCGCTCGG	AGGTGTGCCC	GTCGCATACA	TCGTGCCTAG	TGCTCTGCAA	GGTGCGTGAg	5580
CGAACGGAGT	GCaGGACACG	CGCTTGACTG	CAGCTGAGAG	GAGGGATTGT	ACGAAGACGA	5640
TGTTTTTTGT	ACCATGGCCC	CACGCTGCAC	CATCGGAGGG	TCCCCATGGC	GGTAAACGAC	5700
GAACAGTTTC	AACTCGTTAC	CTTCCAGCTC	GGGGAGGAGC	TTTATGGCAT	CGACATTATG	5760
GGTGTCAAGG	AGATTGTGAA	GGTTCAGGAC	GTTCGTCCTA	TTCCCTGTGC	GCCTGCCTTAC	5820
GTGGAGGGCA	TTTTTAAACCT	GCGCagcGAG	ATTATCCCTA	TTATTAACCT	GCACAAGCGC	5880
TTTCACCTAC	GCGAGGCTAC	GCTCGAGTCG	GGCGACGAGT	ATCTCGGCGG	CTTTGTCATT	5940

697

CTCAATGTGG AGGACAGTAA GCTCGGCATT ATCATCGACC GCATCGCGCG TGTATCGCT 6000
GTCTCGCAGG AGGACGTGCA GTCCCTCCC CAGGTTATCA CCGGcATCGG GGCGGAGTAC 6060
ATTCATGGGG TCGTGCGCCA GGGGACGAGT TATCTTATTG TTCTGGATAT CCACAAGCTG 6120
TTTAGCTCCA AAGAGTTGCA AAAGCTCGCG AACCTCTAGT GCCCCACCGC TGTCTGTCTC 6180
CTGCCTGCAG CTCCAAGCGC CGTGCGGGGT CCATCCCCGT CCACAGCCCC GCCATCCGAA 6240
GgTCCGAAAT GGACGCGGTG CTCACCTGCT TGGTGGATGA AAAAATTGGC CCTGGTTTCG 6300
TTGGCAGCAC CCTCATCCAG TTGGTGC GCG AGGTGTTTTT TCCAATCGAT GCATAcGTgc 6360
TGCGCAGCCC ssTATCGCAC TTTCTTTgC ACTCCGTGCA CTGAAATTGC CTCCTGCTTC 6420
CCCTGTACTT CTTTCTGCGC TTGCGCCCTT CTGGCACTAC CGTGAGGTGC TTCACCAGGG 6480
GCTGCAGCCG CTTGTCTTG ACGTAGACAT TCACAGCGGT TTGTTGTCCC GTGATGTGGT 6540
GGAAACTGGC AtCGCGCGTG GCGCTCGTGC GCTTCTTGTG CCTGAAACAC TTGGAAATGT 6600
GCCTCCTGCA GCGGTGTTTT TGGAACTGGG GATACCCGTC ATCGAAGACA GCTCTCAGAG 6660
TGTCGGTGCA GTATtGGGAG AAAAGAAGGT GGGAAAcTTT GGCTCGTGTG TCATCGTGGG 6720
ATTGGAGGCA CACGATATGC TTACCGCAGG CGGCGGCGCG GTACTCATGG CCTTTGAGGC 6780
CGCCTGCGCG CGTCGGCTTC AGGCGCTTGT GCCAGAAGCG CTTGCCGTTG ATATGCTGCC 6840
GGATATGAAC GCGGCGCTCG CGTGTGTCCA AGTAAAGCAG CAAGAAAAAA ATATTGCCCT 6900
CAGGCGCGCA ATCTACGACC GATACTCCTC TGCGCTTTTG CGTACGCGTC ACGGTACGCT 6960
TCACCGGTGT GAGCAATTGG AACACAGTGC CTACGCTTTT CCTGTTGTCC TTGCTTCTGA 7020
TCTGAAGGAA GTGACGCGTT ACGTGCGGCA GCGCTCCATT GAGATTTCTC CTGCCTTTGA 7080
ACATTCCATT GTGGCAGCGT TTCAATTACC TGCTATGCGC AGACGGTGGC CTTTTCGCA 7140
GTTTCTTCCT ACTTCTGCAT CGCACACGGC ACCTTTTCAG GGTGAGGACA GGGAGGTACT 7200
AGAGACCACG CAGGGCGCGG AAAAAACCTG TCAGGACTCT AGCTGGGAAA GGGAAAGTGC 7260
TGCGTCTGAG ATTACGCCCTG AGATGTGTTG GCCACATGCA TCTGCGCTTT TGTGCGCTG 7320
CGTGCGCTTT CCGTTGTACC CGCGTCTTGC GCCTGCACAC GCACAGGAAA TTGCGCGCAT 7380
CCTTGGGACA CTGCCGTGAG CAGCCGCGTG TGTCTCAGC GGCTGTTGC AAAATCATCG 7440
GGGGACGCGA AgGTGTTGCT TATTGTCAGC ACGTACAAAC CGCGCGCTGC GtGCTCGCTG 7500
CGGACGTTGT GAACTTTCTG AGCATACGTG GATTCCAGTG CCACACCATT GAGTATGATG 7560
GATTGAATAA AGAAAGCTGT GCTCGCGCAG GCTATATGTT TGCAGTCAGT ATTGGGGGGG 7620
ATGGTACTAC ACTGTTTGCC GCGCGCTGTG CTTCTCCTTC TGGTATTCCC ATACTTGCCA 7680

698

TAAATTTAGG GCGTTTCGGC TTTATCGCTC CTATTGAGCC ACGGTATTGG CAACAGGCGT	7740
TGAGCGATTA TTTGGCAGGG GGGGTGCGCC CTGCTGAGCG TCGGCTCATA TCGTGCACCG	7800
TCACGCGTGC GGGTAAAGAG ATTGCTTCGT GTCTGGCGTT AAACGATGTT GTCCTTTCAA	7860
GTGGACCGTC GCGCGTCTTA CCCGGGCAGA GGTGTGCTTC AACGACATT CTTTTGGCGT	7920
GTATGAAGCT GATGGCATT TTTCTGCGAC GCCTACAGGA TCTATGCGTA CTCGGCGGCC	7980
TGTGGCGGTC CCATCCTCGA TCCGGACCTT GATGCGTTTG TCCTCACTCC CATAAGCGCA	8040
CTGTGCCTTT CTAATCGTCC CGTGGTAGTT CCCTCCTCAG GGGTGGTGCG TATCAAGGTG	8100
TTGTCTATGC GACACAAAGA AACGGTGCTG TCTGTGGACG GACATGAATT GTGCACGTTG	8160
CAGGAAGAAG ATCAGCTGCT TGCAAGCAGG TCaTCGTGCA GCGCACGATt GGTTTTCTGT	8220
ACACCACACG TGTCTACCA TGCACTGTGC TCgAAACTGG CGTGGTCAGG GAGTATTTTT	8280
TCTCGCAGGG GAAGACGTCA CGATGATTGA GCAACTTTTCG GTGCGCAACG TTGCGCTCAT	8340
TCAATCTTTG GCGTTGGAGT TTGGTGACA GTTTACTGCC CTCTCAGGGG AGACGGGTGC	8400
GGGTAAAGTCA ATGATACTCG GCGCGCTGTC CTTTCTCTGT GGGCAAAAGG TAGGGCCTGA	8460
TCTTATTCGC AAGGATGAGA ACGAGGCATG GGTTCCTGCG GTGTTTCGCT GTGAtCACgc	8520
ACCGCGTGCG GTGCACACAT GGTGGCAGA ACGGAGTATT GAGCCTGAGC ACCACCGCGT	8580
GTCCTTCGT CGGGTGATGC GCGGTACCGG TCGTGGCAG GCGTGGATTC AAAACGTCCC	8640
GGTCTCTCGC GCAGATTTGG AGTTTTTCAC GTCATTTTTT ATAGACCTCC ACGGACAGCA	8700
TGAACACCAA TCGCTGTTTC GTGTGCAGA GCATCGCCGC TTTCTGGATA CtACGGAGGA	8760
CTCCAGCAAG AAGTTGATGC GTTTACTGCG TGTATGCGG CTCTGCAGA GCGACGCGCG	8820
CAgcTGCAGC GGeTCGCTTC CTGTGAACAC AACC GG CAGG AGCGGCTAGA ATTCTCTCC	8880
TTTGCCCTTG AGGAACTGGA GCACGCAGCG TTGGACGTGC ATGAGGAGCG TGCGTTGGAA	8940
GGAGAAGAGC AAAAGCTCTG CCAGCACGAA AACTCTGTG ATGTGATGCA AAGGGTTGAC	9000
GCTGCAATTA GGGGGGTGGA CCTGCAAGAG GCGCGCTGC TTTCTTCCTT AAAGAAAGCG	9060
CTTGGTGAC TTTGAAAGCGC CTGTGGGATT GATGGGAGTC TTGAGCCGGC GCGTGCCCGT	9120
TTAGAAAGTG CGTACTATGA AATCGAAGAC GTAGCGCATG TTCTGCGTAC GTATACAGAC	9180
GGTATTCAGT TTTGTCCCGA CCGTTTGAG CACGTT CAGG AGCGTCTTGC GCTCATATAC	9240
CGGCTGAAGA AAAAATATGG AGGAACAGTT GCGCAGTTTT AGAATACCGT GCGCGTGCGC	9300
ACAAGAGATG CAGGATCTTT CACAGGCGGT GGGTGATAAA GAGGCGCTTG AGCAAGATGT	9360
TCAGCGTCTG ATGGCTCAGT ATTACACGCG GGACGTGCCT TATCGCTTAA	9410

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

CTCTTAGAAA CCGGTnCACc GATcCACACT CCCTCTGAAC CGAGATATTC GGTACGCCGT	60
CCTTCAATCA AAAACTGCAC CGCATGCACC GTAGGAAACG CAGCTGCCGT GAACACCACC	120
TGCGAAAgTG CGCCAAGTAG CCCTCAATGC CATACTGATT GAACTGAAAC TCCTCGCTCA	180
GATCCAACAC CGCCACCCCT TCTTGCACGC GTGCAGAGCG CAGTCGCGTA CCTTCAGGGA	240
TGAGCGTACG CAgTCCGCGC ACCGCTTCTG CCTCAGACGG ACCAAGGAAC AATGCGCGCA	300
ACGCATCCGA AAGCGGCACC GTCGAATGAG GAAGCGTGCG AGCTACCTCC TCACGAGTGA	360
TCTTTCCATC TGCATCAATG CGCACCCAGC ACAGCGTAAT TGCGCGGGAC TGTGTGCAG	420
AACCGGGCGC CCCAGAAACc GTGCCGACAT CTTTCCTTCG GTACCAGCGT cAsTGGCGCA	480
GGGGATCCTG CAACAGGAGC GTCCGGCTGT GCCACATCCT GCGTAGGGAG CGTGGCTTTA	540
GCATCACTTT CAACAGCCGA GCCGGCCTGA GAACGACGTG CAGAGTCAAA AACGCGCATG	600
GAATCCTGGT TGCCGAACAT CCCTTGCACT GCAGCGCTCG AAAACACACG GTCAATATTT	660
CTTCTATTGA GAAAGAAAAG CACCGCCATT AACAAGGAAA ACGCAAGCCA GAACAGCAAC	720
CCCGCTGATG AGTGTtTCCC CTTCCCGGCC ATACAGCGCC ATCGTACAGG AATTATAAAG	780
CTTTTCCAAG ACATGCTGCA CACACGTCCC TTATCCCCGC CTTGCAAAAA ATATAGGCAA	840
AAAGAAAATA AAGCAGCCGA TATTGGGTCG TGCGCATGGC ATTCATGTTA CTGGCCCTGC	900
TTTTCTCTTT TCGTAATGCG TCCATTcAGG CAGAGGACGC GCGCCTGCTG CAGCCAAAAA	960
CCAACGCTTT GGATCTTGTC GTGCAGGGGG TAGATCTTGT GCTGTTTGCC CAGGATAAGA	1020
CGGCTATCAG TATCAGTACC CCTCCTGAAA AAGACGTGTT CTTACAGAA CACGAAGGGG	1080
TGCTTCGTGT CCGTACACGC ACAGAAAACG CGGAGGGTAC ACGCCGAGTG ATACGCATTG	1140
GCATACCGCG TGCACAAACG CTCGCATGGG TGAAGATCAT TGCGACGGGC GCACATACTA	1200
CGGTGCGCGG CGTACGcGCG GtGTGGTCAC TGCTTTTGTG CAACGAAGGC AACTCGCCC	1260
TCACGGAAAG CACGCTCAAG TCATGCACGC TGACACACAC GCGCGGCGAA CTCCGCTTTG	1320
AAGCGGCGGT ACTAAACGG GCGTCATTCT GTTTGAATGA CGTGAACGCT CGTTTCACTC	1380

700

TTCTCGGATC	GCGCGCCGAC	TACCGTCTTA	TCTGTAGCCC	AGGAGAACGT	GCGTGAAAA	1440
TTGAAGGCGC	CGAACAACGA	GGCGCGCACT	ACACCGAGCC	CGCACGGGCG	AgaCGCCACA	1500
TGGTTATCAG	CGCGAGTGCT	TCGTCGATAG	ATGTAATGTT	CAAAGCGCCA	CCTACACAAC	1560
AGGAAGCGGT	AGACACGACA	CAGAAGGGGT	AATCCAGGAT	AGACTGCCCC	TTTCAATATC	1620
ACCTCAGATA	GCAGATTAC	ACCGCGCACT	ACTCAAGCAC	GTCAGTGACG	ATGCGCACCA	1680
CGCGTTTTTT	CCCCGCGCGA	ACTATTACCG	TCCCGTCCAA	ATCCAACGCT	GA CTGGTCAA	1740
TTACCGCACC	GATA TCTGCC	ACGCGCTGGA	GCCCGACAAA	AGCTCCTCCT	TGTGCAATCA	1800
AGCGCCGTGC	ATCACTCTTC	G TAGTACACA	ATCCAACCTG	TACAAACAAA	TCAGTCACTT	1860
TGATCCCAAC	TTGCAACGTG	CACTGTGTCA	GCTCGAACGT	CGGCAATGCA	CACTTATCGC	1920
CACACCCGCC	GAATGCCGCG	CGCGCTCCCT	GCAACGCCAC	CTGCGCGACA	gcCGTTCCGT	1980
GCATGAGGCG	CGTTACCTCG	TATGCCAACA	GCTCCTTTGC	ACAA TTAATT	CCCTGAGTCA	2040
ATATCGCCTC	GACATCGCGC	ACAGACAAAA	AGGTAAACAG	GAGCAAGAAA	CGCCGCACAT	2100
CTTCATCCGG	AGTATTTTCG	CAGTATTGGA	AAAAGTCATA	GGGAGACACC	AAAGCCGGGT	2160
CTAGAAGAG	CGCACCTTGC	TCGGTCTTGC	CCATTTTTTG	CCCATCCGCC	CGGGTAATGA	2220
GCGGAAAGGT	CAACCCATGC	ACGGTTTTTC	CGCGCACTCT	TCGAACCAAA	TCCGCCCCGG	2280
CAACAATGTT	GCCCCATTGA	TCATCGCCGC	CAATTTGTAA	CTCTACCGCG	TAGcaTnCAC	2340
TGAGCGTTAA	AAAATCATAG	CTCTGCAATA	GCTGATAATT	AAATTCAAGA	AAGGAAAGTC	2400
CTGTCTCCAG	GCGTTTCTTG	TACGCCTCAT	AGGTAAGCAT	TTTGTTTACA	GAAAAATGCG	2460
CCCCAACCTC	TCGCAAGAAA	TCAATGTAAT	TCAAATGTGC	CAACCAATCA	CGATTATTCA	2520
CATAGAACAC	ATGCCTGTGA	TCGAAGGAAA	GAAAATGATc	CAGcTGC GCA	ACTATCGCTC	2580
CCGCGTACGC	ATCGAGCGTT	GCATAATCGA	GCATCTTGCG	CATACTGGTT	TTGCCGGAGG	2640
GATCCCCAAT	ACGCGCGGTA	CCTCCACCGA	TGAGCACGCA	ACCGCGGTGC	CCCGCATCAC	2700
ACAAATGCTT	TAGCGCAAAC	ATAGGGAGCA	TGTGCCCAAC	GTGCAAACTA	CTGCCAGTTG	2760
GATCTACACC	GACATAAAAG	GTGAGTGGGC	CTGCATCCAT	ACGCGCCGAA	AGCGCCGAAA	2820
GATCAGTACA	TTGTCTAATA	AAACCACGCG	CCTGAAGACG	CGCAAGCgCA	GGaTTCATGG	2880
AGCCGATTAT	ACCGCGCATC	GCACACCCCG	ATCCAGGGCA	GGCGGTT CAG	TCCCGAGAAA	2940
AAGACAAAAC	GCGCTGATGC	ACCCCCACCG	TCGCCCCGCG	TG TCACTATT	CCTTTAAAAG	3000
CGCTGCAATC	TTCGGACGAC	TCCAGCGCAC	CGCAACGTCA	TAGGGTGTCT	CTCCCGCCAC	3060
GTTTCGTAAA	AACTTTCCAA	AGCGATT CAT	CGCCAGCAAA	CtTGCAGTGT	CTTTTCATCT	3120

701

GCAACCTTTG CTGCGTAATG GAGAATACTT TCTCCAGCTG AATCTGTCTT ATTTACCGCA 3180
 AAACCCACCA GCGTTTTCAA GATTGACGTG TtCTTGCTCA GGACTAACAA GGCCGGAGnA 3240
 CTTCC 3245

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

ACAGGGAGGT TCAGGCATCA GAGAAGGACG TCTGTACACT CAGGGAACAG GTTGCCGTGG 60
 CGCAGGGTCT GATTGCTGAG GTTAATAAGG AGTCTTCTTT CGTCGACTCG CTGAGTAAAC 120
 gCGTTGCgGC TGCAAAGACG CAGCTGCAGC AAGTGTCGCG TGCGATTCCCT GATATGCAAA 180
 ATGCATTTAC GCGCGAGAAT ACCGCGCTTC TCCACCGGGT GCGAGATGGA GTACTTGCAAG 240
 ACGTACATAA GGAATTAGCG GTGTTGCAAA CAAGGCTGGA AAAAGCGCAG GGGGAAAGCC 300
 AGTCTCTTTT TGAAGTTTCT GCAGTTAAAT TGCGTGAGTT GTATGAAGGG GCATTTTCTG 360
 AAGCAACTGT GCGTGACAG GTGCTGGAAG AAAATGGATT CGGTCAGTTG AAAGTACAGG 420
 CGGAAAATCG CCTTCTCCAG TTGCAGGAGG AGTTTGAAGG GAGCCTCCTT TCTTTGCAGC 480
 AGCACGTTAT GCAGCGTGTC GAACAAACGG ACCAGCACAT CCAGGATTGT GCATCCCAGT 540
 GGTCTGTTTC GCGCGAGACA TGTGAGTCTG ATTTGAGTAT ACGTCTTGCG GACGTTACGG 600
 CGTGTGTGGA TGAAAGCGTG GCGCAACTGA AGGAACAGAT TACTACACAG GAGCGTGAAG 660
 TGCGTGCGCA CCTGGAAGGG ATCGAACAGT CGCTTTCAGG AGCAGAATCC GGTTTACcGA 720
 GCGCGTGAC AAGAGTGTA CAAGTTTTCA CGAAAACCTA AATAAGATTG CAGAGGCTTC 780
 TGATGCGCAG TTACAGCAGT ACAGGAAGGA GATGGATGGA CGCTGTAGCA AGTTTGACAG 840
 AGAGCTTGAG GGTATTGATG TCCTTGAGTC TCAGTTGCaG CTTGCGCGTG AGCGTACAGA 900
 ACAGAAGGTG CGCGAAGAAT TTGAAGCGTA TGCGCAGGAT CGTGAGCGGA AGCAGTTAGC 960
 GTTTGAGGCA CAGTTGCAGC ACAGTATGGA TACGGTTGAG CACCGTATGA AGCAGCTGAA 1020
 TGACGAGCTG CGTGAGCTGA AGGCAAGTGC GTATGCAAAT GCATCCGAGA AACTGCAGTC 1080
 GGTGGAGGAT AACTTTTTTG AGGTACTTAC CAAGCGCAGm aCTCGTTGCA CGCGCGCTTT 1140
 TCCGAGTGA GTGAAGGGAT TGAGGGTCGT TTGACGCAAC TTGCTCTAGA GAGTGAGTCT 1200

702

GCGCGAAAGG ATCTTGAGGA TACGTACCGC AAAGATGCA CACGCGGCTC AAgGATTTTG 1260
TGGAARAAATA CAAGGGGCAG TGTACAAAAC TGGGAGAGCA AATCCTCGCG ATTGAATCAA 1320
ACGTGAAGCA GCACATGCGC GCAAACG 1347

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5230 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

AACTGTTTGC GAAACGGnAT TCCAAC TAAC CGACACATTC AACGTACGCG CAACTTTCAT 60
CGCAGACACA AACGCTTCAT CAGCAGAAAG ACACAGTGCA AAAAAGAAAA CACCACCTAT 120
CAAACACGAA CGCAAAAAC TCCATAATGCC CCTCGCTCGA GATACCCTGT CAAAGTACCA 180
ATGCACACCT GTCCCCCTCTC CCTACTCACA ATAAGCACAT ACGTCCACGC ACCACACTAC 240
CATACCCTTT GCGCATGCAA TCTCTCACCA GATGACAACC GGTGCAC'TTT ACTGAGAACG 300
ACACGCAAAG TACGCAAAAG CTCACGCGGT AGATATTCCA ACcGCTCCCC TAACAATAGT 360
CCTAACTCCT CAGTGCTATT CCATACATCa TGGAAAAGCG CGGTTTCTTC CGGACTCATC 420
AATCCAATTT GGAACCCAAA AATCATCACT CCACGCCGAC GCAGTTCC'TC TATCGTTCGT 480
CGACTCTCAT GAGGGTATGa GGAGCATCCG TCAGTAATTA CCAACACAAC CTTAACAAAA 540
GATGTATCAG ACGACACACG TGCACGCCTG CGTTCCACGT CTGCAAGAAT GTGTTT'TAAC 600
ACCTCTGCAT CATTCTGTCCT TCCGAATCGT CCATCTAAGT TCACCGATGC TTTGATAAgT 660
GCGCGCTATT GAAGTCTTTC GATTTACTCT TTCCAAATGA CTTCACTTTT ATAAACTGC 720
TCCCAAAGTA ATACACCTCA GAATGAATAG TTGTTCTCTC ACGCCTACCT GCTGCGAGCA 780
TGTCTGAGTA CTCTCCAAAA TCTTTCAACG AAAGCATACT TACCGCAAGC GCTTCCCTTG 840
CACTCGCAAT CTTTTCTTTA TTCATAGAAC CCGAGTTATC AACAAACGAAT GAAACTTCTA 900
TCTGTGCCGG ACGTAGCGTA CACGCACGCA CTTCATACAC ACGATCATAC ACGCGCAnTT 960
GtACCTCTGA TCCCTACCCC GAAATCTT'TG AAAATCAGGG AAAACTGAAA CAAAATCGCC 1020
TACGTTTAAC CTCCCCTTCG GGCAC'TTCCC CTCGTAACAG TCTATCCACT GGACTGACTT 1080
TCCAATAAGT GATTTCCAAA ACGAGCGCAT ATCGATACGC AAACGATGCG TTGTACGCAG 1140
CAACCGCGCA AACTCTTTGC GTTCCTTCGG AGAAATAGAG AAGCGCTCGT CAAACTGAGT 1200

GGTACAAGAC TCAAAAACAT CTTCTCTTTT TTTCAGCTCT TGCTGCCCCGT CCCTTGAGTG	1260
CACAGCGTGC AAATTACTTT TAGTGATTTC GAAGGCACGC TCGTTTCTGA AAGGATCATA	1320
ACTTCTGTCC GTTATATTCT TTAACCTCGAA TGTGATATTT GCCACACTCA GATGCCAAAG	1380
CCGCACAAAA TGCTCTAAGA GAAACACAGA GACAATACGG TCCCGGTGCT TGGTTGGGAC	1440
TACCTCGCCA GAAAGGGGGA AAAATTCTGA GTGAATAAAA TTACTCATCT CAGTACCAAG	1500
CACTAAAGTG CGTAgcCTnc CTGTACTACA GGATCCCGTG CGATGCATGC GCGATTGCAA	1560
CCCTTTGGCA TATCATGGAA CAGCACGCGC TCTGCAAGCG CATATGCAAA CTGCAAGTGC	1620
AATGCCGTTT CCGTATGTTT CCAATACACA CCCCCTTCTT TTTGATACAG AGAAGCCAGC	1680
AGCGCACTTC CTTCTGGAGT TGTGTAGTAC GGAGCTCTGT TCCGCACATA GTGGAAGGCA	1740
TACACCGCAT CGAAAAGGTA AAACAGTGAT GCCACTTCTG TGTGGCAGTA ATGCTGAACA	1800
AAGCGCGGAA CACGTATTTT ATCTCTCGCT TCGCGAGArA AAACGCCTC ATACATAAGA	1860
CGTCGCATCC CCTGTGCAGC GTCTTCAAAA AAAGACACAC GGTTCAGTA ATACGCGTAA	1920
TCCGCCTTTA ATTCTCGATA GTAAACAAGC TCCCGGAAAA GgTTCCACAA TATTTCTTTt	1980
CCGTCAAAGT CGTCCTTTAA AAACCACTGC AGTGGAAACC CTACCATCCC CTCCTGCGGA	2040
ACAAACACAA ACCGATCAGC TTGTAAAATA GGTACACAAC GAAAATGCGC ATCCCCCGCA	2100
AArGTGGCGA TATTCGGTGC TTCAGCGGAA AAAAAACGCG CAAAATTCTC TTGCGCACGc	2160
tTcGCATCAC ATTCATTAT TGTCATGCAA CGGCGGCGG ACGATCTTAC TCAGTCTCTC	2220
TTTAAACATA GAAGGTTTAC AAAATTCGTG CACCGTCAAA AGCCTGCACG TACCATTTTC	2280
TGCCGCAATA AACACGTTGA ATACCGACGG GTGTTCACTC TGCAATAAGA ATGCAGAAAC	2340
GACCGTCTCT GTTGTTGTTT CAAATGAGCG AGAATACTGC GCCGTGCCCG TAGCATCGAA	2400
TGACAGCAAA CGCGCTCCC CACCCCGGCC GAAAACAAGC ACCATGCGTG AAGAGAGCGC	2460
CAACGCGCAT AACACTACAC TTTTGAAACC TGTAATCCAT TCGCCATACG CATAGTCCCC	2520
CGCAGCCATG CCATGCTCGT GCCGAAGCac GCGACTTTCC CCGTCATCGC CAAAGACTAC	2580
CACTCGATCC TCAGAAAGCA CGACCGCTTC AGTGTATGGA TTTTCAAATC CATATATCGC	2640
GTCAGAATAC TCTTCATTGT GTAAAAGGCG TGTACCGCTA AAACCACTAA ACACCACAAG	2700
cTGCGCAGTA TTAAGAGCCC GTACTACCCG TATTCCCCCA CCTAAACCAA GAATCGGCCC	2760
ACGATACTCA TATCCGTGTG CACTCTTTTC TAAAATGAAG AGAGCACCTG TCTCATCACC	2820
TACCACCACT CGGTGAGCAT TTACTTTTTC CACACACAGC ACACGCTCAT ACACGCCTTC	2880
AACACGCGCA ACTACCTCAA ACGAAACCCT TCTTCTCTCT GCCTTCTTCG ATCGTTCCCTG	2940

AATAGAAAGC	ACGATCGTTT	CaCCACtTCG	GTAACGACAA	CTACTTCTCC	ATCACCCATA	3000
GAGATAAGCG	CACAAATACG	CCAATCCGTT	TTCACGCTCT	TATGCGTGGA	TTCCGCAACA	3060
AGCCATTGAT	CGTGCACCCG	GTATAAAAGC	CGTATATCAT	CTGTGCCACC	TGCGATAAGG	3120
ACAGAATCTT	CCGCCAAAGG	AATCGCTGCG	GTGATGCTTT	TTCCAAATTC	AAAAAACACG	3180
TCACTGTACG	TGCACTCATC	TCCACAGATA	TCGGGAAAGC	AGTGCCGAAA	CTCGGGAAGC	3240
AGCTCCTGAA	TCAATGCGTC	ACTTGTCTGT	TCTGCACGTG	CAAGATCATC	CCACAGTGCG	3300
CGCGGAGTTC	CTCCCTCACT	GCGCAATCGC	GCGTGCTCAG	ACACCAGTTG	GTCACACGAA	3360
CACTGCAGAT	GGGCAATCCG	ATCCGCACAC	TCACGTGCGT	ATGATTTCCTC	CTGCAAAAGT	3420
CTGAATGCTG	CACACACGCG	TACCAACTCG	TGTATCCGAT	CGTGCAGAAC	CAACATCGCA	3480
CCGGCATCTA	CCACATCCGG	CACTGTATTG	TGTGTATGCA	TGGCGTACGT	AGGTCCGTGT	3540
CCAAAGAGCA	ATACCACCAC	CTCAGCGAGA	GTTTTTACCC	CATCCGGCAG	ACGCGTGTAT	3600
TCGTAAGGAC	GGGTACGGAT	CTCTyCGTAA	GAgTAAAAcT	GCCCCawTCC	CtTGGGCCGC	3660
ACAcTCCACC	cGTCyTTTTc	TTGAAAAAAA	CCAAaTCGGA	CTGCTTGCGA	TAAAATATAA	3720
TTTTGATCGT	CTGCATTCAA	AACACCACCG	ATAAAGCCGT	CCCACAGCGC	CTGATCCACA	3780
TCCTTCTCTT	CGCCCCGATT	CCACTCATCA	AGCACACGGA	TCACATTACG	AATGGAAAGC	3840
ACCGCTTCAC	GCAGCTCAGG	CTCCACATCC	CCAAGACCGT	CATGCGTCTC	ACTTCCCCCC	3900
GTGCTATCTT	TCCATTGCGC	GGAAAATACC	TGCTGCGTCA	CCTTTGCCAA	TTGCGCAAGT	3960
TTAAACAGCT	TGTCCAATGA	ACCATCAATA	TCCGGCAGGC	AAAGTGATCC	TCCAGAAGAG	4020
GCAAGACGCG	CGAGAATGAT	GCGAAAAAGT	TCATTTTTCT	CAGGATGCGC	CTGATTGCGT	4080
TAAAGACCTT	CTGTGGACTG	CGGAGGGTAA	TCATATTGCA	ACGTGTTAAA	GCGCGAAGCA	4140
AACGCGGGGT	TGAGCGCCCC	AGTGCCCTCG	TAATGAACAA	GTCCACTGCT	GATGTTCCCC	4200
GTGGCAATTA	CGCCAAACCC	TGCAGCTATT	TTTACCGGGC	CTACCCCGGG	GATATAGGCG	4260
AAATCCCCTA	CCCGTTTTTG	CAAAATATCA	TTGAGTGCGA	TGAGATGCTG	CATGGGAATT	4320
GCGTTGATTT	CATCGATAAC	AAGAGGTCGT	CCCTCTTTTA	CTGCGCGCAg	CACCTCACGC	4380
TCAATCTTTT	GTACCTCAGT	GCCAAAATTG	CCATACTTTG	CAAGATAGAT	ATCCAGCATT	4440
GGATCAAATG	CGTAACCACG	CTCAGTAAAG	GCATGCACAT	CCTGGTAACA	GTGTTCTGGGT	4500
GTTTTTCCCT	CCAGACTGTT	TTTTAACACA	AGCGTCTTTT	CAAGAAACAG	ATCCTCTGTG	4560
TCGATGTGCT	TTGACCCCGA	AATAAATAGG	GGTTTGATGC	GCTGCAAAAG	CCGCTCGTCA	4620
CCGAGACGTA	GCGCCTGTTC	ATAATATGCC	GCGCGCTGAG	AAAAAAGGCG	TTGAAACTGC	4680

705

GTACGCGCTT CCTGGGAGTT TTGTAAGGCA TCTGACACGC CACGCTCGCT GCCCCGAATC	4740
TCCGCACACG AGCCACCGGT TGCAGCAGTG CACCACTcAT TAAGCGCACA ACGGACATCT	4800
TCAGTGATTA ATTTATGAAG CGCAAAACgc tCCGCGGCGA GCACGGCGAG CTCAGTCTTT	4860
CCCGTGCCGA GATGCCCCGG GAGTAGCACC GCATCCCCGC GGGCAAGGCT TGTGCTATC	4920
CTCTCAAGTG CAGCACTAAC AGAGGGGGTT TGCGCAAACA CCCCCGAGtG ACGCGTTCAA	4980
CTTCCCCAAG CCATTGAGCA GCATGGAGAA CGAAAAAGGA TTCAGGTGTT TCCAACGCGA	5040
GCGCTGCTCG TTGCTCCTCC AGATCCCGTA TGGCATCTGA GTGCACTCTG GTAAAAACCG	5100
TACTCCGCCT ATGGATACCG AAGTGGGCAC AGGCGACTGC AACTCCCAG TtCcGCAAAA	5160
AGCGCTCATA CACAATACGC GCGTCAATAT CTGCCAAACG TGCCCGATAn CCGTGCAAGT	5220
TCTATCCGCG	5230

(2) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

TTGGATTTCGC CAGTCTATCC TCAAGGCACT GAACGAAAAA GCACGCATCA TCCGTTGCC	60
CGTGAGTCGT ATTCTGTCTG CAAAGAGCAC GTATGAGTAC ATACCTCCTG TTACCTCGGT	120
GAATGTTGGT ATATCGAAAA CACaGGGAGG CaACAGATAT GGCaAAAGGC GTGCAACGAT	180
GTGCCGAGCT GTGCCaACAg TGAAGAAGT TCACATCTGG CACACGCCGC TATCTCTAGA	240
TGCTCCGCTT GGAGCCTCGG GAAGTCGTGG TGAGTCTGGG GATGTTGATG GACTGCGTAT	300
AGGTGACTGC GTGCCGGACG ATCTTTACGC GCAGcCTGAG GAGCATATGC TTGCATGTGC	360
ATTGCAAGCT GATATTGCAA AGATTTTACG ACTTTTGCCT GCGCGTGATG CGCAGGTCAT	420
CCGCTATCGA TTTGGACTTG GCGGGTATGA ACGGCGTTCT CTGCAAGAGA TTGGAGAAAT	480
TTTTAGATA ACAAAGGAGC GCGTTGCGCA AATAGAAAAA AAGGCTTTGT TCGGTATCCG	540
TAGCTGTGCC CGTCAACACA GACTGGATTC CTACATAGCG TAGACATCAG AGGCGTATGA	600
AATAGGAGCA GGACGCGTTG GGCATACAAC TTATAGTGTT TTTAGGAAAT CCTGGTGCAG	660
AGTAGAAGA AACCGGGCAC AATGCTGCAT GGTGTCTTTT AACGTACCTT TTCCCATCCA	720
TCGTGCTTCC TTGGCGATGC GGATGTCGGG GGTGATTGC GCGTATTGAA GGGTTTGAAG	780

706

GGTCAAGCGA AGAAGTTTGG CTTTTGAAAC CGCTGACTTA TATGAACCGT TCTGGGAAAA 840
 GCGTAGGGGC AGCATGTGCC TTTTTCAGAG CGGATGCGAA cAGCTcTTAG TAGTGCACGA 900
 TGAATTAGAA TTACCGTTCG GTGTGGTGAG TTAAAAACAA GGCGGAGGGC TTGGAGGACA 960
 CAATGGGTTG CGCTCTATCA AGGAAGTGCT TGGTACCGCA GATTTTTTGGC GGTTCGCGAT 1020
 AGGCATCGGG CGTCCACCCA GTGAGAGTGT GAATATAGCG CAgTACGTCC TCTCTGCCTT 1080
 TTACCCGGCA GAGATGGCTG CATTCCCAA GCTGGGGCGT GCCACGCGAG ATCTTCTGTG 1140
 TCAGCTTGTA GTAACAGATC AGGCAGCGAC AGTCACCTTA CTCAGTGCCT GGAGAAAAAA 1200
 ACGGTTGCTG TCTTTATGCG AATAAGGACA GGGTGACTCc CATACGGTGA AGGAAGGGTA 1260
 AAAAGAGAAA GTGTGGGGAG GACTTGCATA AAGAAAGAAT GGTGGGTTAn TGGCGCGCCA 1320
 CGTGATTAG CTAGGACGAG GAAATCATAT GGCATTTGAA ACAATTTTCGT CATGCTTAA 1379

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

CTGCCCnAGG CGCGTGTGGG TGGTGCGCAT AACCAGGGGA AGGATATCCC ACCGTGTTGG 60
 TAGTAGAAAC CCGTGCTTCA GATTGTAGGG ACCGGTGCCC ATAAGTGCAC CAGGGGCTTG 120
 GCCATGACTG CATACCCCCT TGCCATAGCT GATGCCCCAC TCAAGTGTGG CAGAGCCAGT 180
 TAGCTTCGGG GAAAACTCCT GTCCGAGCAC TCCCCGCTC GTCCTACCC CCACCACCAC 240
 ACACAGCACA CTCCCCCACC GCATGCACCC CATGCTACCT CACCCCCCCC CCGGCCCTGT 300
 CTAGTAGCCC CCTCACCCTG CCACCTGCAC ACACGCAAAA ACTCACCCT CTTGCACCT 360
 GCCTACCCGC CnGCATCGcG CGcACCCCAG GCGCAGACCT TTGCGAGCGC AAACGCACCG 420
 ACACACCCAG CCACACATCC CATAAAAAGC GTAAACTGAT CCTGCATCCC GGCTGCAGTT 480
 CCCCCTGGGA ACAACGTCAC GCTCGATCCC AGCAGGAGCC CACACACACA gCATGCGCGG 540
 aCACCGGGTA CAACCGAAAC CATGCGCGGA GCACCCGCGC CGCCCCAGC AACCTATCC 600
 CCATTCCCAC ACAGAGTGGA AACAGGAGCC CCCACACGTG CGCAGAACAC AACCTGCTTA 660
 TTACCGACGC GCCAGTCACT CCTCCCCCCT GCTCCACCGC GCGCAAAGAC AACACGCTCA 720
 AAAGCGGTTG GTACACCCCC GCCAGCAGCA ATACCAATGA ACCGAAAAT CCTGGCGTGA 780

707

gCATTGCCGC CGCCGCTAGC GCCCCTGCGC ACACGGTCGC CACAAATCCG CGCGTGTGTG	840
CAGTAGTAAG GACCGCCGTA GTCTGAACAG ACGCAGGGGC GGTGCGAGAG GATGCGTCAC	900
GCGCGTGTG CATGCGAGAA AACGCACACA CTGCCACAAA CCCAAGCAGC ACAAAGAAAA	960
TAATTCTAAC TGCACACCAC ACGCGGCGTG CCGGTTCCCC CACATGCCCC CGCGCTGTGC	1020
CTTCCGCTG CACTGAGTGC TCCGCGGcAA CACTGGCGGC ACGCACCCGA TTGCGCAAAG	1080
ACGGCACACT TGCTAACAGC ACCCCGGCCA AAAAGGCATT CGTAAGATGA GGAAATGCTT	1140
CGTACAACGC ACGCATAAAG CGTGGgCACA CCCCTATCCC CAmCACTATT CCCCCGCAA	1200
gGGCAAGCAA GCGTCGCCAC TGACGGCACA GATGCGCTCT ATCCAATGCT ATTGCTGCAA	1260
TCAGTAaTTC CCaCGTGCCA CAGAGCAGCG CAACCGTACC CCCCgAAAGA CCCGGTACCA	1320
CGTTTGCCGC TCCTATTAAC ATTCTATCC ACACGTGCAT GACCGGTGAA CTCATGCTCC	1380
GCCTCCCTG CTGGTCTTCT TTCTGCGAAA AAACGCACCC TCCCCTTCAT CCGGGCACTT	1440
CTCTCAGTTC AACCGCGTCC ATCGCATGCG CAACACACCC TCACCATACA AAAGGAGTCT	1500
GAAACTCTAC ATGCTCAGCG ACAATCTTTA C	1531

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

TCTGCCCGGG TGTGGTGAAG CCGCnCAGTT GCCGGCGCGT TACnCGGATG GGATGCCAGT	60
CCAGTGAAAT GCCGCGTGCa GAAGCgTTGG TGCAAACTGC CcTTTGCCAG AAaGCTGCCG	120
TATCTAGAAaT CcAGTTACAC TTTGawCcGG GTTGTCcTT TCTCTGAAaG GCTTCTACGG	180
TTGCaGAGAC GGTACGTGCC aACGAACTTT TTGCGCCAGC AGTCTGATAT TCCCTTGAC	240
CTTGAGTAA CAGAAGCAGG CCCGCTTGTT TCCGGTATTG TCAAAAGTAC ACTTGCAATT	300
TCCCAATTAC TGTCACGCAA TATTGGTGCC ACGGTGCGGG TGAGTCTTTC AGATAGCATG	360
GAGCATGAGG TGcTGGyCG CGAGAAATTC TTGCTGAATG CCGTAAACGG GCTGGTGGGG	420
TTCGTTTAGT GTCATGTCCG CGCTGTGGCA GGATTGGTTT TGACGTACAC GCATTTGTGC	480
GGAGGTGGCA AAAGGAACTG TTCAGTTTGA AAAAGGATAT CACGGTTGCG GTTATGGGCT	540
GTGTAGTGAA TGGTCCTGGA GAAGGAAAGC ATGCGGATCT CGGTATCAGC GGTGCGGAGG	600

708

ATTTCGGTGAT TTTT TTTAAG CGGGGAAAGA TAGTGCCTCG CATTCAGGTA CGTGATCTTT 660
 GCGCAGACGA GCGCAGCGCG ATAATAGACG CAGCGTTTAA AGAGGAATTG TCAAGTTTAT 720
 GAATAACCTG aTCAAAGCAT ATGCGGcGGG TGTCATGAGT GCTGCGTTTC TTTTGGGTC 780
 AGAGGGGCGG GTGCGCAgTG AATCCGATCG GGTGCGTGGG GAGGATCCGT GGCACCTGTT 840
 ACAGTGGGCA CAGGTTGTCT ATGAGCGAGA GGAATTgGCG ATACGTTGCG CTATGCcAgC 900
 GGGnCACGGG CGCTTCGGCG GGArcAA nTG GAGCACCAGT GCCgAaGTGC TACTGCGTGC 960
 ACGCACACGG GCTGAGTCAG CGGGGATACC CGAAACACTG TCTGATTTAT ATGCACTTTT 1020
 AAAAAAGTCGA GGAGAGACAG ATGCCtGCGA AGTGCTTGAT GCTATTTTTTC TCACTCATGC 1080
 GCCGCACGTT TTTCAAAACT CCGTTTCCAA ACTGCTCCAG TGGCTGAAGG ATTCAGCCGC 1140
 TTTTCCAGAA GCGGAGTTGC TCTTGGGAAA GGTATTCGAG GGTGAAGGAG AGTACGCCCA 1200
 GGCTTTGCAG CATTATCGAA ATGCGTGCGA TACGCGAGCG CAGCTTGTA TCCCGACGC 1260
 TCGCTTTGAT ATTATCTACG CAATGGCGAA TGTGTCTCGT CTGCTCAGTC AGCAGGATGA 1320
 ACGGGAGAAG TACTTGCTCC TTGTGCTGAG CGAAGATCCT CTGTACAGTG CACGTGAGGT 1380
 GTGGGGCAAG ACGCTGCA 1398

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1900 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

AACCGATAGA CGAAGGGACC ACACGCGCTC CTCCCCTTTT TAAATAGAGA AAAGAATAGT 60
 CCCTACGGGA ATTGAACCCG TCTTCTGAGA TTGAAAATCT CATGTCCTAA CCGATAGACG 120
 AAGGGACCAC ACGCGCTTTC CCTAGGGAGG ACTCGAACCC CCACACACAG AACCAGAATC 180
 TCGGGTGCTA CCATTACACA ACCAGGGAGG GAGGCCCAGG CTAGTACGAC ACGTATTTTC 240
 TGTCAAGCAG ATAACGAACA CTCACTCAGA TCAAAAACCTT ACCCGGTACC TCCACTTGAC 300
 CGACGCAGAC TGGGCAGCTG CCATCAGCAG CCCCACAGGC ACACGCGnCA TTCCGGGCAA 360
 AGACACACAA CTGGCACATT GCCGGATACA ATTGTGGCAG TCGCTCCTTC CAGTTCAGTA 420
 GCGCTATTGc AAAGCGCGCC TGGCTGcGAT ACAAGGAGGA GAACACTTAC TCCGTATGGT 480
 TATTTcAGGa TTACGCGCCA TCGAAGAGTT TCTGCGCGgC AGtCCTnTGC GCTAGAAGGG 540

709

TTACACGCGG GAGGAAAAAA CAGCAAGACG CAACAAAGCT GCGTGCGTGT GTCACGCTCT	600
ATTATGCAGC GGAAATGCG CGCATCAAAC GACTCCTTGG TATGGCCGCG GCACGGGGGA	660
TACGGATCAA CACACAACGT GTGCTGTGCT TGATAAGTAG CGCGTAGTTT ACCCnCTGC	720
TGCGCGATCA CCGCGGTATC CTTGCTGTTC TAAGTTCACC GAGCGCAACG TCCGCAGGGT	780
TCTCATACAA GAAAAAACG ACTCCGCTGT GGACAGCTCG CAGGAACGAA CGTTGTTACA	840
TGCACTGGCA ACGCACaGC ACGCGCTTGT GCTCGTCTTA GACGCAATTA CTGATCCCCA	900
CAACGTTGGG GCAATTGTAC GCATGCAGAC CAATTTTCTG TCGATGCAGT GCTCCTGCCG	960
CACCATCATG GGGCAGGAGG TACAGAACT ATCACGCGAG TGAGCGCAGG CGCCGTTGCA	1020
TGGGTACCGC TTGTGCGTGT ACGCAACCTA GTGCGCACTG CAGGTATCCT CAAGCGTTCA	1080
GGATTCTGGC TATACGGTGC TGATGTAGCA GGAGAAGCAA TAGGCGCCCG TACTTTTCCT	1140
CCTAAGACAG CGCTGTGTT AGGCAACGAG GGGCACGGCG TTTCGCTTTG CTGCGCACGC	1200
ACTGCGACGC ACTCATCTCT ATCCCAACGC AGGGaATGTA GACAGTCTGA ACGTGTCCGT	1260
TGCCGCAGTA TTCTGTTATA CGAAATACGC CGGAGTCAGC AGTCTCCCTA CTCCGTACAA	1320
AGGCAAAACG AAATGAACGC TCAATGAAAA CACCAGGGc ATCTTCGCAT CTTTAATTCA	1380
TATTGCATCT TTCACCCCAT TGCCTTACct GAGGGAGTCT CTACGCaCGC GGTAcGGAgG	1440
GACCCCATGG CACATCTTCC TAAAGAGTAC GATTTTTCCTA TAGAGTCATT GGGGGAAAGC	1500
AAAATTCCCT CTCCCATCTA CCTGTCTCAC ACCCTTGGCG ACTTCATTCC TAAcTACGTC	1560
AgTGACAATG AGTACATCAG CCATGAACTG AGTGCGCGTC TGGGGGAGAC GGTAGGGCCC	1620
TTTACTCATA AAAACTTGAT GGAGCGTGCG GGCCCGCGCC AGAAGATTTT CTTCAACCCG	1680
CATCACGTTT ATGCAGGTAT TGTCACCTGT GGAGGGCTCT GTCCCGGCCT CAACGATGTC	1740
ATTGCGCCA TCGTCCGCTG CCTTTGGGGC CGCTATGGCG TTAAGCGCAT TAGTGGTATC	1800
CGCTTGCTA TAAGGGCTC TTGCCCATT ACAACTTCGA TATCCTGCCG CTCAACCCTG	1860
AGGTCATCGA TAACTGCCAC AAAACAGTGG TTCGCTGCTA	1900

(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13969 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

710

TTCGATAGAC	GGACAATATC	GTGTCCCTAC	CGCCTTTATT	CTGCCAGAAA	AGAATGGAGA	60
ACGATGAAAA	TTCTCACGGA	TGAGCTGATG	CGTTCTCTCC	ATTGGTGTA	TTAATATAAC	120
AGTCCCGCAT	GTGGACGATT	GATTTCCcAC	GTGAGCmAG	GAAAAAGGAC	GCATGATAGC	180
GTCCGGCTTCT	TGCTTTTCCA	TTACCGAAAG	ATCTACAGAT	TTTCGTAGTA	CGCGCGCGGG	240
CGTACCCGTC	TTACGCCGTC	CCATCTGAAA	CCCCTTTTTT	CTCAGCGCAG	CTCCAGCCC	300
TTCAGCGGCA	TGTTCCCTTA	ATCGGCCTTC	AGGTGCCTCA	TATTCCCCAA	TATACACACG	360
CCCTTCCATA	AAGGTCCCCG	TAGTCAGTAC	CACCGCACGT	GCAGAGATGC	GTCTGCCGCG	420
TGCGGTAAct	AyCGCATGCG	CTGCCCCATA	CGCTACATAT	CCTGCATCAG	TGGTATTGGA	480
ACACACAACG	TCTACCACTG	TGTCCTGATA	CAGGTGAAGA	TGCTGCGTAC	ATTCCAACGT	540
ATACTTCACC	TTCTGGGCAT	ACAAAACTT	ATCTGCTTGG	ATACGCGGCG	CCTGCACTGC	600
AGGnCCCCGG	CTTTTGTTGA	GCAGTCGATA	CTGAATCATG	CATGCATCCG	CAAACTTTCC	660
CATCTCTCCG	CCGAGTGCAT	CGATTTCTCT	TACAATATTC	CCCTTGAAA	TTCTTCCAAT	720
GGAAGGATTA	CATGAGAGCC	TGCCGATACT	ATCGATTGTC	TGAGTGATGA	GTAACGTGTG	780
CTCCCCCATA	CGGGCAGCGG	CCAGCGCCGC	TThCGGCACC	TGCGTGTTCA	CCACCGACGA	840
CGATAACGTC	ATAGTCAGAA	AATCTGAAAC	CCATGGGCAG	CGGATTATAG	AAGAAAGGTG	900
CAAAAGGCTT	CAATCAGGAA	GCACGACAGA	ATTcAGGAAG	CAACGCACAC	ACAACATCTG	960
AAGCCTGTTT	CTGATAATAA	AGGTACCCGT	ACATCACCGC	TGCGGATAGG	ATCTTCCTCC	1020
CGTACTCCCG	AGGTTC TGCA	AGAGGCAGGG	TTTCGAGGAA	CAGATCATCG	GGCAGACTTC	1080
CCCTCTGTTT	TTTCCATT TG	CGGACGCGCG	ACGGTCCC GC	ATTGTAGGAG	AACAGGGCAC	1140
AGAACACGGA	GCCATCAAAG	CGACGAATGA	GATCGGAAAA	GAACAGACTG	CCGAATCTAA	1200
CATTGATATC	CGGGTCAGTT	AAGTCATAGG	TGTCGATATT	GAGCTTACGA	GCGATATCTG	1260
AAGCGGTTGG	CCTCATCAAT	TGAGCAAGAC	CTACAGCGCC	CGCCCGAGAG	ATAACcTGCG	1320
GCTGAAACAG	ACTTTCAC TC	CGGATGAGCG	CAAACAGCAG	ATACTCCTCA	ATATGATACT	1380
TCCCTGcATA	GCCTTGATATG	ACGTCAAGCC	ACGGACGCGG	GTACGCAATC	TTCAAGTGTT	1440
CTACAGAATA	GCGCGCACCG	TGAGAGCGTA	TTGCGTACGA	CTGAATGCGC	ACGGCATCGG	1500
ACCATCGTGA	TCTTTGTATG	TGTGCGTT CG	CAAAATGCTC	TGCAAGGTGG	AGAGGAATGT	1560
CAGGATAGAA	CTGTACCATA	GCTTGGTAGA	ACATATCGTC	CAAGTGATAG	TCTACATAAC	1620
CTTGAGAAAT	AGCACGCGAC	TCATCGGGGG	TAAGAAAAGG	ATGCGGTGTT	CTCTTACTCC	1680
GCACCTTATA	CAAAGCCTCT	TCCAGAGGAA	TGCCCAATGC	ACATGCAGCA	AGAACACGAT	1740

AGTAAAGGGA	AGAATGCGCA	gTTTCGAAGA	TGGTACGGTA	AGCGCGGCGC	gcAcTCTCTT	1800
CTGAAAGCGT	ACCTGAACGC	GCAAGGACAT	ACGTAACGCG	CGCGGAnTTC	GGGTAATGCT	1860
CTATGCGTCA	CACCTCTTGC	AGTGTAGCCA	GACGCCCCCA	ATCTTGCTGC	GTAGTCAGCT	1920
GGACAATTGC	ATAATCGACA	AGGTCAGAAA	ACCAAGAATC	CGAACGCCAA	CGTGGTGCAC	1980
TTTCAACAAG	CACCTTAAAG	AAAGAATCAA	AGTCCAATGC	ACGCagTACG	TCCAAGTAAT	2040
ACCACAGGGC	ATTATCAGCA	TCTTGCCGCC	TTGTGGCCAC	TTTCTCTGCC	TTTTTGAAAA	2100
GGGGAAGCGC	TTGCTTCTTG	TGAGAAGCGG	ACCGCGAGTA	AAGACGCGCC	GCATAAAAAT	2160
AGCAATAAAA	ACGCAtCGTG	CCTCTAATTC	CGCATTGGAC	AACGTTGAGC	GCGATAGATG	2220
TGCAAGATGG	TCAAGAAAAA	CCTGCGCGGC	TTTAACACTG	TTTTCACTAC	CGTAAAGCGC	2280
TGCTTTCCCA	AAATCGGAGA	GAACCGAATT	TGTAGCGTAC	CgCGTGTGCC	ACGCAGAAGA	2340
GCGCAACAAC	AATCGCACTC	TCTCCCACCC	CCGTTTGTAA	TTCTGTGAA	AGACGTCCAC	2400
ACGAGCACCA	TGTACTTCCT	TAAAGATACG	CGGCAGATCC	GGCAGTGCCG	CAATAAGCGC	2460
AGCAAATTGT	GCACTCGTAT	GGGGCGCAAG	TGCCCTATCG	TTGTACCAAG	ACTCAACAAC	2520
CGTTCTCAGA	CTGTAGTAGC	GTTTCGAGTTC	AAAGAGCACC	CTTGAACGCA	AAAGGCGAAG	2580
TGTCTGTTGC	TGCGTTTTGG	TTCGCGCATC	GCTGCCTGCA	TTAAGGACAT	GCAGCTGTTT	2640
TTCAATAAAG	GCGAGACGCT	GTAGTGGACT	CCCTGTATTG	TGTGCCTCAT	GCGCACATAA	2700
CTGGCGGTAC	GGTGCGGCCT	GCGctGCGCC	ACGTACGAAG	TACTCGTGAG	CTTCTTCGGA	2760
AAACTTGGCC	CGCTTGAGGT	GTAACCCAAT	GAAGTAAC TT	GCACCTTCCC	gCGCGGCGAC	2820
CTGCTCGAGA	AACTCATCTG	TTGGCTTTAG	AAACGGAGTG	TAGTTTTTGT	CTCTCAAAAA	2880
CTGAGGGATA	TCAACCTCCC	TAGCGCCGCG	CGcGCACACA	GTGCCCTCCC	ACGAGACAAG	2940
GACACACACC	ACGCACCACA	CGCGCAGGCA	CAACCTGCCC	TCCCGTAAGA	GAGAGAAAAA	3000
GCCACCTCCC	CACACGAGAT	GCTTACCGTG	ACGGAATTTT	AATTGAGGTT	CCTGCAACGA	3060
TATGATCAGG	GTTTTTCAGT	CGGTAAACT	CAGCAATTCT	CATGTAGCGC	CACGGAGTCT	3120
TGTAATAACT	CCGCGCCAAA	TCCCAGAGCG	TATCCCCCGG	TTTGACCGTA	TAACGCACAA	3180
CCTTGACGGA	TCCAGACCCA	GACTCCTCTA	CAGGTTCTGC	CGCTGCACTC	GTAGCCGTTT	3240
CAGCCCCGGG	AGACGCAGGG	GGgACGTCCT	TTTCCTTG TG	GGTTTCTGGA	AGAGCAGTCT	3300
CAGATGGGAG	ATCGACGACA	CGTGCC TCAA	CCGCAGTACG	CTCAAGCTCA	CGCGCTGCAA	3360
CATGCGCAGA	AGACCTGGGC	AGTTCAACTT	TTTGTGACGG	CACGACCGCA	GGACGAGAGG	3420
CGCCGTGCAT	GTACAGAACC	CAACCTACCA	AGACACCACC	GAGCAGAATG	AGAAATGCGC	3480

712

ACACTGCCAA CAAAATCCGT CGTCTCCTCG TGAGGGTAGA ACCATCCCCT CCCTCGTCTT	3540
CAGGGAAAGA ACTGACATGC TCGATCTGAG CAGCAGGCTG CTCATCCGGT GTCGCGTCTC	3600
CTGAGGATCT CTCCAACACG GAGAAAGAGG TTTCTGAAA AGCACCAGAA CCTACATCCG	3660
TCGCACGCGC ACGGCACCGA CTCCCATCAC ACTCAACCTC GAGGCGAATA GTAGCTCCCC	3720
CCGCCGCAGC AACGGACAAC GTGTCTATCG AAAGCGCACC CATAGGCTCA AGTTCTGCAG	3780
AGGTGACCGA CGCCTCTCCA TCGcCAGGAG AAACCCGTTT AAAAAAGCTC AAAAGAGCAC	3840
GAGACTGTTG GTCATTTCGG GTAACGAGCT CGAGCGTTGT gCGCTGCGCA CCCTCTGCAG	3900
TAAAGAGAGG GaAAAAAGAC CCGTCCGCGA GCTTGATACC GATCTCCTGA CTCATGAGCG	3960
CACCCCCGCC CGAGCATAGT CAGGCGAAAC CCTTTTGTCa ATCTTCAGTC CATAGGGGGA	4020
GGGGGAGGCC GCGCTCGCT GAGACTGCAC GCTCAGAGAC AGCATGCGGT TCACGCTACC	4080
TGTAGGCTCC TCCTACCCCC CCCCgTGCC TGTATTCCGA CTGAGGTTCG TCCGTTGGTA	4140
TATTGCTGTC CAAGAGCCCA CTCAGGCGGG CGATTACCTC CCGCGTATGC AACTCAACTG	4200
CCCGCTTCG TGCAACCAcT TCCGTGAGCA CTTCCACGTT ACCGATCATC GTCTCGACCT	4260
CTGCGCACAC CTTTTCGCGA TCTCGTGTCa ACCGCTCAGC ATGAGCTGCA CCTCGCGTGC	4320
ATACCTCTGC TATCACTTTC CCCTGCTCAC GCGCCGTACA TAACTGCCCT GTCACCGTGC	4380
GCATACGCTC AACGGTACGC TCATTTTCTT CTCCCACCAC CTGAACGGCA CCGGAAATAT	4440
CCGCAAGGAT GGTGCTGAAA CCGTCCACCT TTCTCTAAT GTCTGTAAAA CTCTGGGCAA	4500
CTCTGCCGA CGCGTGCCCT GATTCTCCAA TCACTGCCTC TATTTCTTTT AACATTTTTC	4560
CCGTGACACC AGACTCAGCT GCTGTTGCGG CTGCCAGGGA GCGGATTTCC CCCGCTACCA	4620
CCGCAAAACC GCGTCTGCG TCACCTGCAT GTGCAGCCTC AATCGCTGCG TTCATTGCAA	4680
GTAAATTCGT CCGTCTGAA ATATCTACCA CCAGCGCATT CGTCACCGCC AAACCACGCG	4740
ACCGACTCGT AATTTCTTCG ATCACCTCCA TCATGCGGCC AACGCATTCC TTGCCGGTTT	4800
TACTTGCCGT GGTAATTGCC TCAAAATCTG CGTGCACTGC AGAAAACTTA CCCCAGCAAGT	4860
TGTGCACCGT ACTCCCGAGA CGTCAACTG CCTCAAGCGC TTCTCGTGCA CGTTCCCTT	4920
GTGCTTCCAT TTGTTTCATC AACTCTGCA AGGAGGAACC AAGCTCTTCA TTCACCACAC	4980
GCGTTTGAGA AAACCCTTCC CCCTGCACCG CTAACCTCTC GCGTACAGCA CCCGTGTAGC	5040
GCGTCAAGTC TTGCACTACC TGCTCTGCAC GATCCATGGT CTCGGTCAGA TTCTGTTTCAT	5100
TGTGCGAAAG cTCCTGcGCG GTGCGACGAA CTTACCAAAA CAACCGCTCC AAACGCTGCG	5160
ACGAGGAAGA TAAGTCCTGA GAAAGCCGCT GCGCAGTCCG CCCATCCAAA ACAACCTGCC	5220

ACTCGATGAG CGCaGTTTGC GTAACCAAAA ATCCAACAAA CCCAAAAATC AACAGGGGAG	5280
CTCCTGACAG TACCCCTACA GCCAGGAGCA CATCGTGCAG CGCTGTGACG CCTAACACCA	5340
GCACCCCAT ACTCAAAGGc ACCGCGCCAC GCTTTTTCG GTACAAGACT TTGCACATCA	5400
CCCAGAGCAC AATACCCAGC AAAAGCAATA CGAACAGTTG CTGTAAGGGA AGTAATCGGG	5460
CAAAAGAGGC AGGGGGAAGC AAAAGGATAA TCACCGCGTA CGCAAGCCCC TCTGCACCAA	5520
ACGCCACCAC AAAACTCTGA TTCACAAGCC CAGGGTACAA CGTAGAAAGA TAGTACAAAC	5580
AGGACACCCC CGAGAACGCC AGGGTCAGGT ATTCTAACCG CACCATCGGG TCCCACCCAA	5640
TCGTGATCAA GCGTGGCAGA AACGCATTCC CCGTCAGCAG CAAGCGAACC ACAATCAGCA	5700
ACGAAAAAAG CGAGCACGCA TACAGGCTCT TTTCGCTCAC TCCCAACACC CCTGCAGTAT	5760
CTGCCCCTC ATTCTCCGCA TAAGACTTTC TGCTGCAGGA GGACAATCGC CGGAAACAAA	5820
ACATTGCCAG GTAATACGCG AATATCGTAA ACGCAAAACC AATTGTCATC GCCTCAAGCA	5880
CGTCCTTGCG CAGaCgCGCG TACGAACGCG CGAAACAGAC CCCAAGTGAA CTTCACCGAC	5940
AATGCCCGGT CTTAGACTGT GGTAATTGCT TACCTGAATG CACACGTCAA TTTCAGGTTC	6000
GTGCGTTGGC AACCACACTT CGGCAGGGTG GACGTAGGGG ACGGCATCTG CTCGGTTACG	6060
CGCAACGGTA CCAAGTTCTG TTAAGAGATG CCCGTTTGCG TAGATTCTTG CTGCGTAGTT	6120
AAGCGTATCG CAGGACAGCG CAaGCrACGG AGCGCGAGGG GGAAGCAAGA TTTTCAGCGT	6180
ATAGGTGGCA CATCCGTAGT GAGGATACGC CTGAATAGCG GGTATCTGAA CCGCGCCCCG	6240
CGgTTTGGTC CACAGGGAGG GAACGGTCAT AAACGCAGCA GGCTGCTCAG CTGAGTGAGT	6300
AAGTAACTCG TTCCAGTGAA ACCCCCACGT TCCCGAGAGA GAAAGCAGTG CATCACCAGA	6360
GGAAAAATCC CACTGACGGA GATCGAGCAC TCCGTTTCT GCCGAAGaGG CGCCGGGAGC	6420
GCAGTGTGTG AAACCGCAGC AGAAAGGGCA AAAGCAAAGA CATAAGAGTA CGTAATGGCA	6480
CGATATTTCA CGCCGCGGAC TATACGCGAC ACATCCAAAA TGATCTACGG ACTGCACTTG	6540
CTGTTACGC AATCACACGG GCATGCCCAA ATGAGGAATT TTCATCGCCC GCATCAGGGA	6600
TAGTGCACAC GTTTTGGAA GGTTCTCCC GCAGTGGGGA CTGCAACGCT TTTTCATCCA	6660
AAACAAAATA AACTGTTGA CACGGTTTAT TCTCCTGCCT CAACTGGCT GCAGTCCGCG	6720
CCATTTTAAG TCTCTCCGTA AGGAGCGTCT CATGCACACG CAAAGCCTCA GCCCCAGGCA	6780
GTTCATGATG AAAATACTCA ACGGGTCTTC TGCCGGGATC GTCATCGGTC TTGTCCCCC	6840
CGCTATCGCG GGGGAGTTGT TCAGAGCGCT TGCTCCGCTT TCGCCGCTGT TCGCCGCGCT	6900
CTACCATGTG GTGCTGCCCA TACAGTTCAG TGTACCGGCT CTCATCGGTA CCCTTGTGG	6960

ACTTCAGTTT CACTGCTCCG CGCCCGAAGT GGCTACCCCTC GCCTTTGTTT CTGTTATTGC	7020
CTCAGGAAAT GTCACGCTTC AAAATGGCGC CTGGTTGATC ACCGGTATCG GGGACGTCAT	7080
CAATGTTATG CTCATATCTG CACTTGCAAT CATACTCGTC CGTGCTCTGC GGGGGAAACT	7140
TGGTTCGCTG ACCATCATCG CGTTGCCCGT TATCGTAGCT GTTGTCGCAG GGGGTGTCGG	7200
CTCCTTTTCC CTGcCCTACG TAAAAATGAT TACGCTTTTC GTCGGCAGAG TTATCGCCAC	7260
GTTTCATCGCG CTCCAGCCAT TACTCATGAG TATCCTGCTG TCCATGTCTT TCTCGCTCAT	7320
CATCATCTCC CCTGTGTCTT CCGTCGCGGT AGGAATCGCC GTGGGGCTCA CCGGTCTGGC	7380
AAGTGGAGCA GCAAACATCG GCGTCTCCTC CTGCGCCATG ACCCTCATTG TGGAACCAT	7440
GCGCGTCAAC AAGATCGGTG TTCCGTTGGC GATGTTGCA GGAGCGATGA AAATGCTCAT	7500
GCCAAATTGG ATCCGGTACC CGATTCTCAA TATTCCGCTC CTGCTCAATG GCCTCGTTTG	7560
CGGCGTGCTC GCGTGGCTTT TCAATCTGCA GGGTACTCcT GCAAGCGCag GCTTCGGTTT	7620
TATTGGACTT GTTGGACCGA TCAACGCCTA CAGGCTTATG GCGTACACTC CTATGGTGCG	7680
CGCGGGTATT CTTTTCCTCG TGATTTTCGT TCTTTCCTTC CTTGCTGCGT ATCTTATCGA	7740
CTTTATTCTC GTTGACCGCC TCAAACTTTA CCGGAGAGAA CTCTTTATCC CCGAACAAGG	7800
GTAGATATCC TATATGTTAT GTGTTTCCGC CCAGGTCCTG CGTGAGATAC GTGCAGAACG	7860
TGGGTAAGGA ATGTTGTTTG CCTTACCAAG GAGGTGCGAA ATGAGGTGTG TTGTCTTTAA	7920
TCTTCGAGAA GAAGAAGCCC CTTACGTGGA GAAGTGAAG CAGTCCCATC CAGGGGTAGT	7980
CGTGGACACT TACGAGGAAC CGTTGACCGC AAAGAACAAG GAGTTGCTTA AGGGGTATGA	8040
AGGGCTCGTG GTTATGCAGT TTCTCGCTAT GGAAGACGAG GTGTATGACT ACATGGGTGC	8100
GTGCAAACTA AAAGTCCTTT CCACACGTAC CGCAGGCTTT GATATGTATA ATGCAACTTT	8160
GCTGAAAAAG CACGGCATCC GGCTGACGAA CGTACCGTCC TATTCACCGA ATGCTATCGG	8220
GGAATATGCA CTCGCCGCCG CGTTGCAGct GACGCGACAT GCGCGCGAGA TTGAAACTTT	8280
TGTAAGGAAG CGTGATTTTC GCTGGCAAAA ACCAATTCTC TCGAAGGAGC TCCGCTGCTC	8340
ACGCGTAGGT ATCTTGGGAA CGGGCAGGAT TGGACAGGCA GCAGCAAGGC TCTTCAAAGG	8400
GTTTGGTGCT CAGGTAGTTG GTTTTGATCC GTACCCGAAC GATGCCGCAA AGGAATGGTT	8460
AACCTACGTG AGTATGGACG AGCTGCTGTC CACTAGCGAC GTGATCAGCT TGCACATGCC	8520
TGCGACAAAG GACAGTCATC ACCTGATCAA TGCGAAAACA ATCGCGCAGA TGAAAGATGG	8580
CGGTACCTG GTGAACACGG CACGCGGAGC AGTGATCGAC AGTCAGGCGC TCTTAGACAG	8640
CTTGACAAA GGCAAGATTG CAGGTGCTGC ACTGGATGCG TACGAGTTTG AGGGTCCGTA	8700

715

TATTCCTAAA	GACAACGGGA	ACAACCCTAT	TACCGATACG	GTCTATGCTC	GGCTTGTCGC	8760
ACATGAGCGT	ATCATCTATA	CCCCTCATAT	CGCCTTCTAC	ACAGAAACAG	CGATAGAGAA	8820
CATGGTATTC	AATTCGCTTG	ACGCCTGCAC	CACGGTGCTG	CGTGGGGAGC	CTTGTGCCGC	8880
TGAAATCAAG	CTGTAACCTGA	CGcCAGGTGT	CCCTGGTCCC	GTGTGAGTCT	GA CTGGCTAA	8940
TCGGTCAGTC	TGGAGTCGCC	AGCTCAGGGT	GGGTGTGGG	ctCCGCGGA	CCCCGTCCAG	9000
CCGGTTACGT	GCGGGCGCGG	CCCACCTGTG	TGAGCGCGAT	AACCAACATC	AGTACCACCA	9060
CCGAGACCAG	TGCGGTGAAT	CCCCCTGGGG	CCACGTTCAA	GTAATACGAG	AAGACCAAAC	9120
CCAGCGCCGT	GTCCAGCATA	CTAAATAGAA	ACGCCGCCAC	CAACGTAAGC	AGGAAACCCA	9180
CCCGCAGCTG	TAGCnTGTCG	CAACCGGTAC	GGTCATGAGC	GAGCTCAGCA	CCAAAATACC	9240
GGTAATCTTT	ATAGAAGCTG	CTATAGTCGC	TGAAATTACC	ACCGACGCGA	CGTAGTTTAT	9300
CCCGTCTGCT	GCGACGCCAC	AGATACGCGC	GGTCTCTTCA	TCAAATGCCA	AGTACAGCAG	9360
CTGATGGTAG	CGCAACGCTA	GCGTACCCTAC	GCAGAACACG	CTGAGTGCGA	G CATGATCCA	9420
CAAATCGCGT	G TAGAAACAA	CCAGTATGCT	GCCAAACAGA	TAGCTGTCTA	TATCCGCCTG	9480
GATAAGCCCA	GAGCTCAACA	GCGTGACAGC	AATACCCACA	CTCAGGGAGA	GTACTATTGA	9540
AAGAATCAGG	TCATGATGGT	TTTTTGAAAA	GGCGCGCAAA	AACTCTATCA	AAACCCCCAC	9600
CAAGGCAGTG	AAAAAAAAGG	ATCCCCATCC	TGGATGGATG	CCGCACGAAA	CGGCAATAGA	9660
TACTCCTGCA	AGTGAACCGT	GCGCAAGTGC	ATCTCCCATG	AGCGCGTAAC	GGCGGAGCAC	9720
TAAGTGCATC	CCCACAAGAG	GACACAACAA	GGCTATGAGA	AAAGAAGCAA	CAAAAGCGTT	9780
GCGCATAAAT	GCGTACTGCA	ACATCACC GA	CTCCGACACT	GCGCACAGGC	AAGCGCATCT	9840
TTTTTCTGCA	TATCCAAAAA	CTCACTGACG	TACTGCTGAG	GATTACACAA	ATGGCCATGT	9900
CCTTCGCTGA	GATGAAAAAT	TTGCGTAGAG	TTTGTAATCG	CTGCATCAAG	ATTATGCTCC	9960
ACCGATATAA	CCGTTACGTT	ACGTGATGTG	TTCAATCCCT	TCAGCAGAGC	GTAAATATCT	10020
TTCTGTCCCTC	GAGAATCAAT	ACCTGTTGAC	AGCTCATCGA	GCACCAGCAA	ATCAGGATCT	10080
CCGATCAGGC	TCCGCGCAAT	GTACACCTTC	TGTAATTCTC	CTCCAGAGAG	GGTATACACA	10140
AGCTTTTTTTT	TCGCACCCCG	CATACCCACC	TCCTCCAGCA	CAGCATCGAC	AACCCACTTG	10200
TGCGATATGC	GCAGAAGTCT	GCGATACGAG	TTAAGCATTT	CATATACCGT	AAGCGGAAAA	10260
TAGAGCGTGT	GCATCTTTGT	CTGTGGAACA	GAACCAACAC	GCTGTACAAA	GTGAGCGATC	10320
GTACCGGTGC	TCGGCTTAAG	TAATTTGAGG	ACAAGCTTCA	CAAGCGTGCT	TTTCCCACTA	10380
CCATTTTCTC	CTACAACGGA	AAGGTACGCG	CCTTTTGGTA	TTGCAAGATC	CACCTCGTGC	10440

AGTATAAAGC	GCGCGTCTGC	GGTGACCTG	AACTAACGT	TTGTAAAAG	CACCGCGAAG	10500
GGACTAGCCA	TGATGCGCAT	GGTTATACTC	TATTTTTATG	AATGCAACAC	TACTGTCTCT	10560
GAGAAAAAAG	AGACCACAGC	TGCACAATGC	AAATTGTCTC	TCTACCATGG	TTTTCGAAGA	10620
AATTCCCGTT	CAACATCCTA	AAAAGGAATT	GCATATTTTG	CAGAGAGTGT	GCGAGTACGC	10680
GCCCGTTTGG	GGTGGAAGCC	CCTTCAAAGG	AGCCATCATG	CAACGCTGCT	CAGTAGTTGC	10740
CGCCCTTGCG	GGGGTGGTTT	TTCTTGCACA	GGCGTGTTCTG	CTATCAACAC	CTTCTCGCAT	10800
AACCCACACG	GATAAGCTGC	CTGTTGTGGT	GACATTTAAT	GCTCTCAAAG	AGTTAACACA	10860
GATGGTAGGT	GGAGAAAAAA	TTCATTTAGT	GTCCATCGTT	CCTGATGGGG	TTGACTCTCA	10920
CGACTTTGAA	CCAAAAGCAA	AACACATGGC	CTTCATTAGT	GATGCCAAGG	TCATCGTGTA	10980
TAATGGTCTT	GGCATGGAAC	CCTGGATACA	CTCGGTACTC	CATGCTGCAC	GTAATAGCGG	11040
CAGTATACGC	GTAAGcTG	CGCAGGGCAT	TGTTCCGCTG	AAGGCTCACA	CACGTGGGcA	11100
TACGGCGCAC	CATGTACATG	CACATGCATC	GCACGGGTCT	GCGTACGACC	CTCACGTTTG	11160
GCTCAGCGTA	TGTAACGCTC	AAACGATGCT	TCGTACCATC	GGAAAGGCAC	TGTGTAAGGC	11220
GGATCCGCAG	CATACGCGCT	TCTACAAAAG	GAATGCCCCG	AATGCGGCCG	CACGGCTTGA	11280
GGCGTTGTAC	AAGGAATACC	GCTCCAAGTT	TGCAGCCTTA	TCTCATCGAT	ATTTTGTGAC	11340
CACGCATGCG	GCGTTTGGTT	ACTTGTGCAG	GGATTTTGAC	CTCCAGCAAA	AGAGTATAAA	11400
GGACGTCTTT	AACACAGAAG	AACCTTCCAT	CAAGAGACTC	GTAGAGCTCG	TCGAATTTAG	11460
CAAAAAACAC	TCAGTGCGGA	CCATTTTTAG	TGAACGTGGT	CCTAGTGAAA	AAGTCGCTCG	11520
CGTTCTTGCG	CAAGAGATTG	GTGCTTCAGT	TGAAACCATC	TACACTATGG	AAAAAACGA	11580
GGAGAACCTT	TCGTACTACG	AAAGGATGAA	ACACAACATT	AACAGGATTT	ATCGTGCCTG	11640
TTCAAAACAG	GTGACACCCT	CGCAATAACA	ACCGCTTTGC	ACATTATGCG	TTTTTCTGTA	11700
CACTCACCGC	CATGTACTCT	TGCTTAAGGA	GGCTTTTGG	CATACGGGGC	ACGGGGACTC	11760
TGTGTGCCAT	GTCCGTTTTT	TGTCTACTTC	TTTCCTTTGG	AAGGCGCTGT	GTGGCGGCGG	11820
ATAATTTCTT	TTCTTCTCTT	GTGTGGAATC	TGGTTCTTGC	CTTCATCCCC	TGGCTCATCT	11880
CGGCTATCTT	GCACGTGCnc	GnCTTCGCTG	TCCGCAGTGT	ACAGCTGTTC	CTTATGCTGC	11940
TCTGGCTATT	GTTTTTCCCC	AACGCTCCGT	ACATCCTTAC	CGATATTATC	CACTTGGGAA	12000
AGGGTAAGTC	ATTTTGTCTT	TACTATGACC	TTATTATTTT	ACTCGCCTAT	AGTTTCACTG	12060
GTTTGTCTTA	CGCGTTTGTC	AGCCTTCACC	TTATTGAAAG	CATATTAGCC	CGTGATTTTC	12120
ATATCAAAAG	GCCATTCATA	ATTTCAGTAT	TTGAATTGTA	TCTCTGTGCA	TTCGGTATAT	12180

ATCTGGGGCG	TTTCTTGCGC	TGGAATTCCT	GGGACATTGT	CCTACATGGA	CGCACTATTC	12240
TTTCTGATAT	TGGTATCCGC	GTCATCAGGC	CAGTGTCTTA	TGTTGACACC	TGGATGTTTG	12300
TGTTTTTTTT	CGGCACCATG	CTCGTTCTTT	GCTATCAAAG	CTATCGATCA	TTTCTTACCC	12360
ACACAAGAAA	TGACAAATGA	ATATCGTTCT	CTTTGAACAG	GAAGAGGTAG	TGCACGGTTG	12420
CGCTGTACTT	TCTTTCAGGG	ATAGTCGATT	TTGCCATATC	AAGCGTGTGC	TTAAATTGAG	12480
TGCGGGAGCC	TGCTTCAAAG	CAGGGATTAT	TAATGGGGTG	AAAGGTTCTG	CACGCATCTC	12540
CCTAGCCACA	GAAAAGTATC	TCGTAGCCGT	TTTTGAAAAA	CTGGAATACG	AAGATTGTGC	12600
CCTTTTCCCC	CTTCATCTTG	TCATAGGGTT	CCCTCGTCCC	ATTCAGCTCA	GGCGCATTTT	12660
ACGCGACGTG	TCCAGCCTCG	GGATCTCCTC	TATCCATCTT	GTAGGGACGG	AATTAGGGGA	12720
GCGATCTTAC	CTAGACTCAG	GACTTGCTCA	CATGAAAAAA	ATGCACACGT	ACCTCATACG	12780
TGGCCTAGAA	CAGGCAGGAG	GCACGAAACT	TCCCCTCATT	ACTGTTTCGG	AGTCGGTGCG	12840
CACCTTTTGC	TCACAACACA	CCCACATACT	CGGCGACAGC	ACACACCAAA	AACTAATACT	12900
TGATACTAAG	AACACCCTAA	CCGATCTAGG	AAGCGCCcGC	TGCGCGGGGA	TGTACTGTGG	12960
ATTGCAATAG	GGAGTGAGCG	TGGATGGACC	GAATCTGAAC	GTTTACTTTT	CTCCGCCaTG	13020
GGATTTAGAG	CAGTAGACAT	GGGAAGACGG	ACCTTGCGCA	CAGAGACCCG	CGGCCTGTGC	13080
CsCGTGCGCC	GTGTGTACTCG	CCAACGCGCA	CGCGTGAAA	AGAAAAATCC	CTCGGCCAGG	13140
CAAGAGATCT	TCGCCCATAA	GTCGAAAGAA	TCCCTAGATC	CGGATCACAC	TCAAAAAGTA	13200
AACCAGAAAA	GCCCAGAGACA	GGCTGAAAC	AAGGAAACAC	AACCAAAAGA	TCCACACCGC	13260
ACGCGTCAAC	CGAAAGCCAT	TGCTCCCGAC	CGAGGCGCTA	AGTTTCAACC	TCGCAAACCC	13320
AACGCCGACC	CCTTGAGGAG	ACCTCCCAAA	AAACCGCGGA	AAGAAATCCA	CACGGAGACC	13380
ACCGGCGTTG	TATACACGGA	CCGGAAGCGG	CGCCAGGGGA	ATTACCCGCA	CCACACGCTG	13440
GCCGAGATCC	ACGGGAGACG	CTCATCTCAA	GAGATCATGC	CCTTACGTAT	GACCAATCGA	13500
CCGGCGCTAA	CTAGATCAAT	ACATACCTCC	CATACCTCCC	ATGTCAGGAG	CTGGCGGTGT	13560
AGAGGAACTC	TTTTCGGGAA	TTGCAGCAAT	TGCACATTCT	GTAGTCAACA	AAAGCCCAGA	13620
AACCGAAGCC	GCGTTCTGTA	GTGCTGAACG	TGTAACcTTC	GCCGGATCGA	TAATCCCGAC	13680
CTTAATCATA	TCAACCCATT	CCATCTTGGA	TGCATCAAAA	CCGATGCCAC	GTTTCTCCTT	13740
TGCCTTCTCT	GCCACAAcTG	CGCCATCAAT	ACCCGCGTTC	TCTGAAATCT	GGCGTATCGG	13800
CTCCTCGAGA	GCACGACGCA	CAATCTTAAA	ACCAACCGCC	TCATCTGGAG	TCAGTCCACT	13860
CAAATCAGCT	TTCTCGAGCG	CCGCCGAGC	CTGAATAAGC	GCTAAACCAC	CACCAGCAAC	13920

AATACCTTCC TCTATTGCCG CACGTGTGCG ATTTAAGGCA TCTTnCATa

13969

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

CACAGCACCC TACTGCGCCT TCAGGTACGC GACGCACACA TCGCAAGAGA AATTGCCGCC	60
TCAAAAAGTC TTGCATCGCA CCTTTCCCCC ACAACCGCTT GCCTGCAGGA CGGTCCGCTG	120
CCCACACCGG aCACTGCGCG CATTGCCCAG CCGGATACGA CACCTCAGGT GCAGGGTGCA	180
CAGACTGGAT GCAGTTACGA CTTTCTATTG CCACGCCTCC ACCGAGGCAC CGTTAAACAA	240
TTACTCTTGC GCCACGGATG GCCGGTGCAT GATGAAGTGC CTCTCCGCGA GGGAACTCCC	300
CTATCCTTGC GCTTACGCAT CTCTCCGGCT TCGTGTCTCT CTCTTCTAC TCGGTATCCG	360
TGTTGTCACA CGCCAGGGAC ACCCTCGTTT GTGCCACGTG ACTACCAGTG GGAAGCAGCC	420
GATGCCTTCG TCGGGAATCG CACACAAGGG AGCGGATTG GTGTGGTAGT TTTGCCGTGT	480
GGCGCGGGAA AAACGGTTGT CGGTTTACTC GTTATGGGTC TGTGCAAAC GGATACCCTG	540
ATTCTGACTC CTAATAGCGC AGCTGCACAG CAATGGAAAC kTGAATTgTG TGAAAAAACC	600
GACyTGGACG GGACATCCAT CGGTATCTAT TCAGGAGAtG CAgGAAATCA GACCAGTGAC	660
TATCGCAACt ACCAGATAcT CACCTGGCGT GCGCATGCAG ACGCTCCcTT TTCCCATTTc	720
CGTCTCTTTA TGGAACGCAG TTGGGGTTTG ATTATTTACG ATGAGGTGCA CTGCTCCCT	780
GCACCGCTTT TCCGTATCAC CGCAGAACTT CAGGTGGTAC GACGCTTGGG ATTAAGTGCA	840
ACGCTCGTGC GAGAAGATGG CTGTGCGCAG GATGTGTTCA GCCTCGTAGG ACCGAAGCGG	900
TATGACGTGC CGTGGAAGGA TTTAGAAGCA CGCGGCTGGA TCGCACGGGT GCGGTGCGTA	960
GAAGTTCGGG TAACGATGGA CCGGTCACtC CAGTACCAgT ACATGACAGC TCCTGTGCGC	1020
CTGCGACATC GCCTTGCCAG CGAGAACGAA GCAAAAGTAG CGGTGGTACA GCGTCTATTG	1080
CGCGCACATG CAGGTGCGCC TACACTGATT ATTGGGCAAT ACGTGCAGCA GTTATTACAT	1140
CTCGCACACG TACTGCAGGT GCCACTGGTG AGCGGAAGAC AAACttATGC GGCGCGTGAA	1200
GCCATCTATC AGCGTTTTCG CGAGGGCACG CTCCAGGTGC TCGTTGTATC AAAGGTGGcA	1260
AATTGTGCGC TTGATCTTCC TGACGCGTCG gTTGCAaTTC AAGTTTCCGG GaCATTtGGC	1320

AGCCGTCAGg AGGAGGCGCA ACGCcTCGGA CGCCTCTTAC GGCCAAAGAT ATGCGACGCC 1380
CATTTTTACT CGTTAGTTAC AGAACAAACG GTGGAAGAAG ACTGTGCacT GCGTCGCCAG 1440
CGGTTTTTGG TAGAGnCAGG GTTACACGTA CGAAACCcTT CGCGTAAGCG AAGTaCACGA 1500
ATAAAGGATA CTCCGTGCAG AGTCCTCCCT GTGTGTGTGA GGgGGGGGGG AGGAGGGGGT 1560
GACCGTGCgG TCTCCCTTGT TTTTTTGGT CAAGACCGCT ACAGTACTCC ATGCTCGTAC 1620
GCACTGCACT CAGGCTCATC TTTGGCTCCC AGCACGAGCG CGATCTGAAA AATCTCCTGC 1680
CTCTTTTGAA TGCCGTCAAC GCCCAGGAGT CCTGGGTACT TCCTCTCCAG GAGTCTGAGT 1740
TCAAACAAAA AACAGCTGAG TTTAAGGCGC GTGCCGCTGC AGGAGAAGCG CTTGACGCTT 1800
TTTTACCTCA GGCATTTGCG CTTGCGCGCG nAGGCAGCTC GTCGTGTTTT AGGCGAGCGT 1860
CCCTATGACG TGCAGATCCT CGGTTCCCTC GTCCTCCACC ACGGCAAAAT CGTGGAATG 1920
AAAACGGGCG AAGGCAAAAC GCTCATGAGC GTGGCAGCGG CGTATCTGAA CAGTCTTTcG 1980
GGGAGGGGTG TGCATATTGT CACGGTCAAC GACTATCTTG CTGAGCGCGA CGcggAnTGG 2040
gATGCGTCCA GTATATGATT ATTTAGGCGT TTCCGTCGGC GTCATCCTCT CTTCATGGG 2100
CAGTCAGGAG CGGCGGTGTG CGTACGCGTG CGATATTACc TACGGTACCA ACAATGAACT 2160
GGGCTTTGAT TATCTGCGCG ACAACATGCA ATTTTTAACG GAAGAAAAA CGCAGCGTGA 2220
TTTTTACTTT GCCATTATTG ACGAGATTGA CTCCATTCTC ATCGACGAGG CGCGCACACC 2280
GCTTATTATC TCAGGGCCTg CAGAAAATGA TACCCAGCAT TACGCCGAGG TTGACAGACT 2340
CGTCGGGCAG TTACAGGAAG TGGAGCGAAA TCCTGCCACA GGTGACTACC CCAACGAAgT 2400
GGACGGAGAG GAGGTTCGCG GCGATTATAT CGTTGATGAA AAGAATCGCA AGGTTTCCTT 2460
CAGTGGTCCG GGGATGCTGC ACATTcAGGA wtGCTCACGC ACGCTGGGCT TATCCAAGGG 2520
AGTCTATTTG ATGAAGAGAA CTTCAAGTAT ATCCACTACT TTACGCAGGC aCTCCGTGCG 2580
CACTTACTTT ACCGCGCAGA CGTTGATTAC GTAtAAAAGA CGGACAAGTA CAGATCGTAG 2640
ACGAGTTTAC CGGTCGCATC TTGGAAGGTC GGCGGTATTc TGACGGATTA CATCAGGCAA 2700
TTGAGGCAAA AGAACACATC CGCATTGCGC AACGTAATCG CACTATGGCA ACTATCACGT 2760
TTCAGmACTT TTTTAGAATG TATAAAAAGC TTTCTGGAAT GACGGGAACt GCGGATACCG 2820
AGGCGTTGGA GCTCAATAAA ATTTATAAAC TTGAGGTGGT AGTTTTGCCc GACGAATCTT 2880
CCCGTAGCGC GGGTGGATGA GCATGACGTG GTATACCTGA GTGAAGAAGA AAAGTGAGT 2940
GCCATTTGTG ATGAAATAAA GGAGGCACAC ACACGGGGAC AGCCGGTACT CGTGGGCACT 3000
ATTTCTATAG AAAAGTCCGA AAAACTCTCT GCTCTGCTGA GAACACGCGG TGTA AACAC 3060

720

GAAGTTCTCA	ACGCTAAAAA	TCACGCGCGC	GAGGCACTGA	TTATCGCCGA	AGCGGGGGCG	3120
AAGGGTTCGG	TGACCATCGC	AACCAACATG	GCCGGACGCG	GCACGGATAT	CAAGCTAGGG	3180
GGTAATCCTG	AATTTCTGTC	ACGACAGAGC	GCAACTGCCA	TAGCATCGAA	GCACGGTTCC	3240
TCCTCTGTCA	CTGTGCAGGA	ACATATGCAA	GCGTGCTATG	AGGCGGAATA	CACACGGTGG	3300
CGCGCAGATT	ACGAAGAGGT	TAAGCAGCTC	GGTGGTTTGT	ACGTCATTGG	CACAGAG	3357

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

TTGCCCCCAC	GnTGAAAGCG	CTCCTGGTnA	TCGGCGGCGC	ACATTTCGGCA	AATACCCAGC	60
GTCTACTCCA	CACCGCGCGC	GAAACGTTCG	TACCTACGTG	GCTGGTAGAG	CGTGTAGAAG	120
ATATTCCCCC	CGATATCTAT	GCCTTCAGTG	CGGTGGGCAT	CAGTGCAGGG	GCTTCCACCC	180
CAGACTGTGT	TATCGCTGCT	GTGGAgCAGg	ccTGCGCACG	GGCGGCGCGC	CTGTGCTTTC	240
TCGGGTGTCT	TCCTCTGCTC	TGCCCAAGGT	GAGTACCTGC	AGGGCTGTTT	GTGCGGCGGC	300
TACTTCTTCC	GTCGGTTCAG	CGGGTGCATC	CGGCGCGGTG	TCGCCCAGTG	CTGTCCGACC	360
TTTTGCTGTA	GGCTCCGTGC	GGTGAAACC	GyTTCCCTTT	GTCTGCGAAg	TGCATGGCTG	420
AACGTTGCGC	TCGGCGGGGT	GCTGGGTGTC	CTTTCCGGTT	GTCGTtCTTC	GACGAAAGGG	480
CGGATGTGCG	CGTCGACCGT	ACGGGAAAAG	AATACCTCGA	TGCACAGGTT	GCGTGTGCAA	540
AAGAGGAGCT	GCGCGCGCGT	CCTCTGCGGG	CGCTTATGTG	TGCAATTGCG	CTCAAAGAA	600
ATGCCCCAGC	ACATCAGAAG	GTGGCTCAGC	TGTATGCCCC	AGGgcTTGCG	CGCGTCAAAG	660
AGGCGTTTCG	CTATTCACTG	GAGAAACAGA	AGTGGTCGGA	GGCACTTGTG	TTTTTTCGTT	720
CCCTCTCGGC	ACTTCGCATT	CCGCTGAAGG	ACTGGACGGA	GCGATCGCTG	CATCGTGC	780
AAATTGAACA	GTGGAAGGAG	GAGGGTGC	ACGTATTGGT	TGCGGCGCAA	GAGAAGCGCG	840
CCGGAAC TTC	TgCTGCGCGG	AGTCCGGCAG	CCATGATAAA	GGGGACGGTC	ACCATTTTGG	900
TAGATCGAGG	AATTCGCGTA	GAGCACGGAC	GCGGGTTTGC	AGATCGAGTT	ATCGGGTCAG	960
GTTTTTTCAT	CGACAAGAGG	GGCTATATCG	TCACTAACTA	CCACGTTATC	AGAAGCGAGG	1020
TAGATCCTGC	GTACGAAGGt	ATTGCGGTGC	GTACATCAAG	CTCCCCTCAG	ACAACACCGT	1080

721

GAAAGTTCCG GTGCGCGTTG TCGGGTGGGA TCGCCTTGCA GATCTTGCAT TGCTAAAAAC	1140
AGAAATTACT CCTGAGGTGG TGTTTGGCTT AGGTCCTCA AAGAATTTGG ACGTGGGGAG	1200
TAAAATCTAC GCGATAGGAT CGCCTGCTGG GCTTGAACGA ACGCTTACTT CTGGCATCGT	1260
GTCTGCGAAA AAGCGCaAAC TGCTTTCAGT CGGTGGGGGA GTGCTGCAGA TAGACGCATC	1320
CATTAATCGA GGGAACTCAG GCGGTCCAGT TATCGACGAG GAAGGGTGCG TTCAGGCAGT	1380
AGCGTTTGCA GGTGTGGAGC AGCATGCAGG GCTTAATTTT GCCATTCTCTG TAGAATTGCT	1440
CAAGCAGGTG CTGCCAACTT GT	1462

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4532 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

CTTTTTGATG ACGCACGAGC GCTTGTGCCC CCGCGGGAAT TTTACGGGGG ACAGGCTCAT	60
GCGCGGCAGC AACAAGCGTA ACCTGATGTC CCCTCGCGCT CAAACGACGC GTAAGTTCAC	120
GCCCATTTCGT ACCGCATCCA ACAACAATAA CCCTCATGTC CGAAGnCCAT AGTAGCACGA	180
AATTTTTTTG CATGGCCAGC GCGCAGAACA CGGCGCACAA CGCCTGCCAC TCATATCTTT	240
TTCAAAAGTA CCACTACCTG TGCGGTAACC GCCGCACCAG ATCCAACAGG TCCGAGGCGT	300
TCGGCAGTCT TTGCCTTAAC AAAAACACGT GTTACGTGcG TGTCCAGGGc CTGCGCAAgS	360
GATGcGCGCA TCGcTTcCG AAATGGGTGT AATGCAGGCT GCTCAAGACA GACAACAGCA	420
TCGAGATTCA CCAGCCGcCA GCACGCTGCG CGCACCAGTT GcCAGGTATG GCGGAGCAAC	480
GCGCAAGAAT GTGCGTCTTT CCATCGTCCG TCACAAGAGG GGAAAAACGT GCCAATATCC	540
CCCAGGCCTG CTGCACCCAA AAGGGCGTCA ATGCTCGCAT GCGCAAGAAC GTCTGCATCC	600
GAATGACCCT GCGCTCCCTT CTTACTGGGa ATATGTATCC CTGcAAGTAT CAGcGGTCTT	660
CCTGcACACA GcGCGTGCAT ATCAGTCCCC AGTCCAACGC GCAGGCACCT TCTTCCGTAC	720
ACGGcAGGAC TGATATCCCC CTCGTGAGAG CAGGCTCCGA TGCCCGCTGC TcCAGATCCT	780
CCGGATAGGT AATCTTTACA TTACTGCGTT CACCGGCGCA GACATGTACG GTCCCTCCGT	840
AGCGAGCGTA CAGCTCcTgt TCATCAGTAT ACTGTTCCCC ATCAGTAGCA GCGCGGTGAT	900
GGGCAGCGCA CAGCGAsGCG TAgcAAAAAC CCTGAGGGGT TTGTGCTAAG CGCACTCGAC	960

722

TCCGTATAAG ATGCGTTTCG ATACTCCCAT CGGCAGCAAC ACCCTTGGGA GTATCCGTCG	1020
CCTCTATAAC CGGCACTGCC GCTCCATAGC GACAGGTAGC CTCAAGTACA GAATGAATAA	1080
GCGCAACACT CACAAAGGGA CGTGCGCCGT CGTGACCAG GACCACATCG GGCGCATGCG	1140
TAsCATCGCG TCAAGCCCCG CGCGCACAGA CGCACTGCGT GTATGTGCAC CCGGCACGTA	1200
AAGAATGACT GGACGCGTAC GAGACGGGAA CGCCGAAAGA CGCGAATCAC ACGCCACTTG	1260
ACTTTCCTGCG TACGCAACTT CACCTGCAGG AACGGTAACA ACGACAAGGA AGAACGACCG	1320
CGCCTCAAGG GCACGCACGA GTATCTCAGA AAGGAGGCAG ACACCAGGCT GCCTGGAAGT	1380
TAACGGCAAG TACTCCTTTT TCTGCACACA CGCACCACCT CTGCGCATGC GTGCAGAGCT	1440
GCCTGCAGCG GTGACAAGCA ACGCGGCGCG GgTCACCCGG GcACATCCAC CGTACCCGAC	1500
ACAACTGGGT TTTCTTTTGC CTTTTCAAA TAGCCATGGA TGAGCGTTTC AACCTcAGGG	1560
GGTCGCAGCC CCAGCGCAA ACACATCTCA TCCTGAAAAA TACGGTATGC AGAATCATAG	1620
AGCCTTCGCT CCTGGATAGG CAGTTCCTTG ACTTTACTCC GGTGGTAGAG CGAGCGCACA	1680
ACGCCCGCAT TGTCCAAGAT ACCACCACTT TTAAAAAGGT TTAAATTGAC CTGATAACGC	1740
ATTTTCCAAT CAAGAGGACT AGGATCAAAA TCCTCAGACA GAAACCTCAA CGCGCGCTCT	1800
GCTTCCTTCC TTTTGACAAT GGTTCCTAATA CCCAGTTCCT GTGCTTTATC CACCGGAATA	1860
AGCACCGTCA TATCTGACTC TTCCAAGTAA ATGACGTATA TAGCAGCGTC TCGTTCTTAA	1920
ATGTTTTTTC GCTTATTTCC TGcACCTGAC CGACGCCCTG TCCTGGATAC ACCACGTGAT	1980
CGTGGGGACG AAACGCACAC GCCTTACCCA TGGGGCCAGC GTACACAAAC ACGGAAAAAA	2040
GTCAGTGGGA AGAGGAAGGG GAAAAACGAG GGAActCCAC CACGCCCGAG TAGCCATAAC	2100
ACAAAGAACG TGtagactGG CGCACCCCTT TGTACTACTA TGCGCGCCAT GGCTTGCGTG	2160
CGCCGAGTGC GAAATTTCTG TATTGTCGCG CACATTGACC ACGGTAAATC CACCCTTGCT	2220
GaCCGACTCA TCGAAAGGAC GCGCGCGGTA GAAGAGCGTC TGCAGCACGC GCAGATGACC	2280
GACAACATGG AACTCGAGCG AGAACGAGGT ATAActATTA AAAGCCACGC CGTGTGTATT	2340
CCCTACACGG ATGCACACGG CACCGAGTAT GTGTTGAACT TTGTAGACAC GCCGGGACAC	2400
GCGGATTTTG CATACGAGGT GTCGCGCGCA ATTGCTGCCT GTGAGGGAGC GCTCCTGGTG	2460
GTAGATGCAA CGCaGGGAGT TGAGTCGCAG ACGATCTCAA ATCTCTACTT AGTTTTAGAG	2520
CACAATTTGG AAATTATCCC TGTtATCAAT AAGATcGnAC yCTAcGGcAG ACGTGnCCGC	2580
GTGTGCTCCA ACAGGTAGAG CACGACCTGG GCTTGATCC CGCCTCTAGT GTGTTGATTT	2640
CTGCAAAAAC GGGAGAGAAT GTCGACGCGC TCTTTGATGC AATTATCACG CGTATTCCTC	2700

CCCCGCAGGG	GAGTGGTACG	GCCGCGCTCC	AAGCGTTAGT	ATTTGACTGT	CACTATGACC	2760
AGTACCGCGG	GGTAGTTGTC	CaCATTCGTG	TTTTCGAGGG	ACAAGTCACA	AGTGGCATGG	2820
TTATTTCGTTT	CATGAGCAAC	GGGGCAGAGT	ACCGTGTAAG	AGAGACGGGT	GTCTTTGTAT	2880
TCAACCTTAT	TGCACGTGAA	GCGCTGTGTG	CAGGAGATGT	CGGTTACCTG	AGTGCAAATG	2940
TAAAAACGGT	TTCAGATGTA	CAGGTGGGGG	ATACCATCAC	AGACGCGTCC	TGCCCATGTG	3000
ACACGCCGCG	TGCTGGATTT	AGACGGGTAA	AGCCGGTGGT	CTTTTCCTCG	GTGTATCCGG	3060
TGGACACTGA	TGAGTGTGAG	CAACTGCGCG	AAGcATTGGA	GCGACTTGCC	CTCAACGACG	3120
CarTATTTCC	TGGGAACGAG	ACTCATCCTT	AGCGCTGGGG	cACGGATTTC	GCTGTGGTTT	3180
TCTAGGACTG	CTTCATCTTG	AAGTAGTGCA	GCAGCGTTTA	GAGCGAGAGT	TCAACCAGAC	3240
AGTCATTTTT	ACTGCGCCTC	AGGTGCAATA	CTATGTGTTT	CTAAAAACGG	GACAGCGCAT	3300
AGTGTGTGAC	AACCCAGCCC	ATTATCCTTT	GGAGCAGGAG	ATTGCACAGG	TGCATGAACC	3360
CTACATCCGT	GCAACTATCA	TTACGCCGAC	AGAGGTGCTC	GGTGCTGTCA	TGACGCTCTG	3420
TATTGAAAAG	CGCGCGTACC	AAACAGCGGT	GAAGTATTTA	GATCAGAAGC	GGGTGGAAGT	3480
GGTATACGAG	ATGCCCTTGG	CGGAAATTCT	CTTTGGGTTT	TACGATAGGC	TCAAGAGTAT	3540
TAGCCACGGC	TATGCGTCTT	TTGACTATGA	GCTTATAGAG	TCGAAGCTCA	CAGATCTGGT	3600
GAAAGTTGAC	ATCCTTATTA	ATGGGAAGCC	GGTAGACGCG	CTTGCGCAGT	TGTGCTATCG	3660
ACCGCATGCC	CGCAGAAGGG	CGCAGGCGGT	GTGTGCTCGC	CTGAAAGAGG	AGATTTCCTG	3720
TCAGCAGTTC	AAGATTGCAA	TCCAAGGCTC	AATCGGCGGG	CAGATTATCT	CGCGCGAGAC	3780
GGTTAGTCCG	TTCCGCAAAG	ATGTACTTGC	TAAATGCTAC	GGAGGTGACA	TCACACGTAA	3840
GCGAAAGTTG	CTGGAGAAAC	AGAAGGAAGG	GAAAAAGCGA	ATGAAGATGG	TGGGGGATGT	3900
GGAGATCCCG	CAGACTGCCT	TCCTGTCGGT	GCTAAAAGAG	GCTTCCGACG	CCTAAGGGTT	3960
TCAGCGCTGT	TTTTTAGAGT	CCTCTCCGTC	TTGCAGGGGa	TGTTGCAAAA	GCGATGGTCC	4020
GTCATGCTGC	GGTGTAGACT	TAGGTATCTG	GATAAGTAGA	CAGAACACAC	ATTATACGCA	4080
GCAAAAACAG	AAAAAGAACA	GGCGGGGAGG	GCGACGCGCg	CCCTCCGGGC	CGCAcTAAaT	4140
CTTACCGATT	AAaTCAATAC	CAGGCTTCAA	CGTCTTTGCT	CCAGGCTTCC	AACGAGCaGG	4200
ACAAAcTgAT	CCCCATGCTT	AGCCACAAAC	TGTGCTGACT	GAACCTTGCG	CAAAAGCTCA	4260
TCCGCATCGC	GCCCAATACC	CATGTCGTGT	ACCTCGAAAG	CTTTCACAAG	GsCTTCAGGA	4320
TCGACCACGA	ACGTACCCCG	CAGCGCATGC	CAAGTGTCTG	GCAACAACAC	TCCAAAGrAA	4380
CCCgCAAGCT	TTyCCGCCTT	GTCAGAAATC	ATCTCGTAGG	GcAGATTCTT	TATCGTGTCT	4440

724

GTCGCATCCG CCCATGCCTT GTGCACGTAC TCACTGTCCG TAGAAACCGA ATATACCTTA 4500

CAACCAATAA CTATAGGAAA CAAACGGGGA AA 4532

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6923 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

GTGGTTAGAT TCCCTTTTGG GGATGAGTTG GATGGTGCTG ACTCTGTGTG TCTGTGCGCT	60
GTTGTTTTGC CTGAGGAGGA AGTACGTACA TCTCTTTTTT CCTCGTGGGG TTTCGGTGCA	120
CACGCCCCCT GCGTCTTCGG ACGTGCGGAG TGTGTTGCCG GATATGCCAG TGAGAAGGAG	180
GCGAGGAATC TTTGTCTGAC TCGAATGGGT TGACGCGCTC ACCCAGGCTG CGTGTTCAT	240
GCTTTTGGTG AATTTGTTTCG CGTTCCAGTT GTACGTTATC CCGAGCGAAT CGATGGTCCC	300
CAGCTTTATG GTCGGCGATA GACTCCTCGT GTTCAAGACC GCCTCAGGGC CTGTATTCCC	360
GCTTTCTTCG TTTCGTTTGC CACGCTGGCG TACCTACAAG CGCGGAGACA TCGTCGTTTT	420
TTCCAATCCT CATTACCCTG AACTCCGCA GaTAAGCTCC GCGCCTTTTT AGCCCAATTA	480
GTGTACATGC TCACCTTTAC GCGCAAGAAC ATTAATGTGG ATCCTGTAC CCGTGCGCCG	540
AAAGCTGATC CTCTCGTCAA ACGCATTGTT GCTCTGCCAG GGGAAAAAGT TATGCTCGTT	600
GACGGTGTGC TCTATACGAA GACCAGGCAT GATGCGCACT TCAAGCCTGT CGCACAAGAC	660
CGTACGTACG CCACGTGGGA TTTGAATGCG TTGCCCCGAC GCGATTTGGC GCGTGTTCAA	720
CGGGTCATAT TTAATGCTGA GGAGCTCGCC GCCATCCATC TGGTAGAGCG CCTGCGCGCC	780
CAGGTGGATT TTCGCGATTT AGCAGAGAAA ACGCGCGCGT TGGTTGCCCA AGCGCACGCG	840
TaCGCGGGGg CGGCGTCACG CACCCGACAG GGCATTGGCG TGGCGCAACC GATAACGCAC	900
ACATCTGACA TTCCTGCTTT ACCTCTGTTT GAAAAAGAAA TCGCGGGGCG GCGGGAGATC	960
ACACAGCTCT TCGCCACCGT TGCAGACGTT GCCACGCATA TCCGCGACAC CTCCCAGGGG	1020
TTCGCnCatT CGCTCACTTT GTGCAAAGCT GGATCCCATT TTGGGGGCAA GGAACGTATG	1080
GCTTGACAC GGGACAGGAA GGTCCGTCCC tGCACGCGC AGGCCTCTCG CTCTACCAGA	1140
TAAGATTTGC GCAGCTGAAC GCGTTGGTGA AGTACACGTT CCCCCAGCTA GTGGTAAAAG	1200
GCCTCCAGGT GACAGCACAC CGAACGTCGG AGGCTGGGCA GGACGAAACG CTCACTACAC	1260

725

TTTTGCAGGA CGCGGCCCGG TACATCTTTT TCCTGGGTGC GGCGCGTGGA TTCAACATGG	1320
ACGAATTCCC CGCTGGCGCC GAGCAGTACC TTCCAGAACA CAACTACTTC ATGATGGGAG	1380
ACAACCGATT GAACTCTACT GATATGCGCC ACGCGTACAC CGAACACCTC GAGGCAATCG	1440
ACGCGCACGA CCCGTTCCCT ATTTTCTTTA GCTCCAATGT TGCGCCCAAG TACATTCCCG	1500
ATAGCCACAT CCTCGGTGTG GCGTCGTTCC GATTCTGGCC GCCCTCCCGC ATAGGCACCC	1560
CACAATAGGC TTAGGGGGAG CGGAGAGAAA GCTAAGAAAG GCGGAACCCG CCCAGGCGCG	1620
CAGCAGGcAG AAAGCCCGTA CCCTCAGACA sGTCCCGTTA CACAACAAGC GGGATAGGGA	1680
AGAGCCCTCG CTTACAAGGG CtCAGGAAAG ACATCCCTT ATCGTGCgAA gcGCTcGCCG	1740
AATGCTTTAC AGCTTGCTTG GGCTTCTTCA CTGGGATCGT CGTACGCGAT CTCCCCCTTC	1800
CCCTCGAAGA CATCAGCGCC AgCCGCCTTA CAACGCTCGA CCCAGTTGAC CATCCATTCTG	1860
CCGCCTTCCC CTTCTCCAGC CCACTCATAG GATCCGAAAA GCGCAACTTT TTTCCCCGAT	1920
AACCTTCCCT CAATAGAGGT AAAGAAGGGT TCAAACCTCGC TTGACTCTAG CTCCTCAGAA	1980
CCAGctGCAG AGCAGCCAAA GGCGAAGsGG TCATAGGAAT CAAAAGTACC AACGTCGAAG	2040
TCCATGACGC TAAAAAGGTC AGCTTTTGCA CCACCGACAT TCAAACCTC TACGATGCAG	2100
CGAGCCATCG TTTCAGTGTG CCCAGTGCCA CTCCAAAAAA TGACAGCAAC TTTTGCCACA	2160
AACTCCTCCT CGGGAACGTC ACGCagTGGG TGcACTCGCA AAATAGTGCA GCCACGACAC	2220
GCGCACCCCTG CCCGCGCAAG GGTAGGGGAA AGCTCTGTTG CTGTCAACCG CAGCCACAGC	2280
AGGATCCGgT GCCACCCTGG ACACCGGTAG ACTTGACGGG CCGACATTTT CCGGTACACT	2340
GGGGCTGCG CGCCAACCTTA GCTCACCTGG CAGAGCAGCA CCCTCGTAAC GTGCAGGTAC	2400
CCGGTTCGAG CCCGGGAGTT GGCTTTCTGT TTGGCGTAtT CCGCGCTGTG GGCCGGTAGG	2460
TGAGTCTTGG AAGAGGTGGG GGGGsGCGGg AACGGCGTGC TGTCTGTTC CTACGCGTTT	2520
TTCTCACTT CGGGTGGGGT GTTTTCCCTT TGAAGAACTG GGCAAACGGC TGkTATCGCG	2580
CGAAATCCTG TCCCGGCGCG GGGGATGTGC CCCGTGTCTT TGCGCGCTCA GGGGAGGTTT	2640
TCCCTTCAGG AGCCCGGGGA CGGGGTGCTC TCCGTGAAGG TGTCGCCGTG TGATCCGCAG	2700
gTGCACGCTG CTCTGCCTG AACTGAGGG AAATACGTCT CTTGCCTCG TCAAGCCCGA	2760
TGATGGTGCA GGTGTACAG TCACCTACCT TCACTTTTTT GAGGGGGTTG GAAACAAAGT	2820
GGTCGCTCAT CTGCGACAG TGCAGAAGCG CCGTTTCCTT TATTCCAATG TCCACAAAGG	2880
CCCCAAAGTC CACCACGTTT TTTACCTTTC CCTGTACGGT TGCCCCCACT TTTAAATCTG	2940
CAAAGGATAT CAGACCTTGG CGCAGCACCG GTTTTGGATA ATCCTCGCGC GGGTCACGAT	3000

TAGGTTTTTG	CAGCTCTGTA	ATGATATCTT	CGACGGTTCG	ATCACTGACT	GCGCATTGCG	3060
ACTGCACCTG	TGCCTTTTgC	GCTGCGCTCA	CTGTACCGCC	TGCGCGCAGT	ATATCAAAAA	3120
TTATCTTTCC	CGTTGCATAG	TTTTCTGGGT	GCACCCACGA	GTTGTCCAGC	GGGTTTGTGC	3180
TTTCGGGGAT	TTTTAAAAAT	CCTGCACATT	GCTCAAAGGT	TTTTTGTCCT	ATACCACTGA	3240
CTGTTTTTCAG	TTGTTTCGCG	CTAGTGAATA	TGCCGTAGtG	GCACGATGGT	GCACGATCCT	3300
TTTTGCCAAC	GCGCTATTAA	CGCCAGATAC	GTGCTTTAAG	AGAGATACGC	TAGCCGTATT	3360
GAGATTAACT	CCTACGCTAT	TGACTACAGC	ATCTACTACC	GCGTGGAGCT	CCTCAGATAG	3420
CTTTTTTTGA	TTAACATCGT	GCTGATAGAG	TCCCACCCCA	ATGGATTTCG	GATCAATTTT	3480
TACCAGCTCT	GCTAGAGGGT	CTTGCAGCCT	GCGTCCAATG	GAGATTGCAC	CACGGATGGT	3540
CAGATCTAAG	TCAGGGAACT	CCTCTCGCGC	AATATCTCCT	GCTGAGTATA	CGGAAGCTCC	3600
GTCCTCTCT	ACCACGGTGA	ATGCAACGGC	AGAGTGTGTT	TCGCTAATTA	TGGAGGCGAT	3660
AAGCTCCTGC	ACTGCATGGG	AGCCGGTGCC	GTTCCCAACG	GCTACGAGCT	GAATGCGGTA	3720
gCGATCAAGC	GCCTGCGTCA	AAGCGGCGCG	TGCATGGTCC	GTGTTGTGCG	GATATATGAC	3780
AAAGGAGCCG	AGATATTGGC	CCGTTTCATC	CAGTGCCGCA	CACTTAGTCC	CTGTGCGGAT	3840
GCCAGGGTCT	ATGCCGAGCA	CGCGCGTGCC	CTTGACCGGC	TGGGTCATGA	GCAGATTCGT	3900
AAGATTTTCA	CTAAAAACGT	TGATACCGTG	TTGCTCTGCC	GAAGCGGTAA	GGTCTGCGCG	3960
TATCTCCCGC	AGGACGGCAG	GACTGAGCAG	GCGCACCACG	CCATCTGTAA	TGGCATCGCG	4020
ATGATACCTG	TTGTTGGGGT	GCACCGCCTC	TTGAACCTGC	TCGACAGCGG	CGTCTAAATC	4080
GACGGTGATT	TTTACGTCAA	GGATTCCCTC	ACGCTCCCCC	CGATTGATGG	CTAACACGCG	4140
GTGCGCCTTG	ATGTCGCGCA	CTGCCTCTGC	GTAATCCCAA	TACATTTGkT	AGACGGACGT	4200
GtGgCAGCGT	GCGCGTcCCC	GATTCCGGTA	GCCGTAACGA	CGCCTGCAGA	AAGGTAAAAG	4260
GACTTCAGTG	CGGCACGAtT	GGCGTTGCAG	TGTGCGGTCT	CtCTGCGAGG	ATATCGCAGG	4320
CGCCTGCGAT	GGCGTCTTGA	GCGCTGGAGA	CGGCACGATC	AGAATCTGCa	GCAGGAGCGA	4380
cGAgCGCTGC	GGCAGCGCGC	TCGATTTCTG	CCTGCGTGCC	GCACTGCGTT	TCTATCAAAC	4440
GCGCAAgCGG	CTCGAGTCCT	TTTTCGATCG	CCTGCATGCC	GCGTGTCTTT	TTCTTTTTTTT	4500
TGAACGGAGC	CCAGAGGTCC	TCGAGTGCTG	CAAGGGTAGG	AGCGCTCCTG	AGGTGCTCGT	4560
AGAGCGTgGG	GGTGAGCATG	CCTTCTTTGA	AGACGGCGCG	TATAATCTCG	AGTCTGCGTG	4620
TTTCGCGTGC	AAGGTGGGTG	TGGAAGAGGC	GTTCGCAGTC	GCGGATGAGC	ACCTCATCGA	4680
GGCAGTGATG	CGCTTCCTTC	CGGTAGCGCG	CAATGAAAGG	AACCGTGCAG	CCTTCTTTGA	4740

727

GGAGGGAACG CACGGCAGTA ACCTGCGCGG TCGGGATGTG CAGTTCGCgc GcTACGCGTT	4800
CTGCGAGCTC GTCCTCTTGC ACGCTGAGTG CGTCCACAAA GTCCTGGTCT AAAGTCATGA	4860
GGGGGAGTGT AACGCGTTTG GCTCTTTTTA GAGAAGCGCC GGCCTGCAAC CGGCTCCGGC	4920
GCGGACCCTG GCGTGGCACC GGCCAGAGAA GGGCGAGTGG AGAATAGGGG AGTCGAACCC	4980
CTGACCTCTT GATTGCGAAC CAAACGCTCT ACCAGCTGAG CTAATTCCCC AGGACTGCTG	5040
GCTCCAGCTA TACACCAAAT ATGCGCGTCC TGCAAGGGTG TTTcCTGCGG GTGTGATGCC	5100
CCTCGTGAC CCTGTTCCCT GCGCGACTGC GCGCGGTGT AGCGCTCTAG GCGCGTCGGG	5160
GGGTGTGTGA GAATAGGCCG CATGAGCTAT TCGTGGAAG TGCGCGCGCT GTGcTGCGCA	5220
GGACTGTGTG TAGGTGCGGG GCTTCGTGCC CAGGAGGGCA GCGGAATTCG CGTGCGCGGT	5280
ATGCCGGAAC ACGCGCAGGT GACCGTAAAC GGATATCTGT GCGCAACACC AGAGGAAATG	5340
GTGCTCACCC CTGGTGAGTG TGAGGTAACC GTCTGTGCCT TTGGATATAC CAAAAGACG	5400
CTCCAGGTAG TGGTTGAGGA AgGCTCGTTC ACGGTGGTGG ATGGCCGTCT GGATACGGCG	5460
CGTTTGAGAC TCACGGATGT GACTGCGCAG AGGGCGCACT TTAATCCGCG GGATCCGGCG	5520
GgACTGAACA CGGAgTACGT CACgTTCCGG GTGACAAAAT CTGCAAAGTG TACGGTAACG	5580
gTAAAGGATG CCGAAGGAAA GGTGGTGTGC GAGGAGCCGG TGGAGTTAGT TGAGCTGGGG	5640
TTGAACGTGG GGGGAATATT CGGGGGCAGT AATAAGAACA GCGAGGATGT TAGCGTTAGC	5700
GCAAAGGTAG CGTTCAAGG GAACGTTACG AGCGACCCGG CTATGGGCCA GCTCTATGCC	5760
TCAGCGCTGT GTTTGTACCG CATCGTGAC AACAACGATA GCAGCGGCGC AAACAAGTGC	5820
TTCATGCGGA AGGGTTTGAC GTTTGCGACC ACCTGTGCGT ACGGCATTAA GGGATTACCC	5880
GTGCGCTCT CCGGAGAACT GGGTGCCAGT TCAGAGACGG GGATAAAAAA GCCGGACTTC	5940
TCAACCGATG TCGGCCTGTC GCTCAAGTAC CAAAACAAAA TATGCTCCAT TGCCACGTAC	6000
AGCAAGTGCG GAACCACCAC GGGGAGCAAT AGTGACGGAG CGAACAGTGT GGCGGGTGTG	6060
TCcGGTTATG CGTGCTGCCT GCAAGTCTCG TGATGGGCTT GGAGAACAAT ACGCTTCAA	6120
GGTAACCTCT ACGAGGGCTG GGnAnTACGC GCTTCCATTG GGTACGTTAT CAACACGAAG	6180
CTGAGAGTCG GCGGACCATA GCGGGGCAGG GTACCAGCCT GCTGCGATCG CGCGGGCAAG	6240
TGCCGCCGTC AnCGTGCGCG GTCTGCGGGT ACGTCATACC AAACCAGCGC GCGCTGCTGG	6300
GGTAGCAGCG CACCGTTCCT TTTCCCTGTG CAATGAGGCT GTTTACCGCC GCGGGCAAAA	6360
GGTATTCCCG CTCGTGCTGC GCGCGCgCb TtCTTGAC GAATGTCTGC CAGCACGCTG	6420
CGAGGTGTTC GAACACGCGC GGAtGAAGCC AAAAAAGTTC ATAGACGCTA CTTCTGCCC	6480

728

GGTGAGTGTG CAGGGCGCGC GTGCCGCTGT GGCGGGcAGT CTTCCGCGCG CTGTGnGrTA 6540
 ATGACCCGTC TGcCGCCGTG CGCGTGCCAG CCGATGTGCG TGTGTTCTGTG TATGGCACGC 6600
 ACCAGGCGTC CTGCGGCGGG GACTGCGGGG GTGGGGGGAG AGACTGCGGC GTCAcGTcCG 6660
 CAAAGGTGCA GATACCGCGC GAAACGCCAC CGGTTTCGCT GAGCgTGTGC ACAAGGGGgT 6720
 AGCCGACCAT GGCGTGCGT GTCGAGTCCA GCCCCTGCGC GGCAAGGTGC GCGGCAAGcg 6780
 TTTTGTAcgC GTCGcnTCCG TAGTAGTCAT CAGCGTTGAT AACCgCAAAC GGTGCAGTCA 6840
 GCTGTGTGCG TCGCAaagCA AGCGCGTGGC CCGTnCCCCC ACGGCGTGCG CGCGACAGGA 6900
 TCGGnCAGAG CGGCGCCGTG TGC 6923

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6986 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

ATACCTTACA ACCAATCTCC ACAAAGACG GATATACGCG CGCGAGATCG TCAAGCTCGG 60
 TGGGGCACAC AAAGgTGAAG TCGGCCGGGT AAAaCmTAAA CACCGCCCAr cTACCCTTAA 120
 TGGATGCGTT AGAGACCTCC GTAAACTTCC CCCCgACATA CGCAGGAmGc TTAAAGTCTA 180
 TAACCCTCTT GCCTATGAGA CTCTCCaTAG cAACCTCCCA AACGTTcGCA CTCTAGCGCA 240
 AACTATAGGA AACAAACGGG GAAAAGTAAA GTCTTTTACA CGTATCCCCC GGGTCACCAC 300
 ACCATCACGC AGTACGTTCA GAAACAAGGC GAACGCTGGC TTTTTCCTCT TGTGTAActA 360
 CCTTCTTCGT AATGCATAGC TCCTTTTTC CTTTCAGAGA CGGTGCCTCA AACATAGCAT 420
 CAAGCATTA TCTTTCCACA ATAGAGCGCA AACCCGCGC CCCCgTTTTT TGATCAATTG 480
 CTGCTGAGC TATTGCGTCC AAAGCGTCCT CATCAAAGAC aAGACGCACG kCATCCAACG 540
 CGAATAACGC TTCAAActGA CGGACAATAG CATTTcGCGG TCGTACCAAG ATATTGCGCA 600
 GATCCTCTTT AGAAAGAGCA TCCAAGGCGA CCGTACCCG CAGACGGCCG ATAATCTCTG 660
 GGATTAATCC AAATTTcACC AAATCATCCG GAATGACGTC CTCGTGCATC AGTTGCAGAC 720
 CTCGCTCCTT TACCGTTTTT ACATCTGCTC CAAAGCCAAC CGGATTCTTA CACAcTCTCG 780
 TACcGACAAT ACCATCTAAC CCAACGAACG .cACCACCACA GATGAACAAA ATGTTcGATG 840
 TATCCACCCT GAGCATGTct TGGTTTGGAT GmTTGCGACC CCCtGCGGAG GCACcGATGC 900

729

TATCGTTCCC TCAaTTATTT TCAAAAGCGC cTGCTGAACC CtTCACCCGA CACATCACGC	960
GTAATAGACA CGTTCTCGCT CTTACGCGAA ATCTTATCGA TTTCATCAAT GAAGATAATC	1020
CCCCGTTCTG CGAGGGCAAC ATCTCCGTTT GCATTCTGAA CGAGCTTTAA TAAGATATTC	1080
TCTACGTCCT CACCCACATA ACCGGCCTCG GTGAGCGTAG TAGCATCTGc tATCGCAAAG	1140
GGGACCTTCA TTTTCTGAGA AAGTGTCTTA GCCAACAGCG TTTTGCCTGA ACCTGTCGGC	1200
CCAATAAGCA GCACGTTAGA TTTTCAATC AATACCGAAT CAATATCCAA AGACCTACCT	1260
GCCACCCGTT TGTAAGTGGT GTACACCGCA ACCGATAGCA CCCGCTTGGC CAAATCCTGC	1320
CCAATAACGT ACTGATCAAG GTAAGCTTTC AACTCTAAAG GAGTTGGAAT CTCTCTTTG	1380
GTCATGAGCG CAAGTGCCGA CGGCTTGCGA TCACGCAAGT ATTCTGCACA CCGCTCCACA	1440
CAATAATTGC AAATAGAAAC CCCATGACCG GTCACAATCC GGCCTCGCTC ATCTTCTTTT	1500
TTTCCACAGA AAGAGCAGCC CAATACCAGA TCCCCCTTAG ACCTGAGCAT GCTTCTCCT	1560
CTTCATTACC GTATCTACGA TACCATACGA ACACGCCTGC TCCGCGGAAA GGAAGAAATC	1620
TCGCTCCATA TCCTCCCGCA CCTGCTCCTC TGACTGCCCA GTGTGCAAcG CGAAATACGC	1680
AATCGTCAGC GTCTTTAGGC GCAGGATCTC CTGCGCCTgG GATGCACACA TCACTTGCCT	1740
GCCCCGTGAC GCCACCCAC GGTGATGGA TCATCACCCG AGAAGACGGA AGCGCAAAAC	1800
GCTTGCCAGG CGCACCTCCT GCCAGTAACA CTGCTGCCAT ACTCGAAGCC TGTCTAAGC	1860
AAATGGTCTG CACCTCAGGG CAAATGTGCT GCATCGTATC GTACACTGCA AGCCCTGcAG	1920
TAACCGCCCC GCCAGGACTA TTAATGTACA GGCTGATATC CTTATCTGGA TTCTGAGACT	1980
CTAGAAAAAG TAAcTGCGCT ACAACTAAAT CCGCCACCGC GTCAGTGATC TCCCCGTCTA	2040
CGAAAATAAT ACGGTCCTTC AACAAGCGGG AAAAAATGTC ATAGctCCGC TCTCCACCCC	2100
CCGACTGTTC AATCACGTAG GGAACCAGAT TATGCATACG TTCACGCACG GGACTGCTCC	2160
TGAAGAAAGT CAGTCAAAGA CTGCTCCGGC CCACACTCAG TCACACATCG TCCGAGCAAT	2220
TTCTGGCACA GCTTCCGTTT TCGTATTCCT TCACACAGCG CACGCCGTTT TTCCTCCCCT	2280
GCATAATACT CGCGTACCCG CTCCTCTTTG GAACCTGTTT TGGACGCAAT GCGTACGTAC	2340
TCCGTCTCAA TTTCTCAGC AGAAACAGAC ACCTGCTCCT GCTTAAGAAG GAGCTCAACA	2400
ATCACACGCT GCTTCAGGTG CTCTTCCACC TCCGGACGCC ACTGCTGAAA AACTGCAGC	2460
TTATTCTGCG GGGTGCCCGA CAGGCTCACC CCAAACGAC GCATCACCAA CGCCCAACGA	2520
GACTCCATCT CCCCCACAAC CAAAGATTCC GGCAGAGAAA AAGGATTCTC CCGCACCAAT	2580
ATACGCAACA GCTGCCGCCT CTTATACTCG TGCAGCGCTG CCTCCAAcGC TTCCGCGAGG	2640

730

TTTTGCCGCa	aCTCCGTGTC	AGATCGTCAA	GTGTGCGAAA	AGCATCGCTC	ACATCTTGCG	2700
CAAGcTCATC	ATCAAGACTC	GGCAACTGAC	GCTGCTTGAG	CGCCTTAAGC	GTTACCCTCA	2760
CCTGAGCGGC	TTCGTCCTTC	AGCATACCGG	CCCTTTTAGC	AAAGAGACAC	CGCTGTCCTA	2820
ATTTCATACC	CAATATATCT	TGCCCAAGCG	CAAAGGGACC	TTCTTCCACC	CCAAGCGTAA	2880
AGACAACGCC	GGCGCGCTCA	GTACCCGGAC	GAACGGCACC	TGAATCGTCA	ACCTCGTGAT	2940
AATCGACGGT	GGCAATGTCC	CCTACCTCTG	CACACGAATC	TGCACCCTTA	TCAGTAACCA	3000
GCGCATTGCG	CTCCTGAATA	CGCGTTAACT	CTCGAGAGAC	GTCTCTTCT	GTGACCGACA	3060
CAGTGGGCAC	GGACAGCGAA	AAGCCCGATG	TGTTGCGTAG	TTcAACGGAA	GGAAATACGT	3120
CGTATATGAC	AGCAAAaGAG	AAaTCCTCGT	CAGGATCGAA	CACTGGCTTT	TTCTTAAGCG	3180
AAGGACGGGA	GATAGGAAGA	GGCTGACTGT	CCTGCGACGC	CTGGGCAAAC	CCCTCCTCCA	3240
GAGCTTTTTTC	CATGAGGGCC	GCCGCTGCAT	CTTGCCGAAT	AGCACTTCCA	TACTTCCGCT	3300
CAAGCACTGC	AAGAGGAACT	TTCCCTTGC	GGAAACCAGG	AAGCCGCGCA	CGCTCAAGAT	3360
ATTCTCAAC	AAAACGCTGA	TAATGcCGct	GCGCATCCTC	GCGCGCGACG	ACCACCTCTA	3420
GCTCAACCTG	AGATTGTGCA	AGCGCGGTGA	ATTTTTTTTG	AAGTTCCACA	AGCCCAGATC	3480
CTTAGGAAGA	AATACCTACG	TCCGCAACGC	cTCGCACGGT	CCAAGCAGGa	TGCAGCAAaG	3540
CGCTGaAAAA	GCGGGAAACG	GGGATCGAAC	CCGCGaCTTC	CACtTGGCAA	GGTGGCGCTC	3600
TACCACTGAG	CTATTCCCgc	ACAGGCGCct	GCGAGAGGAG	GGACTTGAAC	CCTCATGCCA	3660
GAGGCACTAG	ATCCTAAGTC	TAGCGTGTCT	GCCGATTCCA	CCACTCTCGC	ACGGAAGAsA	3720
TsCGGCAAGC	AAAAACTCGC	CCAACAGGAT	GCAGACACCC	AACCGCCCCT	GAGCCATGcA	3780
GGCTTCGAAC	CTGCGACCCA	CAGATTAAGA	GTCTGTTGCT	CTACCAACTG	AGCTAATGGC	3840
CCGTCTCCG	ACACCCTCCC	CCCAGGATCA	CATATCATGC	AAAAAGGATC	AAGATGAATC	3900
GTATCGTCGC	GTCCACGCA	CCTCCTCTTT	TCGCTCAACA	TTTCCTTCAA	TCAGTCCAAA	3960
CCTCTAGGAA	GATATCCAAG	TCGCCGAACA	CAACAGGGGC	GTAGTAGGGG	ATTGACTGTG	4020
CAGTCACTGG	GTCCGTCGGG	TTCACCCTAC	AAGGAACACT	CCGTTTGCCG	TACTCGTTCC	4080
GCATAGGCCC	TGTCTTTAGG	TATAAACTCC	CTGCCCCATA	CGCCGGCACC	CCTTTTTTGC	4140
AGGAACGGTT	TCCTAAACGA	GCTATCCGTG	CTACCCTGGC	AGCCGACCAG	GGAGGGCGCG	4200
TATGGATCAG	CATACACGTA	CACGCGATCT	TGTTTCTGCA	TTTTTTGGGC	GC'TTCACTT	4260
TGATGTCCAG	GGACCTTCCG	TCCGCACGGT	TGTCGACGTG	TTGCGCGCAG	ATATGGTGCG	4320
CGGCTTAGAG	GAAGAGGCGC	AGCTTCCTCC	CCGTATGGGG	AGTGCACTTG	CGATGATTCC	4380

731

CACTTGGGTG GCGCCCCCCC GTGTATCCCC CTGCAACCGA CGCGTGATAG TTATCGACGC	4440
TGGAGGAACC AACTTTCGCT CGTGCCCTCGT ACGTTCGGC GACAGTGGCA CACCTCACAT	4500
CGAGAATTTA GAAAAACGTC CCATGCCCCG TACCACCCGT GAGTACTCAA GGACAGAGTT	4560
TTTTGGAGAA ATTGCAGACA ACCTGGCACG TCTGAAAGGT GCAGCGGACT GCATTGGCTT	4620
TTGTTTCTCT TACCCATATC GTATCAGACt GACGGTGACG GTGAGGTTAT TCAGTTTGCG	4680
AAGGAAATCA AAGCTGCTGA GGTCAATCGGC ACGTGTGTCG GTGCTGGTTT GACAGAAGCG	4740
CTAAGTGCTC GGAAC TGCC TGAAC TCCGT TCTCTCAAAA TGCTCAATGA CGCAACGAGT	4800
GCGCTGCTTG CAGgTTTTTT TCGGCACCA GAGGGGTGTT CGTTCAGTTC ATACGTAGgT	4860
TTTATCTCTG GCACTGGAAT GAATCTGCG TATCTGGAGC CAGACCCTAT TCCTAAAATT	4920
CCTGCGCATC ACACACCTCA GGTGGTAGTG TCGGAATCGG GAAAAAGCAA CAAAGTACCG	4980
CGCAGTGCTT TTGACGAATT ATTCACTCAA ACTACTGCCG AGCCGATAT TGCACACCTA	5040
GAGAAGATGT CCTCGGGCAC CTACCTCGGT CCCCTTGCTT CCGTTGTCGT GCGGCTTGCG	5100
GCACAAGAAG GTCTTTTCTC ACACGCAGTA CACGCTGcAC TCAGTACGGT TTCCTTTACA	5160
CTCGTGGATA TGGATCGTTT TTTATTTGCT CCCTCTGTGT CCACCACCAC GTTGGGCGCG	5220
TTGCTCGCAC CGGGCACCGA CACAGACCGA GAGATTCTCT TTCTTTTGCT CGATGCGGTA	5280
kTTGCACGTG CAGCACGCAT CGCTGCGGGA GTAATCGCCG CCTCAGTATT AAAAAGCGGT	5340
GCTGGGTATG ATCCGCTTCG TCCCGTGTGC GTGCTCGCAG AAGGCACCAC GTTCCAACGC	5400
ACCTACCGCC TACGCACCCG GGTTACTTCC CACCTGCAAG CCTTTTGTGAC TGAGGAGCGC	5460
GGTGTGTATT TCGATATCAT TTCACTTGAA AACGCCGTAa CGCTCGGCTC TGCACTCGGA	5520
GGACTCAGTT CGTAGGCATA TGCCTAAACG GACTGATGAT CCTGTGAGAG ATAGCGCCGT	5580
GCAGTGCTTC CTGTCATCTT CTCGTGCGCC GCGTGTGGCT GAGCGGCCGT GCTCGCCTTC	5640
TGGTGCGAAC GCGCTCTCCC TGTCTCTAGG GGAGTAACTT CCACGCCGAG TGTATCTTCT	5700
CAATCTTGTA CACGAGTAGT GCCTTCCCTC CATGGTTCAT GATTACATCC ACTCGGGTCG	5760
GGCTCTCGAA GACAATGGAG TCCACCCGCA CGTTTTCGCC CGACGGCACG AACACGTGTA	5820
TAAAATAATC GCGTAGtGCC GCAAACGAAC ACCCTTCTTT GGCAGGGCGT CCGAGCTCTG	5880
CTGCAATATG TCAGGCATTG AGTACGCGCG CCGATATGCG TCGGAAAGAT ACACAAGCCA	5940
CTTGTGATAG TCACGTTTCG CAGTGATACG ATTCAAATGC GCCACCACAT CTTGCAATTC	6000
TGCCTTTGTA CGCTCATAGT CTGAGCGCGT GATGCGCACG GTGCCGAAGT GGCGACAACG	6060
CCCGCACGCT CCTGCGGACT GTGAACATTC ACCTTTCAT CGTTCTGCAC CCACCTCTGG	6120

732

ACGCGGGGCT GTGTGCATGA AACACTGCCC CACAATACAC TTCCGATTAA GTAGCATACT 6180
 TTTCCTCTTG CAAATGCGCT CCTCACTACA CGCCCACCAG CGTACACAGA GTAGGATCGT 6240
 TGAAGAGCTT TGCGTACCCC TGTGCCGACA AGCCCAACTT ATCCTCCAGG TACGGATTTG 6300
 CACCATGATC CATCAATAGC CGAATTAATA CATGATCTTT CCTACCCACT GCCAACACCA 6360
 GCGCCGTTTG ACCATTTGAA CCTCGCACGT TTGGATCTGC TCCTGCATGC AAGAGCAGAC 6420
 GCGCAACAGT TCGGTTCCCA ATTTGAGCTG CTTCCATCAG CGCAGAATAC GCGCGATCGT 6480
 CAGATAACTG ATCTACTGGc gCACCgCGCG CAATAAGTTG CGCTGCCATC TCATCCTGAC 6540
 CCTCCCGCAC TGCCAAAGAC AACACAGsGT ACCGCGTGCG TCTTTCAACG CAGCGCTAAA 6600
 TCCTGCATCC AAAAAGAGAT TGACAATATC AATATTCCCA TCCATGACTG TCGCGATGAA 6660
 ATTTTCTTCA AAACATGGAT AACCgCGCTC TAACAGCGCA GTGCGTGCGA CACGCTTCTT 6720
 TTTCTGCCTT ACAAATCTcT CGTGCTCGAC ACGAAAGAAA TCCTcAAACG TCTCCTCCTC 6780
 AAGTAAAAAG ACCAAGTCGC GAAATACATG GATATCCCTG ACCTCCGTTG TTGTAGCCAA 6840
 GAGCAGCAGC TGCATACCAC GCCCACAAGC AACTCCAGAA AAGAGnATAA AAGCCGGATC 6900
 GCGCATGGGC TCATGCGGTA CAAAAAAAAC ACATGCGTTG CATCCTGTAC CAACGCCAAA 6960
 GGGTAACTGG CACGGTGGAT GTGGTC 6986

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

ACTGTCTGCC ACGCTACACA CACTCACACA TCAGTATCTT AAATACGAAG AGTGTTCAAA 60
 ACAGCTTGCA CAAAAGACGC AAGAAAGCGC AAAGCTTATA ACTCTTTCAG ATGAACTGAA 120
 TGGGATAAAC CAAAAAATAA TACAATTTGA CGCATGGGCA CTCATTCTT TTCTGCACGA 180
 AATTACTGCC TACGCAAACA TACGTTTGCA AAAATGAGT GAAGGACGTT ACCATCTGAG 240
 GGTAGCTGAC TCGCACGTCA ATGCACGAGG ATATCAAGGA CTTGCGCTGC TCGTTGCAGA 300
 TCGGTACACT GGGAGCGTGC GCCTTCGGCA ACACTTTCAG GAGGCGAAAC CTTTATGGCC 360
 TCTATCAGTC TTGCACTTGG TCTTGAGAT TCTATCCAAA CCCGATCGGG AGGTATTGTG 420
 CTTGACTCGC TGTTCATAGA TGAAGGATTT GGAAGTTTGG ATGAGGCAAG TTTAGATAAG 480

733

GCAATTGGCA TCTTAGATGA AATCAGAGAG GGAAGTCGCA TGATAGGCAT CATTTCTCAT	540
GTTTCATGAAT TGCGCACGCG CATCCCTCAC AAAATTCTGA TAAAAAAAC AAACGCAGGA	600
TCACACGTAA TGCAGGGGGA TGCAGAATGA AAACGAGCGC GCTCTTTCTT GATTTTACG	660
AATTGACTAT GGCGCAGGGA TACTTTTTTC ACAAGCCGCA CGAGTGTGCG tGTTTGAAGT	720
ATTCTTTCGT AAACACCCCT TCGCGGGAGG GTACTCCATT TTTGCAGGAC TCGATCCGCT	780
CCTGACGGCA ATAGAGCAGT TCCGCTTCAG TGGAGAAGAT ATCGATTATT TGCGCACCTT	840
GCACTTATTT CATGATGACT TTTTGTCTTA CCTTGCTTCC TTCCGCTTTT CAGGAGATAT	900
ACACGCGCTA GAAGAAGGTT CAGTAATATT TCCTCACGAA CCGATCATCC GCGTGCACGC	960
GCGCTTG GTT GAAGCACTTC TGCTTGAAGG ATTGATACTC AACACCATTA ATTTCCAAAG	1020
CCTCATCGCA ACAAAGACTG CACGGATGTG GCGCGCGTCA GGTGAAGGTG TTCTTATGGA	1080
GTTTGGCCTC AGAAGAGCAC AGGGCTATGA CGGCGCGTTG AGCgCCACaC GCGCTGcTGC	1140
AATAGGTGGC GCAACAGGGA CAAGCAATAC ACTTGCTGCA AAGCTcTACG GTATTCCGGCC	1200
AATGGGAACT ATGGcGCACG CgTGGGTGAT GTCTTTtGAC AGTGAAGAAG AGGcCTTCGA	1260
ACGCTATGCT GCACTCTATG GAAGCGCGTC CGTATTCCCTC ATCGATACGT ACCATACCCT	1320
GGG	1323

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3076 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

TACTnCTACT TCCATCCCCT CCAGAACTCC TCCCgGATAT TCctTCATCA GTACATGGAA	60
TGCTCCCCCTA CCGCCTTGCA CCAAAAATGC AAGACCCGTA GCTTCGGTAT ACCGCTTAGC	120
CCCgATACAT TATCTGCGCA TGCCTACTCG ACCAGTGAGC TATTACGCAC TCTTTCAaGG	180
AATGGCTGCT TCTAAGCCaA CCTCCTGGCT GTCCAGGTAC CCACACTTCA TTTcACACTC	240
AAGCGGTATT TCGGGACCTT AGCTGACGGT CTGGGCTGTT TCCCTCTCGA CTACGAACCT	300
TGTCGCACGC AGTCTCACTC CCACACGTTG ACTGCCGGCA TTCAGAGTTT GATTGGGTTT	360
GGTAGGCGAT GAAACCCCTT AGCCCATCCA GTGCTTTACC TCCGACAGTT TTGTATAAGG	420
CTGTCCCTAA AGGCATTTTCG GGGAGAACCA GCTATCTCCA GGTtTGTTTA GCCTTTCACT	480

CCTAGTCACA	AGTCATCCAT	ACCTTTTTTA	ACAGATTATA	GTTCGGTCCT	CCACAAGGCT	540
TCACCCCTGT	TTCAACCTGC	TCATAACTAG	ATCACCCCTGG	CTTCGGGTCT	ACGACGTACA	600
ACTCACCACG	CCCTTTTAAG	ACTCGGTTTC	CCTCCGGCTC	CAGGACTCCT	ATCCCTTAAC	660
CTTGCTGCAC	ACCGTAACTC	GCAGGCTCAT	TCTACAAAAG	GCACGCTACC	ACCCTCACAG	720
GGTGTAACAT	CTTGTTGGTT	TACGGTTTCA	GGTTCTATTT	CACTCCCTC	ACCGGGGTTT	780
TTTTCATCTT	TCCCTCACGG	TACTTGTTCA	CTATCGGTAG	TTGTCGAGTA	TTTAGCCTTA	840
GATCGTGGTC	GACCCAGATT	CCGACAGGAT	TCCTCGTGTC	CCGCCGTACT	CAGGTACCGC	900
ACCAGCAGGT	CCGCCCCATT	CCGCATACGG	GGATTTTACC	CTCTCTGTCA	GGCTTTCCCA	960
AAACCTTTCT	GCTATAGGCC	GGATTATTTT	ACCCACCGAA	CGCAAGCCCG	CGCGGCCCTA	1020
CAACCCCTGT	TAGACACAGG	TTTAGGCTCC	TCCAATTTTC	CTCGCCACTA	CTTTCGGAAT	1080
CTCTCTTGAT	TTCTTTTCCC	AAGTTACTTA	GATGGTTTTC	TTCACCCAGT	TTGCCTTAC	1140
CCTCCCTATT	CATTCAGGAA	GGCAATGACA	AGGCTTTACC	TGTCGGGTTA	CCCCATTCGG	1200
TCATCCCCGG	ATCACAGGAC	ATGTGCTCCT	CCCCGAGGCT	TTTCGCAGCT	TATCACGACC	1260
TTCATCGCCT	GACAACTCCA	AGACATCCAC	CGTAAACCAC	TATTCGCTTG	ACCATATTAT	1320
CCATCCCTTC	TCAACTTCAC	ACCCACCCCT	AATACTCTCA	AAAATCACCT	ACCACCTACT	1380
CCTTACCCCA	TAAACAAAAC	AAaGGGACAT	AAaGAATAAT	AGTGGGCTTT	CCCTGGAGAT	1440
AgGGGACTCG	AACCCCTGAC	tACGACCTGC	AAAGCCGTCG	CTCTAGCCAG	TTGAGCTATA	1500
CCCCCTTTTC	AAAAGGGAAG	GGGAGAGACT	GCCGTGCAGG	AGCAGAAAAA	CCtTaAGtGG	1560
CTTCCGCCAC	ACGnCGAACA	CGGCACCATG	CCATGCCCAT	ACCCTTTcTC	TTAGAAAGGA	1620
GGTGmyCCAG	CCGCACCTTC	CGGTACGGCT	ACCTTGTTAC	GACTTCACCC	TCCTTACCAA	1680
ACATACTTCG	GCACCGCCCT	CctTGCGGGT	TAGGCTAGTG	ACTTCGGGTA	TCTCCAATC	1740
GGATGGTGTG	ACGGGCGGTG	TGTACAAGGC	CCGGGAACAC	ATTCACCGCA	CCATGCTGAT	1800
GTGCGATTAC	TAGCGATTCC	AACTTCATGA	AGTCGAGTTT	CAGACTTCAA	TCCGGACTAC	1860
GATTGCCTTT	TTGCGGTTTG	CTCCACTTCA	CAACCTCGCA	TCGCTCTGTA	GCAACCATTG	1920
TAGCACGTGT	GTAGCCCCGG	ACATAAGGGC	CATGATGACT	TGACGTCATC	CCCACCTTCC	1980
TCCGGTTTGT	CACCGGCAGT	TCCGCCAGAG	TCCCCAACAC	CACTTGCTGG	CAACTGGCAG	2040
TAGGGGTGTC	GCTCGTTGCG	GGACTTAACC	CAACACcTCA	CGGCACGAGC	TGACGACAGC	2100
CATGCAGCAC	CTGTCAAGAG	GCGTATcGct	ACGCCACCGC	ATTTCTACGG	CGCTCCTCTT	2160
GATGTCAAAC	CCGGGTAAGG	TTCTCTCGCT	ATCATCGAAT	TAAACCACAT	GCTCCACCGC	2220

735

TTGTGCGGGC	CCCCGTCAAT	TCCTTTGAGT	TTCACCTTTG	CGAGCATACT	CCCCAGGCGG	2280
TACACTTAAT	GCGTTCGCGT	CGGCGCCGAG	ACTCATGCCC	CAACACCTAG	TGTACATCGT	2340
TTACTGTGTG	GA CTACCAGG	GTATCTAATC	CTGTTGCTC	CCCACACtTC	GCACCTCAGC	2400
GTCAATCATC	GGCCAGAAAC	CCGCTTCGCC	ACCGGTGTTC	TTCCAAATAT	CTACAGATTC	2460
CACCCCTACA	CTTGGAATTC	CGGTTTCCCC	TCCGTGATTC	TAGACCAGCA	GTACCCAGTG	2520
CAGTTCCCAA	GTTGAGCTCG	GGGATTTTAC	ACCAGGCTTA	CCAGTCCGCC	TGCATGCCCT	2580
TTACGCCCAA	TAATTCGGAA	CAACGCTCGC	CCCTTACGTG	TTACCGCGGC	TGCTGGCAGC	2640
TAATTAGCCG	GGGCTTATTC	GCACGACTAC	CGTCATCAAA	CGGGCATTCC	CTCCCGTCCT	2700
CATTCTTCGT	CGGCAAAAGA	ACTTTACAAT	CTTTCGACCT	TctCATCCAC	GCGGTGTGCG	2760
TCCGTTACAG	TTTCGCCCAT	TGCGGAATAT	TCTTAGCTGC	TGCCTCCCGT	AGGAGTCTGG	2820
GCCGTATCTC	AGTCCCAGTG	TGTCCGGTCA	CCCTCTCAGG	TCGATACCC	ATCGACGCCT	2880
TGGTAGGCCA	TTACCCCAAC	AACAAGCTAA	TGGGTGCGAG	GCTCATnTCT	GAGCGAGGCC	2940
GCAGCCCTT	TCCTCTCAAA	GACTACGTCC	AAAAGAGCGT	ATTCGGTATT	ACCCCTATT	3000
TCTAGAGGCT	ATCCCCATCT	CAAAGGCAGA	TTACCCACGC	GTTACTCACC	AGTCCGCCAC	3060
TCTAGAGAAA	ACGAAA					3076

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1091 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

CnGATGTGCG	TAAACGCCTG	GAGACGCTCA	AGAACACGCA	ACGTCAAAAG	GGCAGAACGC	60
CGCGCCGCAC	GgTCGAAAAC	TCTTTATAAC	TCATAGAGAC	ATCCTGCTCA	GCACCCGCAC	120
CGTCGGATAT	ACAGCGTATA	ATAACAAAGG	GGACGCCATT	AACTGACGCT	ACATGCGCAA	180
AGGCTGCCCC	CTCCATTTCC	ACACCATGCG	CACCAAATTC	GCGTATAATG	CGTGCACGTG	240
TTTGCGCATC	TGACACGAAA	AGATCCCCTG	AGGCGACGCG	CCCTTCGACT	AAACGAGAAA	300
CGCGAGAAGG	CGGATCCCCC	GAGCCAGAGA	GCGCACAAGC	ACCCTCGGTC	CACTCCGGAT	360
CCCGTGTGCA	GAGATCAAAG	GCTTCCCGCA	CCAAATACCG	CAATGCCGTG	TTCGCAGTCC	420
ACTCTACAGA	ATCCATGCGC	GGAATACGCC	CTTCTGGTA	ACCAAAGCG	GTAAGCTCTA	480

736

CATCATGCTG CACTGCATCG ACAGAACTA GCACATCAAA AACACACAAG CGTCATCGA	540
GAGCACCTGC AATTCTCTGTA TTGATAAGCA CACGCGCACC AAATCCGAA ATGAGTAGTT	600
GAGTGCAAAG CGCTGCATTC ACTTTCCCAA CACCGCCGCA CACATACACC ACCTGAAGCG	660
CACCCACCGA CACAACATAG AACGTGAGCC CTGCCCCGCTC TGTACCTACT CCCCCGAGAC	720
ACTCACGTAC GCGCGCAACC TCCTCTCCCA GTGCAGCAAA AACGCCGACC GTCACGCACC	780
CTCCCCGTGA AAAACACGAA AACGCGCACT CGCAACCCAG GCACGGAAAA AAGCTGTCCC	840
TTGAAGGTCA GGAAAAAGCC CCGACCACAA GGCACACCGA TAAATGAACG GAATATAGCA	900
GGGAGAGGAC TCGAACCTCC GGCTCCGGG TTATGAGCCC GACGAGCTGC CAACTGCTCC	960
ACCCTGCGGT GACGCACAGA GCGTACCACG ACTAGAGCCC GAAGTCAAGC CACAAAGCAG	1020
GACGCTCCGC CCCAGCTTGA AGCGGAGCCT TACAATCATA CATACGACCA GAGGATACGA	1080
CACGCAGTTT A	1091

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

ACGACCTCGC CTGCAAAATC GCTATCCTTT CCCCATCTTT ATAGGTGAAT AGACCCGGCC	60
AGGGAGTAAA GGCCCGAATC TTGCGCTCCA ACACAAcTGC AGGATTAcTC CAGTCCGCCA	120
aTCCCaTCTC CyTACAGAGC TTACCACAAA aTGTTCCTg CGAgTGaTCC TGtGCTGCAG	180
GGGCGAGCGT GTGCCGCTCA ACACCGACTA AAACATCATC CACAAGATCG GCAGCCACCA	240
AAGACAAACG AGAAAGAAGC GCGCCAGTAG TCTCTGTACC GTCGAGCTGA ACACGGGAtG	300
CGCAAGAATG TCCCCTGCAT CCATCTCCTC ACCAATGTAC TGGAGCGTCA CACCCGTCTC	360
GCAGTCCCCC GCTAAAATCG CCGCAGGGAC CGGTGTACTC CCTCGCCAAC GCGGCAACAA	420
CGAAGGATGA ACGTTAATAG CACCGCGCGG GAAAAGCGCA AGGAACCGAG GGCCAAAAAT	480
CTTACCGTAG GCAAAACACA CCAGCACGTC CGGACGCAAA GCCTCCACCG CGTCATAAAA	540
GCGCGATCC AAACGCCCCG GAACGAAAAG AGACGCAGAC TCAGGAAGAA CCCAGACGC	600
TTTTAAGCGA AAAAATTCCC TTGCAACCGc AGAATGGaCA AGCTTcCCCC aGCGTcCGaC	660
AGCAGCAGGA GGATTcGTcA AAACCCCCAC AACCCGaTGA GCGcACGCCA CCCGGCGCAA	720

737

AGAAGGCACG GcACACTCTG GAGTTCCCGC GAAGAAGACC CTcACCATGG GCTAACGAAT	780
CGTCCCGCGc AGCGCgnCAT ACCGACGAAG GGCATCATCC CTCCGCTTTT CGTCAATGCG	840
ATCCAAAAAA AGAATACCGT CAAGATGATC GTACTCGTGC TGGATCACTC TTGCCAGAAT	900
ACCATCTGCA TCAACGGCAC AACGTTTACC ATTCTCGTCG AGGTACTGCA CACTCACCCG	960
ACGCGGACGC AACACCCCTT CATAAATGTG AGGAATGCTC AAACAGCCTT CCTCGTAGGA	1020
AGATTGCTCT TCAGACGCGG CAGTGATCTG GGGATTGATA AAAGCGCGGA CGTGGTGCTC	1080
AACATCTACT ACAAACACGC GGACGGTACG CCCTACTGCG GCGCCGCAAG CCCACACCG	1140
CCTGCCCCAC GCATCACACG AAACATACCC GAGATGAACG CGCGCAGCTG CTCGTCCACC	1200
TCCGAAACCG GCTCGGAAAC CGTTGTCAGG CACGGCTCAC CTAAAACTT AAGCTCCACC	1260
GCCTCTTCCC GCTCTTACCC AAGAGAAACT CATACCCGCC TAGTACAGCC TTGAGTCGCT	1320
GACCTTGCGC CCCTTCTTCA TCAGtTGCGC CGCAACGCCT TCTTCTTGCG ATTcAGAAGC	1380
GTGGAAGGCT TCTCATAAAA TTCTTTTTTC TTCCACTCGC GAATAATACC TTCCTTCTCC	1440
ACCTGGCGCT TGAAGCGCTT AATTGCCTTC TCTAAATTCT CAGAATCATC CACCGTTATG	1500
TGAGCCACCG ACCCTCCCCT GAAAAAACA CAGCCTACCA GGGGTAGnTA GCGCAAAAGA	1560
CGTCCCCTGT CAATCGTTTC TTCCGAAAGC ACTCCTGCCT CCCCTGCACG CACACCTtAC	1620
GTGTCTTGCT TATGCAACCG CTGACCTTCC TAACGTGCGT CTACTTGTGG TACAGTGCAG	1680
CGCTGTGCGT AGAAGTCAAA ATTGTCCGCA CCGACCTCCT TTCGAGTGCA TCCGTGGGAC	1740
GCTAGCCTAC CCTGCACAGG CGTCCACCCC TCCTGGGAAG AGGCCCCGACC TGCCGTGAAC	1800
ATTACCGGAA GCCGCGTTGC GGTCTTTATC TCCTCCCTGA CCGCTGTGCT TCTGCTGCTC	1860
ACCGTTCAGT GCGCGCGGTA TATGCTCATG CGTGGCAACG AGACAAAGGA ACTGAACACA	1920
CTCACTGAAC GCGGCGCGAT CTTGGACCGA AATGGCCGGT TTCTTGCCGT TGGAAACCACC	1980
GTCTACAACC TCAGTGTTAA CAAAAATCTT GTCTCAGACC CACGCACTGC AGCCACGTG	2040
TTAGCACAGG TCCTTGACCT TTCAGAACAA GATATTGAAG AAAAATTCCG CACCGCGCGC	2100
GCTCACTTCT TTTACCTCAA GAAAAAATG AGTGAAAcGG AAAAGAACCT TGTGCTCAC	2160
GCTCTTAAGG AGCACTCCCT GAAAgGATTT GCCTAGAGG CAGTGCGCAA CCGCATCTAT	2220
CCAGAAAGTA GCCTAGCGTC CACGGTCATC GGATACGTAG GTGATGACGG AAGGGGACTG	2280
AGCGGTATCG AGTACAcTG CAGGATGTTT TTTCTCCTGC CCCGTACCAC ACCGGGTATA	2340
CGGGCAAGGG GCATACTGTC ACCCTCTCGA TCGACCGAAC CATCCAGTAC ATGATGGAAA	2400
AAATCGCAGA TACTACGCTC CGGCGTACCC AGGCAGAAG ACTCATGTTC CTTGCGGTGG	2460

AGGCAAAGAC AGGTCAGATT CTATCCTACG TCAGCAAGCC GTCTGCTAAC CTTTCACACT	2520
TTTCCCAAAG TACCCCTGCC GAACGCTTCG ATCGCCCCGC CCTTTTCATC TATGAGCCTG	2580
GCTCTGTGTT CAAAATTTTT TCCATCGCTG CACTGTTAGA ACTCGGGGTA ACTTACACCC	2640
ACGACACGCT CCACTGCGAC GGTTCCCTCT CCTTTACCTC CCCC'TTTTA AAACCAGGTC	2700
AAAAAGGCCA TCTCATCCGC TGcCTGCGCC CACACGGcAC CATCAGCGcT GaAGATATCA	2760
TCCGGcTTTC GTGTAATGaC GGcATGGcAC AAATTGcTGa ACGTGCCGAC AACCACAGCT	2820
TTGAGCAACT ATTGCGCGCT TTTGGATTTG GCGCGAAAAC AGAAATTGAG TTGCCGGGGG	2880
AAACCGTCGG TCTCTTCTCT CCCTCAGAAC GCTGGTCCCA CCGCAGCAAG CACACCATCG	2940
CAATCGGCCA GGAAATTGGC GTCTCTGCCT TGCAGtTGTG GCTGCCGcTA CCGCGCTCGC	3000
CAACGAGGGC GTACCGCTCG GCCTCTCCCT CCTCCATGAG GTCACTACCG CCGAAGtACC	3060
GTGGTGTACC GGCACAAAAA GAAACCCAAA ACACGCGTTA TCTCCGCAGT AAATGCGCAA	3120
AAGGTGTTGC GATACATGCG CACCGCCGCA GAACTTGGA CCGGGAAAAA GGCGCTCGTA	3180
GACGGGGTGC CGATCGCAGT CAAAACAGGC ACTGCGCAAA TGGCGCACAG AAATGGTCGT	3240
GGGTACAGCG ACACCGACTA CCTTGCAAGT TGCATCGGCC TTTTCCCCGC GCACGATCCA	3300
GAAATTATCT TATACATTGC CATCATCCnt CCTATCGGAC AAGCCTATGG AGAGCTCATT	3360
GCAGCGCTG TCATCTCTCA AGCGGCAAAC GAGATTATCG ACTACCGCGG TATGGTCCGT	3420
GCCAACGCCC CGTTAATCCA ACATAGCGGT CTCATCCATA CGTCAGAACG GACACCTCCA	3480
CGGTTAGGAA CCCATATGCC AGACCTCACC GGTCAACCTA AACGTTTACT CCTGGATATT	3540
GCAAAACGCA CCGACGTGCA CCTTGTCcTT ACAGGAGAAG GTTATGTGTA CGAGCAGCAT	3600
CCGCCTGCGG GCACACCTCT GACAAAAGGA ATGACCATTG AACTCAAACCT CAAATAAAAA	3660
GCGAGATCCC GCGCGTTTCC CGGCCGGTGT TGCGCAAGGC TGCAGTACCA CACGCGCAGG	3720
GGATCTGAAA CACAGAAGAA AGCATCCCTT TGAGAAGTTT TTTGCGCAAA ACAGCGCTCT	3780
TTTTGCCCAG CGGTTTCCAG ATCTTGACAG TGCCTGACA CTTCCAAACG AGCAGCTCCT	3840
GCAACGCATC CCTCCTGATT ACCTCCTTGC AGCGGCCCAT GACGGAGACG CAACGCTTGC	3900
AGTACGGGGC ACCTATCTCC ACTCAAAATA TCGGCCGCGG CAAGAGGCTG CACGTCTTAT	3960
CAGCCAGGAT TTTT'TTACGC ACGCGATTGC AAAAGGCGGC TATGTAGGTG CAGGTTTAGG	4020
TCTTGCTAT GTAGCAGAAC TGTACGCGCA nAGCCACCCT ACGCACACGG TAGTGCTTAT	4080
CGAGCCAGAT ATATTCGTGT TCCTGCTTTT TTTAGCCATA GAcTyTCAC TCCCCTCcTC	4140
CGACACGAAC GTCTAAAAaT ACTGCCTGCa CAGACGGTAC CGGATGTGTT GCAGTTCyTG	4200

CGCGCCACGG	GGGATGTGTC	TCTCCCCCTG	TTCCATTCT	TACCAGCCCA	GGAGCTAAAC	4260
ACCGCGTGGT	TTCACGATTT	TACCCAGGCG	CACCGGCACG	CAACTGCACA	GGCAGAAACG	4320
AATAAGCAAA	CGCTGCAACG	GTTCCGGTCCG	CTTTGGATAC	GCAACACTAT	AAAAAATGCC	4380
GCACAGCTGT	GTGTGCGCAC	GCCCCGTAAAT	GCGtGCGCAA	tGCGCGGCAG	GGAGTACTGC	4440
ACTCATCATT	GCAGGTGGCC	CTGGGGTGGG	TGCGAGTATA	TCGTTCCTTC	CGTACCTAAA	4500
AAAAAAACAC	TGATTATTGC	GGTTGAaTAc	CGCGTTnTGg	CGTGTGCaGC	GCGCGCGTCA	4560
CCCCGGACGT	TGTGCTTCTG	TTTGAtCCAC	AATACTGGAA	CTATTTGCAC	GTAGCACGTG	4620
CGGTGGCGCC	CCATGCACTG	CTTATCACTG	ACATTTCTGT	GTTCCCTGCa	GTGTTTCGAC	4680
TCCCGTGGGA	GTACATTGTC	CTTGCaGGTT	CGGCATGCCC	TTTCGCTACA	TCCCTTGCGC	4740
ACCATGATGC	CTCCTGCTCT	CCTTCCCACG	CTCTTCCTCT	CCCTTTTGTC	GCGCCCGATC	4800
TTCTCGCCTC	AGGTGGGTG	GTTGCTACAA	GTGCGTGGGA	ATGTGCCCCG	TACTTGGGAG	4860
CGACAACCAT	AGTGTAACATA	GGGTGGGATC	TGGCATTTC	TGGAGCGCGC	ACGCACTTTC	4920
GCGGAGCGCT	GTTTGAGGAG	CGGGCACACC	TGCAATCGGG	TCGAGTGGCT	CCTGCCGAAA	4980
CTACCTCCTT	CTGTGCACTG	CACTCCCTGC	CCCTATATCC	TGTCCCGGCT	GCATCTGACC	5040
CCCATCCAGG	AAAGAACTCC	CCTGCTTnCC	CTACCGGGGA	GAACAAAGAG	CAAACGGTGC	5100
TAACCGaCGC	GCGTTTTTCA	CTGTACGCCG	TGTGGCTCGA	AGCACACCTT	GCGCGTTATA	5160
CGCACATTAA	AACGTATGCG	CTTGAGCCTG	CAGGAAGGAG	AGTTGCAGGC	ATCACGCCCT	5220
TGCGCTTTTC	CCAGCTTGTC	ACGTTACTCA	ACCGGTCGTC	AGCTGTGCCG	CACTGCCGGA	5280
CCATGTATAG	CCGCCGACGC	AGGCTATACT	CCCGGTATAG	AAACAGCAGC	GTGCAGGTCA	5340
ATTGCACCGA	TGCGGTGCGC	TGGAGGCGCA	CGATGAAGAG	TACACCTGTG	CACTGTCTCG	5400
GTCATTTTAC	GAAGAAAAAG	AAATCCGCAG	AAGGTGCACG	GAACCTATGG	CGTGCTCTCA	5460
GACGTGCGGA	TACGCGGTGC	GCTTCTCCCC	ATAACCTCGA	GCACGCACCT	GAGAGAACTC	5520
GTTCTTCCT	CAACGCGATG	CCACTGACAC	CCACAACGTA	TGAAAACAAA	ACACATGCAT	5580
TGTACACAGC	GCTGTGCACG	CTCCTCCCGA	CCGAGCCTAC	CTACCGCGCA	CGGGCACACG	5640
CACACCTCTT	TGAACCTCTC	ACCCGAACAC	TCAAGTTTTG	CGCCGCCTAT	ACCGAGGAGG	5700
AGGGGGAGTG	GCGCGAGGCC	tGACATCCGG	GGCCACTCAA	AGACGTGTGT	GGGGCgCaGG	5760
GGCaGGGCCC	GTGCGTTCCC	CCTTTCAGGG	AAAGAGCCAA	GCGCGTGCGT	CCTGCATCAG	5820
TTTTAGAAAC	ACCAAGACGT	CTACGTTTTG	CTTCTTGCGA	TTCTCGTAGT	CCGCCAGCG	5880
GCGGGGCGTG	TAGTGTGCAT	GGACGTCTGC	CCTCACCTGT	GCTGCATGCG	CACAGCCGCG	5940

740

CGCAATCAGC	TGGGCGTCGT	GCGCGGGGGC	GCGCCTAAGT	TTTTCAGGAA	GCACTTCTGA	6000
CAGAAGGTAT	GCACTGAGTA	CGCGAATCAA	CGGtGACGCT	TGGTGTGCAC	CAACGTGAGA	6060
AGATGCGCGT	GTGCCTGTTC	AAAGTCGCCG	CACAGGTGAC	ACGCGAATGC	GAGGTAAAAG	6120
CGAGTCCACG	GCTGGACGGG	CGCCTGTGTG	GCGGCAACGC	GCGTCATAAA	GGTACGCAGC	6180
TCCGAGTACT	TTCCCGCAAG	GAGCTTGCCA	ACGGCAAAGG	TGAGCGCGCA	CTTCATGATA	6240
TACCGAGGGC	TGCGCGTGCA	CAAAATGTTC	TAGTCGCTCA	AGTGCTTCAA	AGTCACTTAA	6300
AAGGATCAGT	GACTCTGAAA	GGAGAGACAC	CCTCCGCAAG	GCAACCCTAT	TGCGGGTGAA	6360
CACTTCCTCC	TCCAAAAGAG	CTGCCAATGC	CGACCAATCT	TCCGCATCCA	GGTATCGAAG	6420
CAGTCTCCTG	TTTTTAACAT	AGAGTGATT	TATCAGCAA	AAGAGTAGGA	GAAAAATGAG	6480
AAAAAAAAATC	CCATACGCGC	GCACAGATTG	CCAGCCTGTA	CCCCGGACAG	GAGTGAGAAA	6540
CAGAACATAT	CCGGTACCCA	TACACAGCAG	CAGGAGTGCA	CCGTAAAAa	GCACTACTAA	6600
TGCTTTGATC	TTCATGGGAA	aTCTCCTATA	CTGCCTcCCC	GCCTGTGCGG	GGCGCCATTC	6660
TACTATGGGG	GCGAGCGAAA	CGTGAATACG	TATGCAATTG	TAGATATACC	CGAGGAAACC	6720
CACTTCAGCG	ATGACGTGTA	TCTTGATGAC	ACTTTTTTTAG	TGCTGACCCC	CGCAGgTCTC	6780
TTTGACGAAG	CGCTAAAGAG	TCGACTGCAG	GAGTGGGACT	TCACCACGGT	GCACACCGGc	6840
GGACAACCTGC	TTTCTTCTGA	GACTACACTG	GAGTGTCTCT	TGCCTGCATC	CGGCGATCCA	6900
AACGCGAAGG	GTGCTCCCGG	ATCCGAGGCC	TTGCGTGAC	AACGAAGCCG	TTTTACGCA	6960
CTGAAGAAAC	AGTACAACGA	GTTTCAAATG	TTGCTTGAGC	ACGTTTTTGA	TCAGTATCGT	7020
GCAAAGCAGa	GCCTGAACAC	GCGCGCGGTC	ATTGACCGTG	CGAAGATGCT	TTGCGAATTG	7080
GTAAAAAAGC	ATCGGcAAAC	GCTACTGCGC	GTCCTTCCCA	CCATTCCCTA	CCGGGAGCAC	7140
TACGCGCTTG	AGACACATGC	ACTCCGTTCG	ACGTTGTATG	CTGTTGTCAT	TGGGTTACAG	7200
CTAAAAATGC	AACCGTTCAA	GATCATtGAG	CTCGCAACAT	CTTGCCCTGCT	TCACGAAATt	7260
GGCATGGCGC	GCGTTATCCC	GAAGCGTACA	CCACGGAGGG	GGAGTTAGAT	CCAAAAACGC	7320
AGAAGGCGAT	CTTTGCGCAC	CCTATTATCT	CCTACCATAT	CCTGCGTGAC	CACTCGCTCC	7380
CTCTGCCGGT	GTGTGTGGG	GCACTTGAGC	ATCGCGAGCG	CGAAAATGGG	CTCGGCTACC	7440
CGCGCAGGCT	CGTGGGAGAA	AAGATTTCCC	TCTATGGCAA	gAtAAtCGCA	GTCgCtTGTT	7500
CtTACgAGGC	AGCAACCGCT	CCGCGCTCAT	ACAAGGAAAT	GAAAAACGCC	GCTGAGGGCA	7560
TCGTCGACCT	TGTGCGTAAC	GCGAACACCC	AGTACGATGC	AGTCATTTTCG	CGCGCGCTTC	7620
TCTTTGCCCT	GTCGTTTTAT	CCTATCGGGA	CCCATGTGCA	CTTATCAAAC	GGGAAAATCG	7680

CGCAGtGGTG	GACGTTAACC	CCGACGACCC	ACGCTTCCCC	ATCGTGCAGG	TACACGGAGA	7740
AaTTCACCGC	AACGGCAAGC	CCATCATTCA	CAGCAGGAGC	GCAGACGAAA	TTTTTATCAC	7800
GCGGGCCCTG	AGCGTAAAGG	AACAGCGTCT	TATCCTTCAG	GAAGGTGGCG	ACTGACCCTG	7860
CGCAGGGcAG	ATGCCCCCTC	CTGCTGCTGG	CTTAGACGCT	TTTTTAGCCC	CTCTAGGTCG	7920
TGTTGCGAGC	GAATAACTTC	CTCAAACCTG	TCGCGCTCGA	TGGTTTCTCG	CTCCAAAAGg	7980
CGCGtTGCGA	TGTACTCAAG	GAGCTCTTTT	TTCTCCGTCA	AGAGTGCTAC	CACCGCGCGG	8040
TAGgTcCAGC	TAGAACGCGC	GCCACTTCCT	CATCAACGTA	CTGCTGTGTG	CACTCCGAAT	8100
ACTCGCGCGC	TAAGTGCAGC	TCCGCGAGAT	ACCCGGTTCC	GCGGCGAGTA	AGTGCAAGgT	8160
TTGAAACTTT	TCGCTCATCC	CATAATCTGT	AATCATCTTG	CGGACAATGT	CTGTTGCGCG	8220
AGAAATATCG	TTCCCTGCAC	CAGTTGAAAC	TTCCCCAAAG	GCTACAAATT	cCGcTGCGnk	8280
TCCTGAAAGC	AGCACATCTA	CTCTGCCAA	CAACTGCTGC	TCCGTAACAA	TATGCCGATC	8340
GTCTTCAGGA	ATGTGAAAAG	TATATCCAAG	CGCAGAGGTG	CCCCGGGGAA	TAATTGTAAT	8400
TTTGTGCACC	TTGTCTGCAC	CCTTCGTGAA	GGTACCTGCA	AGGcATGTCC	TGTCTCGTGA	8460
TACGCAATAA	TCCGCGCTC	TTCTTCTCGA	ATTACCCGAC	TTTTTTTCTG	CAATCCTATC	8520
ATTGTCTTTT	CGACCGCTTC	GTCCAAATCC	GTTTCAATCA	CCTGCGCACG	CCCAGACCGT	8580
ACCGCGAGCA	ACGTGCCTC	GTTCAACACG	TTTGCCAAAT	CAGCACCTGA	ATACCCACCG	8640
GTGATGCGCG	CCACTGCCTT	CAAATCCACT	TCTGGCGCTA	ACTTCACGTT	CTGCGCATGA	8700
ATACGCAGAA	TTGCCTCTCT	TCCCTTAAGA	TCGGGCCGAT	CTACGCAAAC	CTGTCGGTCA	8760
AAACGACCGG	GGCGTAGGAG	CGCAGGATCT	AACACATCGG	GGCGATTGGT	AGCAGCAAGC	8820
AAAATGAGAC	CGGTGGTGTT	ATCAAACCCA	TCCATTCTTA	CCAGAAGCTG	GTTAAGCGTT	8880
TGTTCCCGCT	CATCGTTGGA	ATGGATAGCG	TTCAAGCGGC	TTTTTCCAAT	TGCGTCAAGC	8940
TCATCGATAA	AAATAATCCC	TGGCGCCTTC	TCCCGCGCTT	GTTTGAATAA	ATCGCGCACA	9000
GCGGAGGcGC	CAATCCCCAC	AAACATTTTC	ATGAAGTCTG	AGCCACTGAT	GCGAAAAAAG	9060
GGCACTGACG	CCTCACCTGC	CACTGCGCGT	GCAAGCAACG	TCTTACCCGT	CCCTGGGGGA	9120
CCGACCAACA	GCACCCCGCG	GGGAATTTTC	CCCCGATTTT	CAGTATACTT	TTTAGGGAAC	9180
TTGAGAAAAT	CAACTACTTC	CATCAGCTCT	TCTTTTGCCT	CATCCACCCC	TGCAACGTCT	9240
GCAAAGCGTG	TGGTGACCTT	TCCTTCTTCC	ACCGCCgCAG	AGCGCGCGTG	TCCGGCTGAG	9300
AAAATACTGC	TCCCAGCCCC	GCTTACATTT	GAGGCCATCC	GCTTAAAGAA	AAAGCGCCAG	9360
ACAAAAAAGA	GGATGAGCAG	CGGAAAGAGA	TATTGAAATG	TCTCTATGAG	GTAATTGCgC	9420

TCGCGCGGCT TAATACTGTA GACCACCTGC CGCTCATCGA GCATGCTCAA AAAGGAATCG	9480
GAGAGGACAC CGATGGCATG ATAGGTAGGA GCCTCCCGCT CAGAGAGCAA CGAGAAACCC	9540
CGCGCAGAAG GCGCAGGGCG CGCGGAAGTG TACCCGACAA AGTAAGGGGA ACCGACAACA	9600
ACCTTTACGA TTTCCCCACT TGCAATGCGA TCTTTAAATT CCGAGAACGG GATGATGCGC	9660
AAAGCACGGG AAAACAAAA GTGGTTTGCA AGAGCAAGCA GCGCACAAAG AGCAAGGAGC	9720
ACGAGCGAGA GCACCTTACG CGAATTTCTG CGCGGAGGTC TTTCGCGTGA CGACGAAGGG	9780
CCTTTTTGAG GGGGGGGGA GAACTTAAAA AAGCCGAATG GATCTGAAGA ATCATCTGAC	9840
TGTTTGTAGC GCGTATTCAT CTCAGTTAAG GCTCCCTTTT GCAGTGCGCG CGGGCACGCC	9900
GGCCCATGAT ACACGAAAAG AAGGTGAAAC GTCGACAGAC TGTGTGAGAG CCGTACGGcg	9960
CAgCTTAGCG ACGTCCGCTG GGGCGGTATG CACGGTGCTG CAAAAAACA CACGCGCGCG	10020
GCTATTGCTT ACCCTCATGC GCGCGTTCAC CGAAACTTCA CCTAATGACA CCTACCTATC	10080
ACCCGTACCC GGGCGACAAT CGCCCTTTTC TATACGCCGC GCTTCAGCGA CGTGAGCACC	10140
TGTCCCTTAT CCGGTACCGC GCAGAGCACG CGCAGGACCT GGCACCCTTG AGAGCGTTCT	10200
TGGCGCGCAT CGAGGCGCAC GCAACCGTCA TTGGTGACG CACGCGTGGG GACACCCTTT	10260
TTATCCTTGC CGCATCGATG CCGTCTGATG CACTGCGCGA CGAAAAACAC GCATATGTGC	10320
GCACAATCTC CTGGGAACAG GCTCCTCAGA TACTTGAGAC GTTGGAGCGT CCGCCGCTCC	10380
CTCCTTATG CCCGCCCGTT CCTACTTCCT GTTCTTCTTC GCGTCTTATT CCCGACGTGC	10440
CGCACAACAC CAGGTCACAC GCGCAGGAGA GTTCCTACAC CTCTCGGCAT GCGCTTTTGA	10500
CGCTGCTCAT TGAGTGGCGC GCGCTCATGG TAGAGATGGA CTATTCAGTG AGAGCGCACA	10560
GGGTGCAGCG TAGTTCTGCT CCGTTGCATG AAAGACACGG CACTCTTCCC TCTGACGTAC	10620
TGCTCTTCCA AACACAGGGG GAGGTCTGCG CTCTCTGTGC CTTTCAGTTG CAGCACGTGC	10680
GCGCAGTAGG CGGGCAGCGT CATCTTATCA TTCATGAAGC GGCAGGAGGC GGAACATTG	10740
CATGCGAACG CATTTTCTCT CTCAAGGAGA TTGATTTTGC CACTGCAAAA TTTACTGAGC	10800
GSTATCCGTCG CGGGCTGTAC CAGGTTGCTG TGCATACGGC ACACGCAGAC TTTACGGTCA	10860
ACCTCATCGT TCCCTCACTC AGAGAGCAGG GCGGCGCCTA CTCCCTTGCA GAGTCTTCTG	10920
CCTTTCACAG GAGGGTAAGC GCGTAAACTG CAGATTACGC AAAACTAGCG GTTCTAGCCC	10980
GGAGGGtGAA GCGCGCCGTG TGCATCGGCA cGACCCCGCC AGAGAAGGCG GGCGCCCGTC	11040
TTCCCCGCGG TgGCGsGCTG CGCCCTGCTA CCCCCTCTGC TGTGGAGCGG GGCCTTGTCT	11100
TTTTCTTGAG GGCTTGTTAC gcTGCGCGCC AGTCCCCGAG GAAGAAGGAA TTGCTATGAG	11160

TAGAGGTATT	TCTACCTTCA	GGAATATCGG	CATCAGCGCG	CACATAGATT	CTGGAAAGAC	11220
AACCCTTTCT	GAGCGCATTC	TCTTTTACTG	TGATCGTATT	CACGCCATCC	ATGAGGTGCG	11280
TGGTAAAGAC	GGTGTGGCG	CCACCATGGA	CAACATGGAG	CTTGAGCGGG	aGcGCGGTAT	11340
TACCATCCAG	TCTGCCTCCA	CCCAGGTCCA	GTGGAAGGGA	CACACTATAA	ACGTCATTGA	11400
CACTCCCGGG	CACGTTGACT	TCACCATCGA	GGTGGAGCGC	TCCTTGCGCG	TTTTAGACGG	11460
TGCCGTCTC	GTA CTCTGTT	CGGTTGCAGG	CGTCCAGTCC	CAGTCCATCA	CTGTGACCG	11520
GCaGcTCCGC	CGCTATCaCG	TGCCCCGTAT	CTCATTATATC	AATAAGTGTG	ATCGTACGGG	11580
TGCCAACCCt	TTCAAGGTCT	GCGCTCAGct	GCGCGAAAAG	CTCTCCCTTA	ACGCGCATCT	11640
TATGCAGTTA	CCCATTGGGC	TTGAAGACCG	TCTAGAGGGT	GTCATCGATT	TAATTTGCGT	11700
CAAAGCCCTT	TATTTTCGAGG	GAGAAAGTGG	CGCGCACGTG	CGTGAGGCGC	CCATTCCCGA	11760
ACAGTATCAG	GCAGATGTGA	AAAAGTACCG	GGATGAACTC	ATCGATGCGG	CGTCTTTGTT	11820
TTCTGACGAG	CTTGCTGAGG	CCTACCTTGA	AGGAACTGAG	ACCGATCAAT	TGATTGAGC	11880
GGCAGTACGT	GCGGGCACCA	TTGCAGAAAA	GTTTGTCCCG	GTTTTTTGCG	GTTCTGCGTA	11940
CAAAAATAAA	GGTATTTCAGC	CACTTTTTGA	CGCTATCACA	TACTACCTGC	CAGATCCTAC	12000
CGAGGTAACT	AATACCGCGC	TCGATCTGGA	TAGAGCCGAG	GAGCCAGTTA	CCCTCTCCAC	12060
CGATGCAGAC	GCACCGGTAG	TTGCGCTCGG	GTTTAAACTA	GAGGATGGCA	AATACGGCCA	12120
ACTCACCTAT	GTGCGTGTAT	ATCAGGGGAC	TATCAAAAAA	GGGGCTGAGC	TTTTTAACGT	12180
CCGCGCGCGC	AAGAAATTCA	AGGTGGGCCG	TTTGGTACGG	ATGAACTCTA	ACCAGATGGA	12240
AGACATCAGT	GAGGGAACCC	CCGGAGACAT	TGTGGCGCTT	TTCGGCGTGG	ACTGCGCGTC	12300
GGGAGACACC	TTTTGCAGTG	GAGATCTGAA	TTACGCAATG	ACTTCGATGT	TTGTTCCAGA	12360
GCCGGTCATC	TCGCTTTCCA	TCACTCCTAA	GGACAAGCGG	TCCGCTGACC	AAGTTTCCAA	12420
GGCGCTGAAC	CGGTTACCA	AGGAAGATCC	TACCTTCCGC	AGCTTCGTAG	ATCCTGAGTC	12480
TAACCAAAC	ATCATCCAGG	GGATGGGGGA	GTTGCACCTG	GATGTGTACA	TTGAGCGCAT	12540
GCGACGCGAG	TATAAGTGTG	AGGTGGAGAC	GGGCATGCCG	CAGtGGCGTA	TCGGGAGGCA	12600
ATTAGTGCGC	GCGCGGATTT	TAAC TACACC	CACAAAAAGC	AAACCGGCGG	TTCCGGGCAG	12660
TTCGGGCGTG	TGGCCGGCTT	TATAGAGCCC	ATCGCCGGGC	AGGACTATGA	GTTTGTAGAT	12720
CAAATCAAGG	GAGGAGTAAT	CCCAAATGAG	TTTATCCCTT	CGTGTGACAA	AGGCTTTTCGC	12780
ACAGCGGTaA	AGAAAGGAAC	TCTTATTGGT	TTTCCGATTG	TGGGGGTGCG	CGTTACCATT	12840
AACGATGGGC	AGTCTCACCC	GGTTGACTCC	TCAGACATGG	CGTTCCAGGC	GGCAGCGATT	12900

GGTGCCTTTC GTGAAGCGTA CAATGGGGCA AAGCCAGTAG TCTTAGAGCC AATCATGCGA	12960
GTGTCCGTGG AAGGGCCCCA GGAGTTCCAA GGCAGTGTCT TTGGGTTAAT TAACCAGCGG	13020
CGGGGAGTGG TTGTATCGTC AGCGGACGAT GAACAATTTT CCCGCGTGA CGCGgAGGTC	13080
CCGCTGAGCG AGATGTTTCGG GTTCTCCACC GTGCTACGTT CTTCACACA AGGTAAGGCT	13140
GAGTATTCTA TGGAGTTTGC TAAATACGGC AAGGCACCGC AAGGTGTGac GGA CTGCTC	13200
ATAAAGGAAT ACCAAGAGAA ACGAAAAGCA GAACAAAGGT AAGCGTAACG TGCTAGGCGG	13260
CGCGTCCTTC TCGACGCGGT GGCGAAGTCT TGAATAAGGG GGCTTTCTGG TGTacCCTCC	13320
CGGGCCGAAC GGTACTCTCC TCACATGAGC CGAGGAGGTA TCACGTGGGA GGTTAACATC	13380
ATGAATGCTC ATACGCTTGT GTACTCCGGC GTAGCACTTG CCTGCGCGGC TATGCTCGGC	13440
TCCTGTGCCT CGGGCGCCAA GGAGGAAGCT GAAAAGAAGG ctGCAGAGCA GCGTGCCTT	13500
CTGGTCGAGA GTGCGCATGC TGACCGTAGG CTTATGGAGG CGCGTATCGG CGCGCAAGAG	13560
TCTGGCGCAG ACACCCAGCA CCCCgAACTT TTCTCCAGA TTCAGGACGT TGAGCGCCAG	13620
TCTACCGACG CCAAGATTGA AGGGGACCTC AAGAAAGCTG CCGGTGTCGC CTCAGAAGCT	13680
GCGGATAAGT ACGAGATTCT CAGGAACCGA GTTGAAGTTG CTGACCTACA ATCTAAGATC	13740
CAGACTCACC AGctTGCGCA GTACGACGGG GACAGCGCGA ACGCTGCGGA AGAATCGTGG	13800
AAGAAGGCAC TTGAATTATA CGAGACCGAT AGCGCGCAGT GTCTGCAATC CACCGTCGAA	13860
GCGCTCGAGT CGTATCGGAA AGTCGCGCAT GAGGGATTCTG GCCGCTTACT ACCCGATATG	13920
AAGGCACGTG CGGGTGCTGC AAAGACGGAC GTTGGCGGTC TTAAGGTAGC CGTCGAGTTG	13980
CGTCCACAGC TGAAGAAGC TGACAGCCAA TACCAAGAAG CACGTGAAGC TGAAGAGGTA	14040
AATGCACGTG CCAAAGCTTT TAGCGGGTAC CACCGTGCCC TCGAGATCTA CACAGAAGCTG	14100
GGGAAGGTTG TACGCCTGAA GAAGACCGAG GCGGAAAAGG CGCTGCaGTC TGCAAAAACA	14160
AAGCAAAAGG CGTCCTCTGA CCTTGCGCGG AGTGCGGATA AGAGTGCCCC aCTTCctGAA	14220
AACGCTCAGG GTTCTCTCAA GGAGCCGATT GAGGTAGAGC CGCTTCCAAA CGACAGGCTT	14280
AACACAACGC AGGCAGATGA GTCTGCGCCG ATCCCCATAT CTGACACCTC TTCACCTTCT	14340
CGCGTGCACT CTCGGGGTGT TGAAGACGGA GGACGTCTC CAAAATCCTC TATGAACGAA	14400
GAAGGAGCCT CTCGATGAAG ACACGTAATT TCTCGCTCGT ATCCGCGTTG TACGTACTGC	14460
TGGGTGTTCC TCTGTTTGTG TCTGCCGCTT CCTACGACGA CAATGAATTT TCTCGCAAGA	14520
GTCTGCGTA CTCGAGCTT GCAGAGAAGA CATACGATGC GGGAGAGTAT GACGTCTCTG	14580
CAGAGTACGC CCGGCTCGCT GAGGATTTTG CGCAAAAATC CTCGGTCTAC ATCAAGGAAA	14640

745

CTATGGCGCG CACCACTGCC GAGGACGCTA TGAACgTGC GCGCACCCGC CACGCGTGGG	14700
CGAAAAATGA GCGCATCGAT CGCGCCTATC CGACCGAGTA TTTGCTCGCT AGCGAGGCTA	14760
TCAAGACCGG AGGcTCGCTT TTGACAGCAA GCAGTACGAC GTAGCGCTCA CGTGGGCGCG	14820
TAAGGCGTTG GACGCACTCA AAAACGTAAA GCCTGAAAGT CAGTTGCTTG CAAAGGCCGC	14880
GAAGGAGGag GCTGCGCGCA AGGCCGCCGA GGCACGAAAA CTCGAAGAAC AAAGAATTGC	14940
AGCCCAGAAA GCGCAGGAAG AACGTAAGCG TGC GGAGGAG GAAGCTGCGC GCAAGGCCGC	15000
CGAGGCACGA AAATCTGAAG AACAAAGAAT TGCAGCCCAG AAAGCGCAGG AAGAACGTAA	15060
GCGTGCGGAG GAGGAAGCTG CGCGCAAGGC CGCCGAGGAA GCAGCGCGAA AaGGCGGAGG	15120
AACTCGAGAA GGGTCGTGTG CTACCTGCGC AATACAAGGT GACTACGTGG TCCATTGACC	15180
GGGAATGTTT CTGGAATATT GCCAAAAACC CCGCCGTTTA TGGCAACCCC TTCCTCTGGA	15240
AGAAGTTGTA TGAGGCGAAC AAGGACAAAA TTCCTCAGTC CAAAAACCCC AATTGGGTAG	15300
AGCCTGAGAC AGTCCTGGTC ATCCCCAGTC TCAAGGGAGA GGAGCGCGAG GGTCTGTATG	15360
AGCCCAACGT GAAATACCGT CCTCTGCCGT AACGGATAGA CAAGAGCGTA TACGCTTTTT	15420
CCCCTTTTCC ACAAGGGTGC AAGGGGCGTG GTTGGGAGCC CATAGAGAAA GaGCTyCCCA	15480
GAGCGCTGGA ACGCTACGGT GTCCaGCGCT CTTTGTGTGT TTTGTCTCT ACAAGAAAGT	15540
TCCACTTTTT GCTACACTTC CCTTCTATGG ACGTGTCTT TGAAGAGCTT GGTTTGAATG	15600
AACAATgCTT GCAGCGGTGC GACTCAAGGG GTTTCGGTGC CCAACTCCCA TCCAGGCTGC	15660
TGCCATTCCC CACTGTTGG CAGGGGATGC GAATATCATC GCAAAGCCC GAACCGGGAC	15720
TGAAAAACG GyCCCTTCGG CCTCCCCCTT ATCCAAGAAC TGGGAAGCCC GTGCGAACAC	15780
CCAGGGGCCT TAGTGCTTGT TCCTACAAGG GAGCTCGTGC GCAGGTCGCA AGCGAACTGA	15840
GCTCCCTGAG GATACAAAA ATACCTCGGA TTCACACCGT GTACGGTGGG GTCTCCATCG	15900
CGGAGCAGCT GCGTAATCTC GAACAGGGTG GAGAGATAAT AGTAGGAACG ACCGGGCGCG	15960
TCATCGATCA TATTGAGCGC GGTCTCTCG AGCTGTCTTA TCTGCGCTAC TTCATATTAG	16020
ACGAAGCGGA TGAGATGCTA AACATGGGTT TCGTTGAGGA TATAGAGTCT ATCTTCTCTC	16080
ATGCAAATAA AGACGCACGC GTCCTTATGT TTTCTGCCAC TATGCCCAGG CAGATCCTTT	16140
CTATTGCCTC TACCTTCATG GGAAGCTACG AGGTTGTTGA AGAAGTCACT CCAGAAGAGG	16200
CGCGCCCGCT CATTGAACAA TTTATGTGGG TTGTAAGGGA CGCTGACAAA ATCGAgGCGC	16260
TTGTGCGCCT TATTGATGTG AGCGACAAC TTTACGGTCT GGTGTTCTGT CAAACCAAGG	16320
CGGACGCCGA cACTGTTGCG AAATCTCTAG ACGAACGCCA TTACCATGTT GCTGCACTTC	16380

ACGGAGATAT	TCCGCAAAGC	CAGCGAGAAA	AAATTCCTCGA	GCGCTTTCGT	ACAAAACGAG	16440
CGCGTATCCT	CGTCGCCACT	GATGTTGCCG	CTCGCGGCAT	TGACATCGAA	GGAATTACGC	16500
ACGTGGTGAA	CTACTCCATT	CCTCATGATA	GCGCTACTTA	CACGCACCGc	GTcGGcAGAA	16560
CTGGACGCGC	AGGATCACAG	GGTATCGCTA	TCAGTTTGT	ACGCCCACAC	GAGACACGAC	16620
GGATGGAGTA	TCTGAGTAAA	CACCTGTAATG	GCGAATTGAA	AGCTAGTACG	GTACCTTTGG	16680
TGGAGCACAT	CCTTACTCAA	AAGGAGGGGC	GTATTTTCTC	GTCCCTCAAG	ACTCATCTTT	16740
GCCAATTACT	CTCTGAAGGG	GTGCACGGAA	CCTTTTACCG	TTTTGCGCAc	GGCTGCTCCA	16800
AGAAGACCTT	AAAGCTCGCG	TGGCAGAAGC	CCTGGGTaCT	TCCGCCGACG	TTCTCAGGA	16860
ACCGAACGTG	TCGCTTGTCG	CCGCGCTCCT	GCAAATCCAC	TACGGTACTG	CGCTGGACCC	16920
CAGGCAKTAC	CGGGATATTA	AAACGATTAC	GCCAGAGACG	GCCCGCGCAC	GTCCCCATGA	16980
mGCGGAAAAG	GCGTATGTGC	GCATTGAGTA	CGGAAAAAAA	AGCTACCTCA	CTCGGAAACG	17040
TGTTGTGCAG	TTCATCTGTG	CCCTGGTAAA	AATCCCCGGT	CATCTTGTAG	ATCGCGTTGA	17100
CATAACCGAA	CGTTkCGCGT	TTGCcGCATa	CCCCGACGCG	CAGgaGGAaG	CAGTTcGCTT	17160
ATCCAAGAAG	CGCAAGGACC	TGCCGCGCGT	TTCCTTCGTT	GGGCACGCCA	GTcGCCTAAG	17220
AAATACCGCT	ACCCCTGCAG	AAAAGTCTAC	CTATCCAAGG	CGCCTCCCTT	CCGGAGAAGG	17280
CCTAAGGGAG	CAGATCTCAA	GGAGAACCTC	TTCTCTAAG	AAGGCTTCTG	GGAAACCGGA	17340
GGATTCTCTT	CCCCCTCCCC	AAGAACATCG	CCTTGATTGA	TGCAGCGGCT	CACTGCGCCA	17400
CTACAGCATT	CGTGCAAGCC	AGCGCGAGAT	ACTAAGGGCA	TAGTTACCGA	CGGCTTCTAT	17460
ACCACGCACG	ATGTCCATAT	ACAGGAGcTC	CGCCTTTACA	TCTGCACCCT	GCTCAAGACG	17520
TCTGCGCACA	AGTCCtTTTA	GATGGGCCCC	CTTGCTTTTCG	ATAGAGTGCG	TCATTTGGTT	17580
TACGTGCAAC	ACCTGCTTAT	CTTCCaGTGG	ACGGTTCaAG	TGCGAATACA	CAAAGTCAAC	17640
GCACTCATCC	ACCATGCCgA	CGTACGGGAC	TAACCTCTCG	ATATCATCAC	GCTTGAGCGG	17700
TACATTTCCC	TTGATGCTCT	TATGGAAGTA	CAACCCTATA	CCACACAAAT	GGTCAGTAAT	17760
ATTTTCAATA	TCGTCTGCAA	TGGAaaACAT	TAATTGCACG	TTATGTTTTCG	CTTTCTCGCT	17820
CAAAGAAAGA	TGCGATGTTT	TAATCAGAAA	GCGCGAAAGC	TGTTCCCTGCA	TTTGATCTGC	17880
ATAATCCTCT	TCCTTTGTCA	GGCGTGTAC	GATCTCATCA	GTAAGAAAGCA	TACACGTTCC	17940
CTGAATGGAC	TTACGGATAG	TAACAAGCAT	ACCCTGTGCT	ATTGAAAACA	TTTTTTTCAG	18000
TTCAATTtCC	GCACGAAAAA	TATGTGCCTC	AGCGCTCTCT	TTTACCGCAG	TTTCTTGAAA	18060
AACAAGCTGA	TACCTwTCTG	GAGCGTCGTC	ATACCGAGGA	CGAATTAACC	ACTCTACAAA	18120

747

CGCTGCAAGG TGCTTAGTGA AGGGAAACAC AATAATAGTG TTGACGATGT TAAACATACT 18180
 GTGAAAGAGC GCAAGCCGCA CTGTGATGTT ATCAAAACCC GAATTCTTTG GAGTCAAAAC 18240
 ACACAAGAGT GCCAAACTG GATGAAAAA CATCAAAAA ACCAATGCAC CAAACACaTT 18300
 AAACAGCACG TGGAcTGC GG CAGtCTCCGT GCGTTCAATT TACTCCCAAT GGCTGCAATT 18360
 GCAGCATCAA TGGTAGAGCC CACATTACTT CCTAATACGC TTGCTGCAGC GAACTCCACT 18420
 CCGaTGACAC CACCGAACGC CATAGTCAAC ACGATCGCAG TGGTTGCAGA CGAGGAGTGC 18480
 AAGATGACCG TTAACACAAA GCCTGATAGG AGTCCTACAA AAACACTGAG CGCACGATCC 18540
 TCAACTGCAA TTTTAAGGAA GGAAAGCTCT TCTACAGAAA GTGGAGGAAT GAGCGAAGAG 18600
 AGCAAACCAA GCCCCGTAAA GAGAAGACCA AAGCCCATGA TGCTCTCGCC CAAATGTCCT 18660
 TTATGCAAGT GTTTAAAAA AGTCAGAAAA TAGCCAATCC CAAAGGCGGG GACAGCGATT 18720
 GACGCAAGCT TAAACTGAAA ACCCACAAGC GCAACAATCC AAGCAGTAAC AGTGGTACCG 18780
 ATATTGCGAC CAAGAATTAC GCCGATTGAC TCGGTCAAAG AAAGCACTCC CGCGTTAATA 18840
 AAAGAAATCG TCATAACCGT CGTAGCCCCT GACGACTGCA CAATAGCGGT AACTGCCATG 18900
 CCGGTTAGCA CCGCGAAGAA ACAGTTACTG GTCATCACTT GGAGaTTTT GTGGAGGCTT 18960
 TCTCCAGTAC CCTTTTGGAT ACCGTCACTC ATCAGCTTCA TACCAAAGAG CATGAAGCCA 19020
 AGGCTTCCGA TACCCTGCAA AAGGACAGCC ACAAGGTGCA TCGGCGCCCA CCATAGCAAA 19080
 AACAGGGGAT ACGTATCAAT TGTCCGAAGC GGGACACTGC GCCGTACGGA CGTATGTTTA 19140
 TTAGTCAATC TCTCTTTTCT CAAATAGTCT CGCCGTGACA TCGCTT 19186

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4901 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

TGGTATGTGG TGC GCGATTC ACGTAAACGA AATGTTTCTT TTCGCAGAAC AGATGCTAAA 60
 TAGCTGGCGC ACAGCGATAC ACGCCATAGG GCAACTCTTT TTGCGCACGA GTGCGCACGT 120
 GCCGGTGACA CCCATTCAATC TGTTAGATCC TGCTCACTAC CTGGAACGCA TTCCCATCGT 180
 GTTGTCGGTG CACGCGCTCT GTGGCGTTGC AGGAGGCACG CTATGCCTAT CGTTGGCGGT 240
 ATGCATCATT CCTGCGCTCC GTGCGGGCCG CGTGCGTCCC CTTGACCTCA TGCGCAAGGT 300

GTGATAGGAT	GCCCCAGTT	TTTTTGATTT	CTTACATCCG	GCTCGCAGAC	GGATGGGTAC	360
CATCTTTTAG	AAGAGCACGC	GGCCGGTGCG	GTAGGGGCTA	TGGAAGAACG	CAAGAACTAT	420
ATGGATCGGC	TTGCCGAAGC	ACTTACGCGG	CGCAAGGTGC	AGCTCGATCG	GGACATCCTA	480
CCAAAGGCGC	TGGAGCAGTA	CCGTGTCCAG	GTCACAGCGG	TAAAGGCAAT	TCGCAGTAAT	540
TTGCTGCAAA	AAGGTTTCTT	GCACGATGAC	GCGTACAAGT	ACGACAGCAA	GATGACTGAG	600
ATTGAGTTGC	CAGAAACTTc	CCctACGGGG	AAAATGAGAA	GCCGATGGTC	ATTGGTTCTC	660
GCCTTTCGCA	CTATCAGACT	ATGCTCGGTT	TTTTGGACAA	CTACTACCGG	TTCGATTCGG	720
AGTTTCTAAT	CCCGAAACGT	ATTGCAAAGC	TCGTTGCGCT	CAACGGTACg	TTCATGTGGA	780
AAGATTTTAC	TGCTACCACC	AAAGACGCGA	ACACACGTGG	GCTATTTGAC	ATAGTGCAAT	840
CTTTCTATGG	CGCTGCTGAT	CCTATTTCTGA	TAGGACTGGT	GAGGGATTCTG	TTGCAGTACC	900
TAGTAAAAGC	CCATGAGGTA	ATCAGCACAG	CACTTAAGTC	CCTTTCGGTG	TTTCATCGCG	960
AGCGCTACAA	ATTGCTTATT	CGCCAGCATG	CTCTGGATGG	CTTGGACGAG	ACAACGGTGG	1020
ACGTCAACAA	CCCAGAGGTT	GCGCTTGACG	CGATGAAAAA	GAACTTTTCA	GAAAATGCAA	1080
AAGGCCATCC	GTTCTACAGC	GAGTTGGCAA	CCGTGGTTTT	GAGAGAAGAC	TTCTCTGCCA	1140
ACGCAGAAAA	GCTGCGGGCT	GCAATCCTCC	GCGAGTTTGA	AGAATCTTCT	GCACCCAAAA	1200
GATGcCGCGG	TGCTATGCGC	AATCCACACG	CCGTACTACT	TTCTGGTTTC	AGATCGCTTG	1260
GAGCTACTTC	TAGCCACTTT	CATACTGCTC	TGGAAAAGAT	TCGCTTCAAT	GAGGAGCTCG	1320
TGACTCAGTC	TGAGGCGGCC	TTCTTTTCAA	AGGTAGTGTT	AGCCTTTCTC	AAAGCTTTCA	1380
ACATTCAGAC	GCGTTCAAAG	GACGTTGAAA	TTGTCGTCTG	CGACCCGGCA	ACACAGATAC	1440
AGAAAAAGGA	ATGCGTAAAC	GTTGAGCTCT	TTCAAAAAGA	GCTGGCCCGG	TGTGTCAAAC	1500
TGTATCGGGG	TTTTGTGTCT	CCAGACACTC	CGATTCATGA	AAAGTTAATG	GCGCTCAAGG	1560
ACGAGCAGct	CTTCGAGCTC	CTTTTTTAAAC	ACGTAGCAGA	GGCGCATACG	CTGGTTAAAC	1620
AGCTTGCAAG	TCTTGATGAG	TACTACAAGA	CAGTGAGGTC	TGATGTGCGC	GCGAAAATTA	1680
AAGGGGTCAA	GATTGAAGTT	ACAACTATCA	CCACTTCTGT	AACCAAGGCA	AATAAGTGCC	1740
GCGCAGAATA	TGCCTCGCAA	CTAGAGGAGC	AAAAACATAT	GAAGCGTTTA	GGGGTAGCCC	1800
GTGCGTAGAA	TGCGGCTCTC	GCGCCGCGGc	ATTCTCACGG	TAGTAGGTAC	CCTTCTTCTC	1860
CTACCTCTCT	TTCTTCCGA	AAAAAAAAAAG	ACTCACGCGC	CGCTCCCTCG	ATCTGAAAGA	1920
AAAGAGTTTG	TGGTGTCTT	TTCTCCGTAT	AGGCCTGTGC	TACACCCGCA	CGTGGCATCG	1980
CGCGTGGACG	AAGCACAGCT	GCTCACAGCC	CTATATGAGG	GACTTGTCAC	CTATGATCCG	2040

TACGATCTCC	ACCCAATCCC	GGCGCTCGCA	CAACACTGGT	CGGTAAGCAC	CGATGGGTTG	2100
ACGTGGACGT	TCTATTTACG	AGATCAGATT	TTCTTTCAAA	ACGGCGACCC	TATCACTGCA	2160
GAGACGTTCC	AGCAATCCTG	GCTCAATTTG	TTAAATCCTG	AATGGAATGT	GCCGTATGCG	2220
TCTTTTTTGG	ATGCAGTTGA	GGGGGCACGT	GCGTACCGCA	GCGGCACTAC	GGCTGACTCT	2280
CACACGGTTG	GGATTCTCGT	AGAGGGGTCA	GACAAAAAGA	CACTCGTGGT	CAAGCTCGCG	2340
TACCCAGCAG	GACACTTCAT	TCAGATGCTC	TGTCACCACG	CATTTGCCGC	AGTCCACCCC	2400
ACCCAATCTG	CAAGCGTCGG	CACGCTGCAC	GCGCGTACGG	CAAGCGCCTC	AGCACACAAG	2460
CCGTTCATC	CTATCGCAAG	CGGTCCTTTT	GAATTACAAC	AAATGCAAGC	AGATCGCGTG	2520
GTGTGCGTG	TTAACACCCG	CTACTGGGAC	AGGGaCGCGC	TTGCCCTCCA	CGCCATCGTG	2580
GCGCTgcATT	GCACAAGACC	CTGCAGCGCG	CGATGCGGGG	TTTAACGATG	GGAGCATCCA	2640
TTGGATTAGT	GGAGCGCTGG	AGCACAGTTC	TTTGCAGGAT	GCAGCTACAC	TTCAGATCGT	2700
ACCGCTTCTG	GCAACAGAGT	ATCTGTGTTT	TAAAACGGCA	CATGAGCCGA	CGTGCAAgCC	2760
ACGcTGCgCA	AGGCACTGCT	TTTAGCTACT	CCGGTGGAGG	AGCTTACCGC	GCGCTATTTA	2820
TTTCCCGCAC	GAACGCTCGT	AACTCCGTTT	ACCGGCTACC	CGGTACCGCC	TGTAGTACAT	2880
GAATACAATC	CTGCGCGCGC	ACGCTnTtTT	AGCAGAAGCG	AAGATAGGTG	GGAAGACAGC	2940
CCGTACTCCT	CTTAAAATTC	TCGTTTCCGA	CACCGAGGCG	TGCCGGGCAC	TCGCACTTGA	3000
ACTTCAGAAG	GCCTGGACAG	CCCTCGCACT	TGCAGTGGAA	ATCTGGGCAG	TGCGGCCTGA	3060
AACGTACCGG	GAATATGTGC	AGGATGAAAA	ATACCACGTG	AGAATCGTGT	CTTGGGTTGC	3120
GGACTTTGCA	GATCCGATGG	CGTTTCTGGA	GCTGTTTAGA	AAGGGATCAA	AGACACACTC	3180
AACCGGATGG	ACCCATGAGG	AATTTGAGGC	ACTGCTGACA	CGCGCAGGAG	CAGAACCGCA	3240
CGTGCTTCGT	CGTTGGGAAC	TTCTTGCGCA	GGCAGAACGT	ATCCTCTTAC	AGGAAGCAGT	3300
TGTGCTTCcG	CTTTCGCGTT	TGCATGCACT	GCACGCGGTA	CAGCGGCGCA	CGGTGCGCGG	3360
CTGGTATGCA	AATGTGCTCG	ATGTGCATCC	ATTTAAGTTT	ATCTCGTTAC	AAGAAGAAAT	3420
AAAGGTCAAC	CTAGACTCAT	AGAGGGGCTG	CAACCCGTGC	ACACCCAGGT	GTACCTTGCA	3480
ACGTAGATGT	ACCGGCGTGT	ACAATGCCCT	CTGCATACAC	AGAGGGGATT	ATGGGGTATC	3540
CGTTTCGCGC	TCTAGAGAAA	AAATGGCAGG	CCTATTGGCG	CGACAAGCgs	GTCTTTTGTG	3600
TGTCCGAGGA	TGAGCGCTTC	CCTCCTGAGC	GGCGTGCGTA	CGTGTGGAC	ATGTTTCCCT	3660
ATCCTTCAGC	GCAGGGACTT	CACGTCGGAC	ATCCAGAAGG	CTACACTGCA	ACTGATATTT	3720
ACTGCCGCTA	CTTGCGCATG	GGTGGTTACA	ACGTGCTCCA	CCCTATGGGT	TTTGATGCCT	3780

750

TCGGACTTCC GGCAGAAAAC TTTGCACTCA AACTGGTAC TCATCCGCGC GTCTCCACCT	3840
CCGCCAACTG CGACACCTTT CGCAGACAGA TCCAGTCGTT TGGTTTTTCC TACGATTGGG	3900
AACGTGAAAT ATCTACCGCA GATCCAGAAT ACTATCGCTG GACTCAGTGG CTGTTCTCTCA	3960
AACTTTATGA AAAAGGATTA GCCTATGAAG CAACCGCGCC CATCAATTGG TGTCCCAGCT	4020
GCAAAACAGG CCTTGCAAAC GAAGAAGTAA GAGACGCGTG CTGCGAGCGC TGTGGTGCTG	4080
AGGTGACGCG GCGTGGTGTC CGCCAGTGA TGGTGCGTAT TACAGCGTAT GCCGAGCGTC	4140
TCCTTTCAGA TTTAGATGAA CTTGACTGGC CTGAGTCAGT TAAACAAATG CAGCGTAATT	4200
GGATTGGAAA AAGCTGCGGC GCGGAAATG ACTTTCCCGT AGATGCGCCT GCGTGTTCAG	4260
TGCACGATAA GCTACCACAG ACAATTTCGCG TGTACACCAC GCGTGCGGAC ACGCTTTTGT	4320
GAGTAACGTA CCTGGTACTT GCTCCCGAGC ATGAAGCGGT AACGGCGCTC ACTACACACG	4380
CACAACGCGC AGCGGTACAG GCGTACGTGC AACGTGCAGC AAAAAAGAAC GATCTCGAAC	4440
GCACTGATTT AGCGAAGGAA AAGACCGGTG TTTTCACCGG CGCGTACGTG CGCAATCCAA	4500
TCAATGATAT GCGCATACCG GTGTGGGTAG GTGATTATGT GCTCGTTTCC TACGGCACGG	4560
GGGCAGTGAT GGCAGTTCCT GCACATGATC AGCGCGACTG GGATTTTGCC ACTCGGTTTG	4620
GCTTACCCAA GTTAACCGTG GTGTCTGCAG ACTACACTGC AACAGTTCCT AATAGCAACT	4680
CCCCTCAAGG CGCGGTACTC CAAAGATGCG TCTCAGACGA GGGTTTTGTC GTCAACTCTG	4740
GAGCTTTCAA TGGTCTTGCT AGTGCCGACG CGCGAGAACG TATTGTTGCC CATCTTGAAA	4800
TGCGTGGCGC AGGTGCACGG CGCGTCACCT ATCGCCTACG CGACTGGGTG TTCAGCCGTC	4860
AGCGCTATTG GGGAGAACCC ATCCCTCTTG TGCAGTGTCC T	4901

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

CCCACCTGTC TCACCGGCCT GAACGCCGCG GTCGAAGCAC GCGTGATACA TCCCCCTCAC	60
CTACATCCGT TACAGAAATA ACGGAGGGTA CGAACTGAAT GGAGCTGTGC CCCCTGGGAC	120
TATCAATATG CCAATTTTGG GGAAGGCGTG GTGCAGCTAT CGCATCCCCC TCGGTTCCCA	180
CGCCTGGCTT GCACCACACA CATCCGTGst CGGCACAACC AATCGCTTTA ACATTATTAA	240

751

CCCCGCGGGC AACCTGTTGA ATGAACGAGC GCTCCAGTAC CAGGTGGGAC TGACGTTTCAG	300
TCCCTTcGAG AAGGTGGAGC TCAGCGCCCA GTGGGAACAG GGCGTGCTTG CTGACGCTCC	360
TTACATGGGC ATTGCCGAGA GCATCTGGTC CGAACGCCAC TTCGGCACCC TTGTCTGCGG	420
AATGAAAGTG ACATGGTAAA AACGCGTGCT GTTCGATTCC ACCTCCCCTA TCAAACCCCG	480
TTTTGTCTCGT CTTGCCTTTG CAGTTGCAAA ATTTTGTCCTC GGATGAGGGC TGCCTCTTCA	540
AATCGTAACT CACGCGCACA AACCTTCATG TGTAGGCGCA ACGCCTGTAC CATTTTTTTTG	600
CGTGCAGCAT GTGTGCGCAC GTCTGCGTCT GCTGCGCGCA ACAGGGGTGC GACCTGTACa	660
cGCGCAGtCT TTTTTTACTT CCTGCTCAGC GACCAGAATA TCTTCAATAG ACTTTTTTAAT	720
CGTACGGGGT GTAATCCCAT GAGCACGATT ATACGCCATC TGAATCTTTC TCCGTCGAGC	780
AGTTTCCTCT ATTGCTTCAC GCATCGCATC GCTGATTGCA TCCGCGTACA TTACCACAGT	840
TCCGCGAGCA TTACGTGCTG CTCGACCAAT AATTTGGATG AGACTCGTCG TCGAACGTAA	900
AAAACCGACT ATATTGGCAT CAAAATAGC AATGAATGCC ACCTCGGGCA AATCAATACC	960
TTCTCGTAAT AAATTTATTC CAACTAATAC CTCACATTCC CCCGCACGCA GACTCGTGAG	1020
AATTTCTACG CGTTCAATAG TTTCAATTTC CGAATGAACA TACTTTGTCC TTATTCCAG	1080
TCCATTGAAA TAATCTGTTA AATCTTCAGC CATTTTTTTTT GTCAATGTTA GCACCAAaA	1140
CGTTTCGTCC gCGcACTACA AGCTTTTACC CGcTGaCATA TATCTTCTAT TTGTCCATCC	1200
GTTTTTCTCA CTTTCGATGCA TGGATCTAAA AGTCCAGTGG GACGAATCAG TTGTTCAACT	1260
ATTTGCACAG ACTGTGTGCG TTCCTTCACC CCAGGAGTTG CAGAAATAAA AACTGCTTGA	1320
TTTAACAATG CCTCAAATTC CGAATCTTTC AGTGGACGGT TATCTCGTGC ACACGGCAAG	1380
CGAAAGCCAA AATCGATGAG ATTCTGTTTA CGCACCCGAT CTCCTTCATA CATTCACCA	1440
AGCTGCGGAA GTGTTACGTG ACTTTTCATCA ACAAAGAGCA CAAAATCCTT TGGAAAATAA	1500
TGAAGAAGCG TCACCGGCGG TTCACCAGAT TTTCTACCTG CAATCGGCGC AGAATAATTT	1560
TCTATACCGT GGCAATACCC CATCTCTCCG AGCATTTCAA GATCGTATTC TGTGCGCGTT	1620
TTTAAACGTG CCGCTTCTGC AAGCTTATTC TCTTGAGTTA ATTGTACCAA CCGTTCATCG	1680
AGTTCTTGTC TAATACGGTC CATGGCGCGA GGGATTGCAT CCTCTTTAAG TACAAAATGC	1740
TTTGCAGGGT AAACGGTAAG TTCTTCAAAT TCCCTTAGAA CAGCACCGCT TACAGGATGA	1800
ATGCGACGGA TACGAACAAC TCGATCCCAA TCGCACTCGA TACGATAAAA TTCTTCTAAA	1860
TACGCAGGGA AAATTTCAAT AACGTCTCCC CGAACTCGGA AGCGACCGCA CTCGAGCACC	1920
GCGTCGTTAC GCTCGTATTG CAGAGATACA AGTTGCCGCT TGAGATCTTC AAGATCAAGA	1980

752

CACTGGTTGA CTTCCACGTG GATACGCAGA TCACGCCAGG ATTCAGGCAA CCCAAGACCG 2040
TAAATACACG AAACAGTTGC GACTACAATA ACATCACGAC GTTCCATGAG ACTAAACGTT 2100
GCAGATAAAC GCATTCTATT TATCTCTGcA TTGATAGAAG CATCTTTCTC AATGTAGAGA 2160
TCACGAGCAG GGACATACGA TTCAGGCTGA TAATAATCGT AGTACGACAC AAAATACTCC 2220
ACCGCATTGT CTGGGAAAAA ACCTTTAAAT TCCCCGG 2257

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 992 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

TACTCATCGG CGTCGCGCnT TCnTACTCCT TGGGCATTGA CTA CTTCAAC TACCCCGTCT 60
GATACCATGA CCATTACATC CCCAGGACAC AACGTACGCT CATGAATCTG TATAGGGGGC 120
AGATCCACAA TGCCAATAAC TGGACAATTC GAATGAAGAT GATACACTTC GTGCGCCTCT 180
CCCGCCTGGG TAAAGACAAG GGGACTTTCC ATCGATGCGT TAATGTAGCG AATATTCATA 240
CCCGCTGTGT CAATTAATCC CAAGAATAAG GTCGTGTACT TATCGTGGAG ATGCATACGC 300
TTTACTGCCC GGTCCACCGC ATACAAAATC TCAGGAAGAT TCTTTTGTG TTCCACGATG 360
CGAATCGTAC TGAGCACAAC ACCCATAACT AACGACGCGG CCAAACCTTT GCCAGAAACA 420
TCTCCAATTA CAAATAAAAA CAGGTGTTCA TCAATTGAAA TAACGTCGTA ATAATCCCCA 480
GATACATTAA CCAGTGGCTG ATAGAATGCC CCGACGCATA TTTCTTGGT ATGTGGGAGC 540
GCCTTAGGCA AAAGTGC GCG CTGTACACGC GCCATCATTG CCCATTCTG GGATACATGG 600
GAGTACAACA ACAAAGTGCT CATGTTCTC TTTGATTTA AATACTCTT AACTCTTTG 660
AACAAGAGCG ATATAACTTC GCGCTCAACA GCACGGATAA AACGACATAC TATAAAAAGA 720
CGCAGCTCTC CACTGGAAAG ACATACCCCA CGAGCCCGAC GTCGGTCAGA CATAAGACAC 780
AGATCATCAT CAAAAAATA TATACCGTCT GACCAAGTGCC ACGTGTAGTC CATAGAAAAC 840
TTATGAAGCA CAAGATCATA CGTGCGTGTG TCTGAAACAA ATCGTGGCAG CACTGTTGTA 900
AATAACACGn TTA CTTATCG TATCCATTAA GAGCACTGCG CAATCGGAGC GATATTCAAG 960
CACCTCCTGG AAGGCAGCAA CAAGTTGTTC AT 992

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

GTGCAGGATC CGTCTCTTGT TCACGAAGAA CTCAGACACG GTTGGCGTAT CTGCAGATCG	60
CCTATGCTCC ACGGGGATAT ATTAAAAAAC ACGCGCACGC TAGAAaCctC GCCGCATATA	120
AACgGCGGTC AAgAtTTGTC CAATACGCGA TTAAGCACAA TTACACCACT GAGTCAAAAA	180
GCAGTATCAG GATAGACAGG GGAACAGGTA TGCCTGATAC GGTAATATTT AAAAAATAA	240
AGGTCAITGA CAAAAGCTG GCTTCCTTTG TAAGGGAGCT CATGTCTCAC CAGGTAGATC	300
AACTCACGGT TTTACAGAAA ACGGAGGAAA TCTACGGTAT GCTCGTGGAC CTA CTGATCT	360
AGCACTAAGG AAACCTATCA TGATACCTAA ACTGAGCCCA AATGCTGACC CCTGCACAGC	420
GTGTGCTTCC ACCCTGCCT TTCCGCCGCA GCCCATGGAG GAGGAAGGAG AGTTTTTATA	480
TCAGTTGCGT CTTGAGTACT CCCGCGAAGT GTTATATGnC GTTTTCACGC GgTACGCGT	540
GCACACTTTT GnTnGGTACC CACGCGTTAT GGCAACGACA TTGCTCGGTG CGTAGGGCGT	600
ATACGTACAC CCGTACAAAC CGATATCGCG AGTGTGGTAC GTGTTGCATC AGACCAAGAT	660
TTGTGCACAT GGCACATACA TAGGGAAAAG GAACGTGCTG CGGAAATGAT TTTTCGGGAT	720
CGCATTGAGC ACTATCAACT TGaGATGaAA TGTATTTGCT GTCACATACC TTTAGAAGAA	780
gCACsCsTGG TaTTTCTATA CAgTGCGCCA GCACGTkTTG ATTTCaGAGA ATTAGTTAGA	840
GACTTAGGAG CTACATTTGG TACGAGAGTC GAACTGCGAC AGATAAATGA ACGGAAGAA	900
GCGCGGATAG TAGGCGGAAT TGA CTGCTGC GGGCGCGCGC TATGTTGTTG CTCAGTGTTT	960
AGCAGGTTGC GTCCAGTCTC GGTA AAAATG GTAAAGGAAA AAAATCTATT ATTTCTGTTCA	1020
ACCCAGATGA TGGGTCGTTG CGGACGATTG CGCTGTTGTT TGACGTTTGA GGAATGATCG	1080
TTACACACGT AGCCTGTGTG GCGCACCTAA GTCGCTGCAC CCACTCGTAA CACCACACTC	1140
ACATGTGCAG TGTGTTGCGG TGTACAACCG ATGTGAGCGT GGTGGGGTTT GTTAGCAAGG	1200
GGACGTTGAT CTGTTCTGTC TGCTGAkTGT CTTTGTCCCG TCGTATAGAA CACACTCGCA	1260
GGTTTCCCTG CCCAATACCA TTACTTAGCC CACCTCCTCT AGGAAATTTT CGTAAATGCA	1320
GAACGTTTGG TAATACTTGA TTTTTTATAA GTCTCCATTG AATATAGGAA ACGAGTATAC	1380
CCGTAAAAAG CATAGCATTG CTCGACATTA TCTATTGTTT TACGCAAGAG GATGCAGAAT	1440

754

GAAGAGTCTT GAATATTATC GATCACAGCC AAAAGCAGAT GTGCACACGC ATCTGAATTT	1500
GAGTATGAAA TACGAACGAT ATAAGCAATG GTCAGGAGTA GTCATTCCAA ACTTTCCACG	1560
TAAAATGCGC GGGCTCGACG AAATGCATGA AATTATTGGT GAGTACACGC GTCCTCAGTG	1620
TAAAAGTGGC CAAGACGTGT TGAATTTGTT TACCATGTCC ATAGAGGATG CCATTGCAGA	1680
CAATGTCGTC GTAATGGAGA CATCAGTTGA TATTGGCTTT ATCACCATT ATGAAGAAAA	1740
TTTGGATCAT TTCTTATGTG ATTTAAGCGA TCTGCATCGA CGCTACAAGC GCAATGTTAC	1800
CCTTCACTTT GAGCTCGGTA TCTCCAAAAT ACGAGAGCGC AGyTnCGTAG AACAGTGGGC	1860
TGAGCCCATG ATGCGAAgCG GTATCTTTGA AAATATTGAC CTCTACGGTC CAGAGATTTT	1920
CGAAGGAATC GAAGATTTCA TCTATATTTT TAAACTGGCC GAGAAGTATC ACTTAAAAAA	1980
GAAAGCCAC GTAGGCGAGT TCTCTGATGC GCAATCGGTA CGGCACTTTG TCGAAATATT	2040
TAACCTGGAC GAAGTCCAAC ATGGCATCGG AGCCGCTACT GACGAGAACG TTTTGCGGTT	2100
TCTAGCTGAA AGAAAAGTTC GCTGTAACGT ATGTCCAACC AGTAATGTCA TGCTCAACGT	2160
CGGTGGAATG CCCTAGAAAA ACATCCTATA AAAAAAATGA TGGATGnCAG GGGTCCGTGT	2220
TGGGTTAGGA ACTGACGATC TTCTCTTTTT TGGAAAAACA AATAGCGAAC AATTGTTTGA	2280
TATGGTTTCC T	2291

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2169 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

CCGCCAGTCC ACCGGTGnCA CCCTTCAACG CCGGTTAGGG AAAGCGTGCG GCACGCCAGC	60
GAGCGCAGCG CATGCTGGAG CkCATTCCAA GAATGGAGTA TGCCACGCAC AGGCTCCTGG	120
GTACGAGCGT GCATTTCTTG AGCcGctGTT GACACACGGC CGAGTGTAac GGAGCACTGT	180
GCCTTGCTGCT AGTCCCTGAG CGAGAAGGAT GCAGCAGGAG AGGGCAAGGG AGGAGAACAG	240
GAAGGAGCAC CGGTAGTAGT TGATGGGGTT AATTTTTTTC CGTTATGATC GCTGCTATAT	300
GTGTGCGGTG TTGTCTGATC TTCACGTGTA CTTTGGGCCG TTTCGTCTGT TGCAATCTTA	360
TGCGGTGTTG ATGGGGATTG CCCTGTATGC GGGATTCTTT TTTACGTATG GGGTGTGTC	420
CAGTGCGTAT CGCTTTTTGC CCCAAGACAG GGGGCGTGCG TTTGCGCCGT GTGCACAGGA	480

755

AGCAGCGGGT AAACCCACAG GGGCAGGAGT GATTTTTGTG TCCGTCCTTG TGTGTAGT	540
GTACCTGCTT ATGCGTCCGA GTTTTGTGCA TCGCTTATA TTGCTGCTGA CGTGGGGGGT	600
GATGCTCACC GGATACTTAG ACGATTGCGC GCAGGTGTGC TGGGGGGAGT ATCGCAAAGG	660
CGCGTTGGAC TTTTGTGTTG CCGTGTGAC AGCAGCGCTG TTGGGTCATT TTTATTTTCA	720
CGATCAGGTG TTCTGGTGGT TTCCTTTTTT TTCAGATCCG GTGTTGCTCT CTCCTTTTTT	780
ATTTTTTGCC GGTTCGGTGG TGATTTTGTG GATGTCAATT AACGCAACCA ATTGCACAGA	840
CGGGGTTGAC GGGCTTTCGG GAGCGTTGGT GTTGATGGCG CTTCTTTCGA TGGGTACGAT	900
TTTTTACTTT TTGTTGGGAA ATGTGCGTGC GCGCAGTAC CTAAGGTGC CGTTGTAGT	960
GGATGGTGC CAATGGGCAC TGATGAGTTT TGCACTTGCC GGGGCGCTGA TGGGGTATGT	1020
GTGGCGTAAT GCACACCTA GTACGGTGTG GATGGGAGAC GCAGGCTCCC GTGCGCTGGG	1080
GTTTTTCATT GGGGTGTTGG TGTGTGCTC GGGCAATCCA TTTTGTGCTGT TGATGACAAG	1140
CGGTGTTATT TTGGTGAATG GGGGTACGGG GCTTCTAAAA GTGGTGTGTTG TGCGTTTTTT	1200
TCATGTGCGG ATCCTGAGCC GGGTGCCTT TCCGCTCCAT GATCACATGC GTGAGAATTG	1260
GCACTGGTCT ACGGCGCAGG TATTGCTGAG GTTTATGATT TTACAGGGAC TGCTCACGAT	1320
TGGTCTTTTG GGGGTTTTGT TCAAACGCG GTAGAGGGAG GGCACCCCTT GCGGGGCACG	1380
CCGGGCCGAG CGAGGGCGAC GGTGCGGAGT ATCCGGCGCC TTGACGTGCG TTTATTTCTT	1440
TTGCTAGCCT GCCCCTAATT GCTTTCCTT TCCGGAATGA TGGTAGAGGA GACAGGGCGG	1500
AAGGCGTGGG GTGTGTATGG TGCCGGTGAG AAGGTTTCATA GCGGTGTGTG CGGTGACGGC	1560
GTGTGCCGGG CCGTGTTTTT GCGTTCAAGC GTTTATCTCT TCTCGGATCG GGTATGGGCG	1620
CTTTGGGATA TATGGGAACG AGATAAAGGA CTCCTACTAC AAACATGTTC CGATGACGGG	1680
ACTAGGGGTT GACGTGGTAA CGTCTTCAGG CGTTGCGATG GTGTTCAATG TGGAGAAATG	1740
KTGACGCAG CTCATGTTTC GCGCGCAGGC GCTGCTGGGG TACGCGTTT AGGTGGCAG	1800
GTTCCGCTTT ACACCTGCCA TTGGCGGCAG TTTCTTTCG TCGCACGACC ACGCCGAGG	1860
GGTGGCTCTG TCGCTTGACT TTCAGTATTT CTTTAATGAT TGGGTCGGGT TGGACCTGAA	1920
CATAGGCGCG GGGGTGGATG TTCCGGTGAA CAGTAACCTG CGTTACCTGA TGCGGGTGGG	1980
GACGCCGGAG TTAGCGAAGA TTCTCATCAC GCATACAGTG ACGCATGGAC TGGCTAATCG	2040
CTGGATATCA GGTCCCCACT GGTGGAATTC TCTTCTTCG TGGGTCGGGA ATACCGCGGG	2100
AAAAGTGGCT GGATTTGTAG CGCGTTTGAT AGCAAATTAT CTGCTGAAAG GCTCACAGTA	2160
CAGCATGTT	2169

756

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

```

TACCACCAGC AAACGCCGTG AGGTCAGTCC TTCCCGGCAA ATTTCAAAAA AGAGCGCAGG      60
GAGCCTGTAC ACATTGAGTG CCAACACCCA CAGCCCAGAG AAAACATAAC CCACAGCCAT      120
CACTGGTACT ATCACCGAAC TGACAACACT AATGCGCGCG ACCCCCCCAA AGATAACAAA      180
CGCAAGGAGA AAAGACAGCA ACACCGCTAG GATCTGGACC CACAGAGAAG AATCCTTTCC      240
GTAGTAAGAG AGAGTAGAGA CAATATTATA AGCCTGTAGT GCATTGAACC CGTACGCGTA      300
TGCAAAGACA AGACACAGCG CAAAAGCAC CCCCATGGAG CGACTTTTCA GACCCATTTT      360
GATGTAATAG GCGGGACCAC CTCGAAAACC ACACGCAGTA CGCGTTTGTG ATGCTTGGGC      420
GAGCGTACTT TCGACAAAGG CACTTGCAGC GCCAAAAAAG GCACTCACCC ACATCCAAAA      480
CACTGCCCCCT TTTCTTCCAA AGGCGATAGC GTwAGcAACG CCGACAATGT TCCCAGCCCC      540
CACACGGCTC GCAGTGAAA TCATAAGCGC TTGAAATGAT GAAACTcCTT TCCCCCTCTT      600
TTCAGCCAGC GCTGCAAACG CrGGtTCAGA AGACTAAGTT GAACACAGCC AGTC'TTTATG      660
GTaAAAAGAn ACCGCAGACG ACAAGCCAAC CGA                                     693

```

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4835 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

```

CCACTTCACA TCTTTTCATC AAATTACCGC ATAATACGAT CAACCCTCTT TCCAAATACG      60
GACACCAATT GCCTGCAAAC GCTCCACTaG ACGTTCATAT CCACGCTCAA TTTGATACAC      120
GTTACGGATT ATACTTACCC CGCGCGCACA ACACGCTGCA ACACCATCGC CATTTCCGCA      180
CGCACATCAG GAGATACCAG GTCACTCCCA TGCAATGCAC TCGGACCTGA AACAAGCGCC      240
CGATGCGGGT CACACAGGAT GATACGCGCA CCCATGGTAA TTAAGTTGTC CACAAAAAAC      300

```

757

ATACGCGACT CAAACATTTT CTCATGAATC AATATAACCC CTTGACTTG AGTCGCCACC	360
ACTGTCATAA TGCTAGTCAG ATCCGGCGGA AATGCAGGCC ACGGGCCATC ATCTATTTTA	420
GGAATCATAC CGCCAAAATC GTAATTTACC CGCAGATCCT GCGACGCaGA GACGCTTACC	480
GCGTGCTCTT GCTCGCTCCA AATTACTCCA AGTTTTTTTAA ACGCAAAACC TAGTGGACGT	540
AGATCACGTA CGTTCACATC CGAAATCGTC AATGCTCCAC GCGTTACTAC CGCAAGCCCA	600
ATAAGCGAAC CTACTTCCAT GAAATCAGCC CCAAGTGTAT ATGTGGTACC ATGCAACGCG	660
CTACCCCCCT CAATTGTTAA AACATTCGAT CCGATGCCAG AGACGCGCGC ACCCATCGCA	720
TTCAACAAAT GGCATAGATC TTGCACATGC GGTTCGCTCG CCGcGTTTCGT GATTACCGTA	780
ACCCCTCGG CAAGAACTGA AGCCATAAGC ACATTCTCTG TCGCCGTCAC AGATGCCTCG	840
TCTAAGAAGA CATCACATCC CACCAGCTTA TTTGCAGAGA AAGTAAACAC CCCATCTAAA	900
CGAACTTGTG CGCCAAGTGC GGCAAgCGCA AGAAAATGCG TATCAAGTCT CCTGCGCCCA	960
ATAACATCAC CACCAGGTGt GGAAGCACT GCTTTTCTAC CACGCGCAAG AAGTGGCCCT	1020
GCAAAAAGAA TGGAAGCACG CACTTTCTGC GCAGCTtCGC ACGGCACTTC GCACGTCTGT	1080
AACTGAGGAA GATGTAACAT GTACTCATGA TTACCACGCC TTTCAACACT CCCACCAAAC	1140
GCACGAAAGA TAGTTAACAT CACCGCCACA TCCTCAATGT CGGGCACATT TTGCAGTAAC	1200
ACTGGCTCTT GTGTGAGAAC TGCCGCCGCA ATACAGGGAA GCGCTGCATT CTTATTTCCA	1260
CACACGCGAA TACAACCTGA AACGGGAAAC CCACCTTCAA CACGATAGCA ACTCATGCTC	1320
TCACCCCTTT GCGCACACAT TCCTGTAGAA CACCGATCAA CATACAACTT AATTGCACGA	1380
ATACCGCAAA AGTACGGCCC CATCCTGTGT ACTTACTTAG GCGTCAGCaA ACGCTTGACC	1440
TACATGCTCG AGTGTCACG AGGGCAGACA CAACATACCG ATCGAGTACA CGGCGTATCT	1500
TAAAACGCAA TCCTTCAATT ACCAACTCAT CCCCTACCGT AGGAGACGTC CAAAACGTTC	1560
CAGGAGTAAA CCTCCACCG TGTGGTACAc GCGCGACTGC AAACGCGTAC CTAACACTTC	1620
GTTAAAATAT TCAAGAGGAA CCGTTCCTGA ACATAAAATC TCATGAGTAC CGACGCTTTT	1680
CATCTGAAAA TCAACACGAG GTTTTGACAT TCGCTGcACC ATTGACCCAT GCACTGTGTA	1740
TCCTTCTACT CCTTCGAAA CTCCAGCAAG TGAACCAAAA ATTACCTCCA TAATGTCTGT	1800
CATGGTTACT AATCCTTCCC CATCGCCCCG CTCGTCTACC ACTAACGCCA TCTGcTGCTT	1860
TGATACCGAG AGCATATCTA AACTGAAAA AAGGTCAGCT ACATTCGGTA CACAACACAA	1920
CTCCTGTGCC AAATCACCCA CCCGATGCAC CGCAGCTCTG GTGTTGCTA CACATGCCGA	1980
CACCATCTGA TCTGATGACT GCGAGGGTAA TACTTTACTT TCTCCAAAAA TATCCCAGTA	2040

GTGTACGAAA	CCCCAGACGA	TCCCCGCAGC	ATCATGCACG	AGCAACTGAG	AAAAGGAACA	2100
GGTACGAAAA	GCATCCCACA	CATGAGATAG	TGGTGTGTCC	TGAAAACTG	ACACAAAGTG	2160
TGTGTGCGGT	ACCATAACGT	GTGCAAGCGG	TATGCGTTTA	AACTGTAAAG	CGCGCTGGAA	2220
CAATTGATTT	TCGGTTGACG	AAATCACCCC	TTCTCGTGCC	CCAACTGCAA	TAAGCGTTTT	2280
AATTTCTTCT	CGCGAAAGAC	ACGTCGTATG	ACGCGGcAAA	AAAATACCCT	CCAGCACATG	2340
CATCAATGCT	GACGACACAC	ACGCGCAGGG	GTACAGCAAC	CAGTAACTCA	ATTGCAAAAA	2400
AGGCGCAATC	CACATCAAGA	ATCCCAGTGA	GTACCGTGCA	CCCAGCGCCT	TCGGGAACAT	2460
TTCTCCACAA	AGAATAATCA	CGCACGTCAC	CGCAACCACT	GCCTTCCACA	CCGACTGTGC	2520
ACCCCAACAAC	TCCATAGAGC	CTAACGTCAC	CACGCTAGAG	AGCACCATAT	TCAGTGCAGT	2580
GT'TTTGCACA	ATAACTGTGG	TAATCAGCTG	TTTCGCGCCG	GCCAGAAGCC	AGCATAAGCG	2640
TTGTGTACAA	CGTGTACTGT	GCCgCTTAAG	CTTACGTTCA	TCGTCTTGGT	TCACCGACGA	2700
CAACGCGCTT	TCTGAACCTG	CACATAGGGC	CGAGCACACA	AGTAAGAACA	TGAGTTCCAA	2760
TCCTACCAGA	AAAGGGTATG	CCACGCGCGC	TTCCCTACTA	TCCTTGAAAC	TCAAACCGAA	2820
CACGTACGAT	TCTGCGCACA	TGCAGTTGTA	GCACCACACA	ACGCCAAGAA	CCGAATACAA	2880
CCGTGGTGCC	AGGATCAGGA	ATACACCCTG	TATACTCCAT	GATAAGACCT	GCAAGGgTCT	2940
CACTGGTACA	CGAAGAAAAA	TCGGTGCCGA	GTAGATCATT	TATCTCATCC	AAGCGCAgcG	3000
ATCCAGGAAA	TATATACGCC	CGTACCCCCG	CACGCGTAAC	cTGCGGACCT	GTTGAATTCA	3060
CAGGGAATTC	ATGCGCACTG	CTCTTAAAAA	ATGCTTGSTA	TATATTGTGC	TTTGTACAA	3120
GACCTGCCGT	CCCGCCATAT	TCATCAAGCA	CAATGGCGAC	TGCGCGTGAG	TGTGCGCGCA	3180
ATTTGTGCTG	CACATATGCA	AGTCGTGTAC	ATTGGAAGAC	AAAAACCGGC	GCGCTCACAT	3240
GTTGCATCAG	TGTTCCGCAC	TCTTCTAAAT	CTCGTCCGTC	TACCTCTTCT	GAGCACAAGA	3300
ATTTCTTCAC	ATCGAAAATA	CCAATTATCC	AATCAACACT	CCGTTCATAC	ACTGGAACAC	3360
GCGAAACGCG	CATCTTCTGT	GCACAGGCAA	TTGCCTCCGC	CAGAGAACTC	GCGCGCGGAA	3420
CTGCAATCAA	TTGCGCACGA	CAGGTCATAA	TATCTCGCGC	AGTAAGGGAT	GCAGAATGCA	3480
AAATACGTTG	ATACAATGCG	CGTTGCGGGG	AAGTCACAGT	GCCATCCGCC	TCTCCAGCGT	3540
ACAGTACGGT	GTGCAGGTCG	TCATCCGTAA	CACGCAGCGA	GGGAGTGTGG	CACGCGACAC	3600
GCGCAAGACG	CAAGAGCGCA	CTCCGCGCCA	TACAGAACAC	CTGTACAAAA	GGAGTAAGCA	3660
TCAAAGCGCT	CCACTGCAAG	AATCGCGCAG	TATGCAGTGC	CAtGCGTTTCG	GCCGGCACAA	3720
GGCAAGTGAC	TTCGGAATAA	TTTCTCCAAA	AAGAAAGTGA	AGCACCGTTC	CTGCACCGAT	3780

759

GCTCCACCCC ACTGCGTGGA TGCCAAAGAG GGCACGTGCA AAAAGCGCAA TGA CTGCAGA 3840
 CAACGCACTG CTCGCCAGGG TGTTCCCGAT AACCACAGCA GCAAGATAGA AGTTTTTCCG 3900
 TCGAAGGATA CGCATTGCCA CTCGAGCGCG AgCATGACGT TTTTCGTACA GGTAGCGAAG 3960
 TCTTAAGGTA TTTAGCGCAC AGAACGCTGT TTCCGCAGCA GAGAACAACA TGGAAAGCAC 4020
 CAGCAGCACT ACCAACACAC CGAACGCAGC GGAAACGGAA AGAACACTCA CACGTAATTC 4080
 CCCC GAAGGc tAAAACACCA GAACCGAAGA GACAACGCCA TACATCCTTG GACCCCTCCC 4140
 CGCTGGGGGG GGGCACCTTT TAAGGTGCTC ACGCCCTTGT GTCAAGAGCA CACCCTCCAC 4200
 TACAATGAAC TGCGTGTCG GAGACGCGC GGAGTCCTCT TTCTATGAAT AGAACCGAAT 4260
 CTCTCGTGG CTTAATCAAA GCCACCGTAC GTGAACAAGA CCGAGGCCGA ACCGTTTATA 4320
 AAAAGATTGC CCAGTTCCTC TCCCTCATTG GAGAAGAGCA GCGGCGCTG GTGCTCAAGC 4380
 AACTTGAGCC TGCACAGATT GAGGCGGTGG TTGCCGAGCT CCTGACACTC AAACCCCTCA 4440
 GTCCAGAAGA AGCGCGTGAG ATcTACGGGA GTTTTCTGCC CTCTGCGCTC GTGTGTCGCC 4500
 TGTTACCGGT GGATGCGTnT GCGCAGTCGA TGCTTTCCAA AGCGTTTGGG GAAGAAAAGG 4560
 CCGATCTTAT CTTGAAGCGG GCGGTGCCAG CGGCACAGCC GAAACCTTTT GAGTTTTTGG 4620
 TGCGCTTGAA GCCTCCCAAC TTCTCCCCCT CCTGGAAGGA GAACTACCTG CCACCAAAAC 4680
 ACTCATCCTC TCGCAGCTGC CTCCAGAAAG CtGCGCACTA TTTGAGTAAT ATCAGcACAG 4740
 AGGAGAAGAA GGA CTTGATC GTTCGCCTTG CAAAGTTAAA GCACGTTAAC CCTCAGGTGC 4800
 TGCAAGTCAT GAGTGACTCC TTGCACAAAA AGTTT 4835

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

GGCTTTCCCT GCGTTATAGG AGGTAACGAT TGCACCGCCT GTTCAAATTT TTCCACACA 60
 CCTGGTGGTG ACTGCGATCG CATCTGTGCG GCGAGTTCAT TGCGTGCTTT CGCAGCAGCA 120
 ACAAGTAACC CAAGCGCGTG CATGAGCGCG GTGTCAAAAC GATTACAACC ACGCTGTGCC 180
 GCAAGCGTTT CAGCGAGGGA CTCCCTCGCG GCACCTTCT TGTACGGTGT CCCAGCATCG 240
 AAGGCACACA CGATCTTGAA TCCTGCTCCC GGGGAAAGCG TCAAACGCGC GCCTACATTC 300

760

CACAGCACAG TATCTTTGTT TTGATGATGC GTCTGATCAG GTCCAGTTCT GTACCCTGcA	360
GAAAGAGTAG CACAACCTGc TGcCTCAAGC CTGaCCTGTT CCCGCCCTT TCGGGCGTAT	420
ACGAGCGTGA ACTCAGTACC AAGGCCATAT TTACTGTGCG GGTCCGCTGG CATGCGCCGA	480
CTATTGGTGC CCTTTCCTTT CACCTTAGAG GTGACAGAAG GAGCACTTTT CCATATACCG	540
TTCGACGAAA AGGAAAGGGC ACAGTTGAAT GTAATGCCAC TGTTCGAAAT ATTCCGTGCC	600
TGATATGCGA TTTTTCGCGC AACCCACCA AACCTGGAG CGTATTGAC GCTCCTTGAC	660
TCATAACTAG TAGTAATAAA GGGGGTCCAC AACTGCGCAA AATTAGAGGG AAAAACGGGA	720
TCTTTTCCTA CAGAAAAAGA GACATCGTAG AGGTGGAGTG TGGCCTCAAG GGAAAAATCG	780
CTTCTTCCTG ACTTTAAGAA AGGAGAACGC GTCGTCATAC TTGGATCCGC AGTTCCCGAC	840
CCTAAAGCAC TTTCAAAATC CACCTTCAAT CCCTTGAGAG AAAGCTCAAC CCATATGGGA	900
TCCTCACCTG AAAAGCTCGT ATACGTGGCG CCTTTCCTGG GCAACAAGGG AAAAGCAAGC	960
TTCCAGCTGC TCTTCGTGCG AAACCCATGT CGTATGCTTT TACCCGCTGT AACTGGAGAG	1020
GCACCTTCTG CATCAAAGAC GACACCCAG CTAAGTTCAG CAGAAcCGCT GAACGCGGCG	1080
GAGGACGAAA AGGCGCGTGA AACCCCGTCC AAAACCGCAC CATGAAGGAA AAACACCCCA	1140
CACCCTAACG CAAAACGCGC ATATACGGAT ATACAGGCGC CCATAGGGCA GCCATTATGA	1200
CCCTTTCATA AACACGATCA ACATTTTTTC CCGTCAGCGG TAATTTTTTT CACTACTTCA	1260
CTCAGTTTTC GCACAAATGG CACAACACCA CGCCCGTTT CTTCTATACG CCTCCCCAGA	1320
AAGTGACTCT TCTTCCCACC CACGAATATC TAATGTACAC CAACATACAT TACAGATACT	1380
GCTAGATCTG ACACATGACA TCGTTGTACT AAATGTGGT GAAAACACGG TACACTACTG	1440
TATGCATGCG TCTAGTGTTA GGCTCGTGCA TTTTATACT TTTACTCCGA GGGCGCGCTA	1500
CCGTATCGCG TCTGCACGCG AGCCCGGCCG TCACCATTTT GGGGAGTACT CGTCTTACTT	1560
GGGGCATTAA CTTAGGCGCG AAGGCGAACT TCGTGCTACC CGTAGCACCG CTTGGGGCAA	1620
CCGGCACTGT GCGAGAGAAC CCAATCATC GCTTCCGTCA TCGCAGACAC GGTTTTAGGA	1680
GTTCCAGTAC TCTCTTTTTT TCGCTGACGC TTTGTCCACC GAAAACTCGG TCGAATCTGC	1740
ATAAAAGCAG CGGTGTGTAT GCAGAAATCC TGTAAAGGAA CCTAGAGTGT GCGCTCCCC	1800
TCGGTTCCTT ATCTGGTGAG GCTTTAGGCG AACTCACGCC CACAGAAAA CAAAGCTTCT	1860
CCGTAGAAGC GACCCTTCGC TTCTACGGCG CATATCTCAC TATTGGAAAA AATCCGACCT	1920
TTTCTAAAAA TTTTGCCAAA TTGTGGCCCC CGTTCATCAC CACACGATAC AAGGAAGCAG	1980
ACACCCAATA CGCCCCTGGC TTTGGGGGTT ATGGAGGGAA GATTGGTTAC CGCGTAGAAG	2040

761

ACGTCGGGAA TTCCGGGCTA GGTTTTGA CT TTGGGTTCCCT TTCCTTCGCT TCAAACGGCG 2100
 ACTGGAGCAC GAGCGGGACT AGCCATAGCA AATATGGGTT TGGTAGTGAC CTCTCTATGG 2160
 TACAAGAGAA ACAAGAAGCT GTTTTAACT GTGGAAC TCG CCGGTAATGC TACCCTCCAG 2220
 GAGGGTTATG CCACGTTAGC TCCAACATTT TCGGGAGCAC CCAACAACAA ACGGGCATCC 2280
 CACGCGCTCT TATGGAGTGT GGGAGGGCGT CTTTCGATCA TGCCTGGTGC AGGATTCCGC 2340
 TTCATTTTAG CTACG 2355

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 718 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

CGGGCGCGTC GAGTAGTCGG GTGCAGGAGG GATCTGCAGC GAATGACCAT TTTCAGGACG 60
 AATCGACCAC GGCAGAACTC CTTTAGTCAG TGGCCGCCAG CGCGTGAAA TAGATGTGGA 120
 TGGATGAGTC TCCCGTCCCT GTGCAAGAGT TTAAACTTTC TCAGTTTGAG GGTCTTTGG 180
 ACCCTCTGCT GTTCTCATC AAAAAGAACG AGCTGAGCAT TTACGATATT CCTATTTGCG 240
 AAATTACTGC TCAGTATCTG CAGTACGTGG ATCAAACCGT CTCGCCCGAT CTCCGTGGTC 300
 TGACGGAGTT TTACGCAATG GCTGCGGTTT TTCTGTACAT TAAAAGCTGC ATGCTCCTCC 360
 CAATGGAAC AGATCTAGAT GGTGAGGATA TCGAGGATCC TCGGCAGTCG CTGGTGAGC 420
 ACCTTATCGA ATATCAAAAA TACAAGCAAC TTGCAAGCT GATGGAGCTG TATGAGTGTG 480
 AAGACATGTG GTGCGTTGAG CGAAAAAGA CGCAGCATCT GTTTTGTCT CCAGCAGAAG 540
 TGCTCTCCT ACACGGTGAC GTTCGTGATT TGCTGATGCT CTTTATTCGG TTAGTGAGAA 600
 AGACGCCTCA GTGGATTATG GATTTGTACG AAGAAGTTTC GGTAAATGAG AAGCTGACAT 660
 TGCTTTCGGA ATTGCTTGGG GTTCGGGGC GGTGTGTATT TACTGAGCTT ATTAAGCA 718

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1959 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

CAACTGTGCA CCGCCGnTA nAATAAGTGG ACTCGCACA CGCCAACAGT GTGGATATGC	60
GTGCGAAATC TGTTCGCGTC TAAATAACGC TCCCTGTTTC TGCACACGTG CAATAATAGC	120
CTTATCAGCA GCTTTTACAA AAAGCCCCTG ATAATCTGCA ACCTCTGCGG TAAAGCGACA	180
CTCTGCATCA AGAGGACACT GAATCGAAAT ACCCGCATCC TTAAATACTT CATAATCATC	240
CTCTCCGAAC GCAGGTGCGA CGTGTACAAC ACCAGTGCCG TCTTCAGTAG AAACAAAATC	300
CGCAACTCGC GTACAGAACA ATCCCTCCTC TGAATCTCCT TGTACAGAAG GATCCGGTCC	360
CTGCCCCAAC ACAGGATAAG AAAAAAGCGG CCGATAGCGA ATCCCCGCAA GATGTTTACC	420
TCTTTTTC CACACTACGC GGTAnAGnAC GAATCTGGAT AaTAGAaTTC AgACGAGAAC	480
GAGCCAAAAT ATAGTGCTCA TCATTTCGCT CTATTAGCAC GTACAAAATT TGTGGTCCCa	540
GCGCAAgcGC TGctTGccGG AgCGTCCAGG CGTGGTGGTC CATGCAAGAA AGCACGTATG	600
CGCAGGAAGT GATGCACTTC CCCAAGACGC TGCCGCACAA AACTCCCGTG CAGCAGGACT	660
ACCAGGAACA ACAGATGTAC ACTCAAAACG CACAGTAATG GCAGGATCAG ACACATCCTG	720
ATATCCACCT AAATTCAATT CGTGATTAGA AAAGcTGTCG CACACCGTGG ACAGTACGGG	780
AGTATTTTAT AACCTTCATA CAGCAGTTTT CGCTGCCATA GTGCGCCACA ACCCACCACA	840
CGGACTCCAT GTAGCAGACA TCCATGGTTT TATAGTCATT ATCGAAGTCA ACCCAGCGCC	900
CAAGACGCGT GAGTGTGCGC TGCCACTCCT TCACATATCG CAGCACACTG GAGCGACATG	960
CCGCGTTAAA CGCGCTGACA CCATACGACT CAACATCACT TTTTGAATTC AAATTGAGCT	1020
CTTGCTCAAT CAGGTGTTCA ATGGGCAGAC CATGACAATC CCATCCAAAG CGACGCGGCA	1080
CGTACGCACC ACGCATTGTC TGATAGCGCG GAATAATATC CTTAATCGTG CTGGGCACAA	1140
AGTGACCAA ATGTGGCAGT CCAGTTGCAA AAGGGGACC GTCAAAGAAA ACATAAGACT	1200
TCCCTGCGC ACGCTGCGCC ACAGACTGCT CAAACACCCG GCGTTCCCGC CAAAAGGCGA	1260
GAATACGCC CTCTGCGCG ACAAATCAA CCTTTGGGTC CACAGGCGTA TACATACAAC	1320
CTCCGTTGCT CAGAATCGCA TAAGGAGCGT AAGGCATTAT ATCATTTTCG TCCTTCCTTT	1380
TCCCATACG TCTTATGACC GGGCCACAC CTTTCCCCAC CTGCACCAGA TACCCACGT	1440
GTGCGTAATC GCACGTGCTC TGCCAATTAC TGCATTGAGT ATTACGTATG CAATAATGCC	1500
CCACATTACA CCTTCTGCAA TCGAATACGA AAAAGGCATC ATCAGAACTG CGACGAAGGC	1560
AGGAAACCCT TCCCACATC TTGAAATCC ACATTGCTTT CCATGCAGCT CGTTACCGTA	1620
ACAGTGCAGG GAGCGATGGT AGCCGACATT GCAGTTGCAG TGAGAACCGC ACCCATCCA	1680

763

TTCCTGTATG CGAGCGTATT GCAGGATTCG CCGCAAGCAC GTAAGCCAGT GCGAGAAACG 1740
 AGGTATCAAA AAATGAGCGC ATTCTTATGC ACATGATTCA AAATGACTAA ACCTCATAGT 1800
 AAATGAGGCG CCACCACGGG ATGCAGAACG CACATCGGTA GAAAAACCAA ACATTTTCTT 1860
 CATCGGAGCC TGTGCATGCA CAAGCTCCCG TCCGTGTTTT GAATCCATGC CCAGAATTAT 1920
 TCCCCCCCCG TGTATGATCA CATTATCAC ATCTCCTAC 1959

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

GTTCCGTCAG CAATTTTCAGT ACGCGGTGTA GGTATTGGGC GAAAAGGTTC TCTCGAAGCA 60
 GGAGACCGAA GACAGCAGGG GAAGAAAAAA GTGGGAGTAC GAGACTGACC CAAGCGTTAC 120
 TAAGATGGTG CGTGCCTCTG CGTCATTTCA GGATTTGGA GAGGACGGGG AGATTAAGTT 180
 TGAAGCAGTC GAGGGTGCAG TAGCGTTGGC GGATCGCGCG AGTTCCTTCA TGGTTGACAG 240
 CGAGGAATAC AAGATTACGA ACGTAAAGGT TCACGGTATG AAGTTTGTCC CAGTTGCGGT 300
 TCCTCATGAA TTAAGGGA TTGCAAAGGA GAAGTTTCAC TTCGTGGAAG ACTCCCGCGT 360
 TACGGAGAAT ACCAACGGCC TTAAGACAAT GCTCACTGAG GATAGTTTTT CTGCACGTAA 420
 GGTAAGCAGC ATGGAGAGCC CGCACGACCT TGTGGTAGAC ACGGTGGGTA CCGGTTACCA 480
 CAGCCGTTTT GTTCGGACG CAGAGGCTTC TGTGAtGCTG AAAAGGGCTG ATGGCTCTGA 540
 GCTGTGCAC CGTGAGTTCA TCGACTATGT GATGAACTTc AACACGGTCC GCTACGACTA 600
 CTACGGTGAT GACGCGAGCT ACACCAATCT GATGGCGAGT TATGGcACCA AGCACTCTGC 660
 TGACTCctGG TGGAAGACAG GAAGAGTGCC CCgCATTTTCG TGTGGTATCA ACTATGGGTT 720
 CG 722

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

CGACGAACAC TCCAACCCCA AATGACACCT TCTCCGGAAG ATTACCCAAC TCAACCAAAT	60
TCCGACAACC TTCAAACAGA CCATCTGCAA GATTCTTCAC TCCAAC TGGA AGACGAACCG	120
ACGCTAATTC CGCGCAGTCT CGAAAGGCC CAGATCCAAT TTCCTTCACG GAATTAGGTA	180
AAACCACGTC TACAAGGCTT CCACACGAAG AAAACACATC CTGCCCAATC ACCTGCAGCG	240
ATCTCGGAAA CACAATTCCCT GCCAGACTCA CACACTTGTG AAATGCATGA TGACGAATCT	300
CTCGCAAGCC GTCCGGAAGT TCAATACGAG CGAGTTTGT ACACCCATGC AAATGGCATG	360
GCTGGCCCAA TnCATGGCGC ACCGAAACTA GGCAACGnAC ACCCGACACC AGCGGAAACG	420
GCACCCATAA AACGCCTTGG TAGCCACCTC GGACAACCGG CAGCCCATCA ATCTGACTGG	480
GCAGTACCAC TGCAATGCCC TTGCCAGAT ACCGCGTGaT AATTATCCCA TCACGGTCGG	540
GAGTCAGACC GTACTGaAAA AACTTCGCCG GCGTCTCTTT CACCTCCgCA CGAGAGACAG	600
CATTCTGCTT CGCagAGACA GGATGCGATA CCAGTACGCC CAAACCGATA CACCACATAG	660
CAAAAACGAC TACTTGTTTT GGCATTATTT CGTCCTCCTT TTAAATCAA CACGAGCCAA	720
AAACTAACAC TCACTTCAAT GGATACGCGT CCCACACAAG CGGTGCGCAA sATGgACGAA	780
CCCCCTTGAA AAGGTCAACT TTAAAAAAT TAAGCACTCC CGCAGATATG CGCACCGTCT	840
CCTACAGGGA CTCCATACCT CGCCGGTAAA ACTAAGACCG TGAGCCCTCA CCAACGCAAG	900
ACAGTTGCAC AGCAGTATGT ACAACTGCGC GCAGACCCGC TCGATAGCAG GTAACTCAAG	960
TGCGCTGAAA cCACTCGAAG ATGCTGCTCA TCAATTGCCA CAGTTCTTAT TCCGCACTGT	1020
TCGAGCAGAT ATTGGCGCAG TGTTTCTGCA GAAAAACCTA TGCAACGGAT ACAGGTAAAA	1080
TAACCAGAAT TACACGGCAA AAACTCAACA CGCAGCGGTA CCGCAGCCCC ACACTCCGTT	1140
GTGCTCCAGG TAAGATCAG TACCACGCGC TGCACCTCTC GGTAGCGTGC ACACATCAAC	1200
TGAAAAAATT GGTGTCTCTC ACGTGCCGTG GCTGAACCCA ACCCAGCAGG CTCATCCTCT	1260
TCAGCCAACA GACGCAGCGC AAGGTTCTGC GTAAGGTGGC AGTACATGAA AGTGATGCAC	1320
GGATCATCCC CATGACTTTT TTTTCAAAG CCTGGTACTG GGAAACACCA AGAGCGAGTC	1380
CTGCACAGCT TAGAAAACCC ACGCGTAATC CCCATGCGTA CTCTTCCTTC GTTAACCCAT	1440
CTATCTTTAA CGCGCAGATA TTCTTGTCG CTTGCGcAAA GcGGGCAAAA AAAGAGCCAC	1500
GCATCAAAGA CGCCTCATAC TCGAACCCGC TATACGCATC GTCACAAATC ACCAGTACCG	1560
CACACCCTGc GTCaTaTTAA GCATACACCA CCTCGTATAA TTGCTGTGCC TCCTCTTCCG	1620
TGGGGGTATA ActGACGGAT TATGGGGGAA ATTCAAAAT AACCTTATCA CCCCATCCGA	1680

765

```

AGCCTGTGCG TCCAGCGCTT CCTTGACGCG GCTCAAATCA AAGCGCCCCG CTCGAAAAAG 1740
AGAAAAGGGA ACCGGcGTTG CCGCACAAACG CACTGCTAGC ATGAGATCAT AATTTTCCCA 1800
GCGCGGTGCC GGCACCAAAA CCGTCTGTCC TGCACCCACA AATAAGTCCA TAGCACAGGA 1860
CAACGCTGCC GTAAGTCCCG GCAACACGAT AGGAAGCGAC ATCTTTGGAA AACTTGCCGC 1920
ACAAGAATGC TCTCCCTGCT CTGCTGCACT CTGCATTGCT GCAACGTCCG GTTCATCCGG 1980
ACACAACACA GGATCACGCG CACACAAACG cCGCGCCCag cGCTCGCGGA GCgCAGGAAT 2040
ACCTGCAGTC GGCGCGTAGG AACTATTTTC AGAAGAAGAA AGATCAGGAA CAAGCGCATG 2100
CAACGTATCA CGAAGCACCG GCACCCCATG ACGCAGAACC ATGCCAACCG CCCCATTCAT 2160
ATCAGGCGCA GCATCCGCGC CTCTGCATTC TGTGCAACAA TCCCGTGGGG AAAATACGCG 2220
CGCAAACCAA GAGGAGATAA CAGCGCGTGC ACCACCGTTC CTCAAGAGC AGCGTTTAAC 2280
GCACGCGCGC CTTCAGAGAG GTCCATGT 2308

```

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

```

CTTTGACCAC TCGGGAAACT CCCCAAACGA ACAAGCCAAC TTAGGGATTG GAACCCTAGA 60
CCTCGAGATT ACAAATCACG CGCTCTAGAC CGACTGAGCT AAGTTGGCGA TGACTACGCG 120
CCCCGGACTG TACGCGCGAA CCCACGGCTT TGTCAAGCCG CTCTCACTGC ACTAAGAAAA 180
ACTACACGCG CAGAACAGCA GAGCACGTAC AATGCGGACT CTATACCTTG AATTCTCCA 240
CCTCATCTGC AAGACTGCTG ATGCTCTGct TGCTACGCTG TGTATCTCA TTAACCTCGT 300
GTAtGCGTTA TTGATCTCGA TGGCACCAGC TGCCATCTCA TTCATACTTC TGGCAATTTT 360
ACTAGTTAAG TCGTCCAAGC GCTGCATCTC GCGTGCAATA ACCTCGCCCC CTTTGAGCAT 420
ATCCGCAGAC CCCTCCTTCA CGTCTAcGGT GCGGGCATTG ATGCTCTTAA TCGCAGCTAG 480
GACtCACGGC TTCCATCCGA CTGCTCTTTC ATCGCCTCTG TCAGCGACCG GCTCATTGTA 540
CGCACCTGAT CGGACAAACG GAAGaTGGTA TCAAAC TGCT CCTCAACCGC TTTGAAGAC 600
GTGGAAAGCG TATCTATTTT CACACTGAGC GTCTTGAGCG TCTCAGTAAT GGTCTTTCCT 660
TGGGTGCTAG ACTCTTCCGC AAGCTTACGG ATCTCATCCG CAACCACCGC AAAACCCTTT 720

```

766

CCTGCCTCGC	CCGCATGCGC	CGCCTCGATA	GCGGCGTTCA	TTGCAAGCAG	GTTCGTCTGA	780
CTTGCAATGT	GCTGAATAAC	ACTGCTCGCC	TCAAGCAAGC	TTCCCGATTG	CTsrcTGaTC	840
TTTTGCGTAA	TACCGCTAGa	GCTAACCAGC	GTGTACGCC	CATCAGCGGT	GGCAATAGCA	900
AGACTGTGCA	CCGCCTCATC	ACTCCGTTCA	AGTGTCTGCG	TAATAGACAC	AATGTTGGCA	960
ACCATTTGCT	CAACTGAGGA	GGAAGACTGT	GCGACGTTCA	CCGCCTGCGT	CTCAATGCTA	1020
CTGTTcAGCC	CCTTAATTGT	CTTGATGATA	CTTCCACCGT	GTCCGTGGCC	TcAnACACCC	1080
CACTCACCTG	CAATTCAACT	CGGTGCTTGA	CACCATCGAT	ATTGGCGGTA	ATCTCGTTTA	1140
CCGCACTGGC	TGTTTCAGTC	ATGTTACTGG	CAAACCTGTC	CCCGATGCGC	CGCATATCGT	1200
CAGAGCTCGA	CCCCACCGTG	GCGATACAAA	GCGAAT			1236

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3856 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

CCTTGGTGTT	GATTTTTTTTA	TATGTGGCGC	nTCGTTTTCG	GTGGTTCTTT	GCGCTTGGAG	60
CGATAGTCGC	GCTCGTGcAT	GATGCGTGCA	TTATGGTGTC	ATTCATGGTG	TGGTTTGGTT	120
TGGAGTTTAA	TCTGCGAGTA	TCGCGCGGAT	TCTGACGATT	ATCGGGTACT	CGATCAACGA	180
CACGGTGGTA	GTTTTTGATC	GGGTGAGACA	GACCATTCTC	CTGGATCCTA	TCGCGTCAGT	240
GACGACAGTA	CTTGACCGAT	CGCAAACAGA	CATGCTCACG	CGCACTGTAG	TGACAACGGt	300
GACGACGCTG	CTTGcAGcGC	TGATGTTGTA	TGTGTTTACC	GAGGGAGGCA	GTCGGGATTT	360
CTCACTCGCG	CTAATGGTGG	GGATGGTCAG	CGGCGTGAC	TCGACCATTT	ACATCGCCGG	420
TGGCTGTATC	GCCCTGATCA	GCCGGGGGAA	GAGCGGAGGT	CAGCTGCTCG	GACTCTGAAA	480
CCCCGCACGC	GCGGCTGTGT	GTAGGAAAGG	AAAGGAGAGA	GGAAGAGAG	GGGACTCGgC	540
GCTGCCGACT	TTGCTATTTT	TTCTTTACAA	TCGTTTTTCT	TTCCCCGCGG	GTGTGcAGGC	600
TGCGCGCTTG	CCTAAGGTGG	AGCCGTTCTT	TTTTGTTCTT	TTCCAGAAAG	TCAAGTGACC	660
TGTTAAAACC	TTGCAGAAAT	TTCTGCATCT	CTTCTTCAAA	CACCACAACC	GCGTGCCGGT	720
CAAACCCGGC	ACCGTCGACG	TTTTTGCTTT	CTACTACCTG	CAGAAATACA	TCTCCGACCC	780
TATTTTCCTT	CACATTGAAA	AAGTAGGTCC	GATTTTCCGC	TTGCACCTCT	GTAGTAAACA	840

GCTCACC GCG TATCCCCATG CTGTACCTTC CTTCTGCTTA TGAAGTCGTA TCCGCACACG 900
AAAGCGCACA GCGATCTGCC TCGCGCACCA TGTCCGCGTG CAGCTGCAAA AGCGCAGyTy 960
CCCCCGCCTC GTCATTACCT TTCAGATCCG CAGAAATTCT AAATATTGGT TCTGTCTTTG 1020
AACC GCGCAT CCACACGAAC GCCACCGCTT CTTGGTGCTC GTTGTA AAAAT TGGATTTTCA 1080
ATCCTCCGTC AGCCGACCGG CTAAATCCC CCGCCGCGTC CTGCTGCTCC CTCCCGCGGT 1140
ACAATATCGG GCGGTACGAA CAAATGCCGA AGCGTTTTTT TAACGTGTCT TTCTCCTGCG 1200
CCCACCTGCG TTCAAATACC CGCTGaTATG CGCTCTTGAG GAGTGCA TGG TCAGTCGTTC 1260
GTATCTGcAA GAGCGCGCGC GTATCGTGCG TTGGTGTAGT CGTG TACGCA GgTAGGCTGG 1320
CAAATAGATC CGATATCGTG AAGGCATGCT GCGCGCGTTC TGTTTGGTGT GAGTGCGCGC 1380
ACCACCAGGC AAAGAGTCCT GGCTGTTTCC CATCCCCCG CAGGAGCAAG AGCTTTAAGA 1440
GTGCAAAAAC AGTATGCAAA GGATCACGTA CTGCCGCCGG ATGGAGAATG CTGCCCCCGT 1500
TTGATCCTTC CCCTAGAATG CGCACGCagT AGCCTTCTTT CCGTAGAAGG TGTGCCTTCT 1560
CAATGAGGTG CGCCTCTCCT ACCTCCGTGC GAAAAACGTG CACGTCTAAG AgCTGCGCGA 1620
TAGCTTCTAC ACGCAGCGAG GTGGGACCAT TGGTAACCAG CGCGATAGGC GCGCGCGGT 1680
GTGGCTGCAT ACGGAGGTTG CGACTGAGTT CACAGATCTC CGACACAACC GAAAGAGCAA 1740
AGACTGCCTG TTCGTGCGGA ATGACAGCGC GATTAAGGGT TTGGTCGTAA TAGACAATAT 1800
TTCCCCGATC TCCGTCACAA TCTGGCACAA AGCCGAAGGc AATGGAGCGT TCTTCTGGGG 1860
ATGAACCTCG CGTGGCTGCC TCGGTCAGTG CCTGCGCGCA CGCGgTAAGA GAGGACCCTT 1920
CAGGA ACTAT GCGATGGCGA ATATCCCCTG GCGTTTTCGGC GATACTAAAA AGGGCGACAC 1980
CGAGTGATTC TAGGAGGCGC CTATCTATGG AAGCTGCACG CGCACTTCCA TTGAAATCAA 2040
TGAGGATAGA CAGGGGTGTT CCCTGTTTCG TG TAGGCGGC ACGCTGCTGG GTAAAGCGAT 2100
GGAAAAAGGC ACGGTGCTCA GTTTCTTTAG GGGAATTTGC GATCACTTCC CTTATGAAGA 2160
GATCATAGCT GTGCAGGCTT TCTTGTTTGT GTGTTTTGTT GTACAGCAGC GGTTCGAGTA 2220
TAGAGGCGTT GAGCGTGGCA CAATGCTCTC GTATTTTCTG GAAAGAGGCG GGCTGTAAAC 2280
ACTGTGCGAC GAAgTCTTCG CTCAGCTGTT GTGCCTGAGT AGGACTGAGC ACGCCGCCGT 2340
CATTTAGGCC AAATTTAAAG CCATTGTATT CGATAGGATT GTGACTTGCG GAGATGTAGA 2400
GGAAAGCGTC GTAGTTCCTC GCGTAGCTTG CAATTTCTGGG TATTGGTCCG ACTCCGACAC 2460
AACGCAGCGA ACAGCCTTCC AGATGGAGGA TAGCGGTGCA GATAGAACTG ATAATCTCTC 2520
CAkTAGGGCG CGAGTCGCGC GCGATGACAA CACGTGGTTT TGGGACCTTT TTTTCAAGA 2580

768

ATCGGGCGTA GCTGAGTGCT ACCTGTGCGC TGAGTACAGC GTCAGCCTTT TGCCTGAGGG 2640
TGACGGTGCG CTCAGGGGTA AAAGCGTAGG GGAAAACCTT GCGCCACCCT GAGGGTGACC 2700
GGGTGAGTGA TAGATGAAGC GCTGCGCaGG CTGCGGCAAG GTGAGGGAGG TGATGAGTGA 2760
GTTGAGCAGG GACATGCGCG GAGGATAGGG CGCGGGTGAA GGAAGTGCAA GGGAGGTGGT 2820
GGTCTTGACA GGATGAAATC AGGTGTGGTC GGGTGTAGGG GCGGGGGAGA GGTAGGAATG 2880
GGAGTAGTGG AATGGGTAGG TGAGTGGATG CACGCGGTGG TGTGGAGCTT TCCGATGGTG 2940
GTGCTGTTGC TGGGGACGGG GTGCTACGTG ACGGTGTGTA TGAAGTTTTT TCCTGTGGTG 3000
CGGCTGTGGT ATGTATTAAG ACAAACTATT GGGGGTCGCG GAGGTAAGAA GGGCGGCAGT 3060
GGTGAGGTGA GTGCGTTCCG TCGGTGTCC CACTgCtTGC AGCGACGTTG GGGTCTGGAA 3120
ATATTGTAGG GGTTCGCACG GCGATTGCGA TTGGGGGGCC TGGGGCGATA TTTTGGATAT 3180
GGGTGACGGG GATATTCGGG ATGGGAACGA AtTCGtGGAA GTGGTGTGG CGGTGTACTA 3240
TCGGCGTCAG ACTGGTGATG GCGTTTTGT GGGGGGGCCG ATGTATTATC TGAAAGACGG 3300
AGTGGGAGTT CCAGGGGCTG GGGTACTTGC GAGTTTGTTC TGCATATTCA GTGTTATCGC 3360
GTCCTTTGGG ATAGGAAATA TGACGCAKCG AAcTCGGTGG CTCTAGTGTT CGAAGATGTG 3420
TTTTGTGTGG ACGTGCGGGT GACCGGGGCA GTGCTGATGG TCTTGGTAGG CTTAGTGAGC 3480
GTGGGTGGGT TAAAAAGTAT CAGTTGGGTG ACTGGGGTAA TGGTGCCTGs GATGGCGATT 3540
TTGTATGTAT GTGTGGGCGT ATGCTGgTGT GTTGCAATAC GCGACAgCTG GTGCCAGTGT 3600
GCTGGGATAT CGTGTCGGG GCGTTTGCCG GGACTGCAGC AGTTGGGGGG TTTGCAGGGA 3660
GTGTGGTGCG TCAAGCGATA GCGGnTAGGT ATTAGCCGGG GGGTAGCGGT GAACGAGGCA 3720
GGGCTTGGA CTGCTCCTAT TGCGCATGCG GCGGCTATTA CAGACCATCC AGTGnCGACA 3780
GGGGCTTGTG GGGTATCTTT GAAGTTATTT GTGGGGACAA TGGTGGTATC TTCGGTGACG 3840
GCATTTGCGA TACTGC 3856

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

CGACCTAGAG CGTAnACTGC TGGAGGGACC GCTCCGTCCA TTATACGGAC GATGGAGGGA 60

AAAGGCAATG TTCTGCCCCG CAGTTGCGTC CGGTGCACGT GGAGGGTCAG TGACGAAAGA 120
AGAAGCAATC GAGGTGGACG GAGTGGTTAA GGAAGCGCTG CCGAACACCA CCTTTAGAGT 180
GCAATTGCAG AATGGGCACG AGATCCTTGC GSTATCTTTCA GGTCGGATGC GCAACACTAC 240
ATCCGTATCG TGCCCCGAGA CTCGGTGAAG GTCGCGCTCT CACCCTACGA CCTCTCCCGC 300
GGCAGAATTA TGTTTTCGTGA GCGTTAGATT CCTCTCTCGC AGgAGAGAGG TGCTTGCTCC 360
TCTTTAGCAG CGGGGTTGCT CATCCTTCAA GGAGGATTGA GAGTCCTGCC CTCAGGGTGT 420
GCACTCCGCG CGCCAGGCAG GACACGCTGA ATGCGATCCC GAAGAAGCCA AATACTAAAA 480
AGAAGCGTAC CCGaATAGAG CCAGGAGGAC GAGCGCCGCT CCCTGAATGA GAAGGCGCGC 540
CCCGTCTTTC CTGGAGCCCG TGC GCGCGGT AGGACCCGCC GGATCGGGCG GAGGTCTGCA 600
CTGCTCCAAT AACTCCACCC ATTTCCAgGA AAACCACCgA AGAAAGTGTA CCATCCCTCG 660
AAGTGTTCGG TTTCCCGCGC GTGCCCTCTC CAGGGACCGT GCGTGTGTGT GTAGCGGGTG 720
CGCGCTCCTG CTTGTGTCGTC CGTACCTGGA GGTCCAAGCG CCAAAGCCCT CTGaGGCGTc 780
GCGTcCTGcA CGcGaGGaCC AAAATGcGcC ACCTGcGcGT TcGGcATcGT aGCGTGCGCG 840
TGATGCACGG TCAGAGAGGA CGGCGTAACt GcGTTGaTCC TTTTAAACTG GTCTCCGcA 900
CACGCGTCGC CCGGATTTTT ATCCGGATGA TACTTAAGCG CCTGCGCGCG AAAAGCTTTC 960
TTAATGTGTT CCTCAGAAGC ATCGGCAGCA ACGCCCAGTA TGGCGTAATG GTCAGGAACA 1020
GTGCGCTCGC TCATCGTTTA CCAATGGTG GTCCCCACGA ACTCTTGCTT GTTCAGGATG 1080
CGCTCCAAAT TCGGTAAGTC ACGCCCTGTT GCGCAAATGA CCTGAATTCC CGACTTTTTT 1140
GCCCGGACAC TAGCGACTGG GTCAAAGGGG ACATGGCTGC CCGGTACCCA CTCCTTGTCG 1200
ACAAGGAGGA GGAAATCATC CCAGGAGAGG GATGTGAGCG CCTTCGCATC CTTGTCTGAA 1260
CGAGGATCCC CCGTGTAACAC ATGCGCAACG TCGGAAAGGT TAATAACCGT CTTTGCAGAA 1320
TAACGCTCTG CAAGGAGCAC AGCGTCGGTG TCGGTGAAA AACC CGGTTT CCAACCAGCA 1380
GCAACGAGCA CCTGACCTGA AAAACGTTT GCCGAGTCG GGTCATACAC GACCGGATTT 1440
GGACAAAGGA TTCCAAAAAG GGATTTGAGC AGCTGCGCGT TCAAACGCGT AgCCATGaTG 1500
CCAATCCAGT CAAGTTCAAC GTGTTGCGCC GTGGCATACA GCTCCCTGTC TTCTTGATTA 1560
TCGCCCTCGT GCGCAGGTTT CGCACAGGCC GGAGAAGACA GGCTCCGGCG TAgcGCACgA 1620
TAGGCGTTTT GATAAGTGCG CGCAGGTGCA CCACCGCCTG AAACGACAAT GAGCTTCCGT 1680
GAGGCGTCTT CGTATAGGTA CCGTTGAACG GAACGAACGA ACGCCCCGAG AAGCTCTATG 1740
TCGGGCGTCT CAGGCGCAAC GATGGAACCT CCAAGTGACA GAACGGTGAC CATGAAACCC 1800

770

TCTCGCCGGC ATCGTAACGC AAAGAGACCC TTTGGATCCA GGCCCTGTGT GTATCTGGCA	1860
TTGCGTCCCA GCGTGCACGG GGCGATGGAG TGTCTACAC GGGCGACACA GACTCCTAGT	1920
TCTTGATTC TGTGCAAAAA CCGACGTAAA AACTGTATCT CCGTAGTCTA GTGAGTGTTT	1980
TCTGTGCATG AGTTGCTCCC GTACGACCGG TGCTTTACGC GCGGTCCCCC TTGTGTTCCG	2040
TTCCGTCTCTG GTGCTTGCGG TGTGGGGTGT TTCCTGCGTA CAAGCCGCCG ATGTGGCGCA	2100
CAATGCGGAT GTACCTTCCC GCTCGCTGAA GGCGCTCGAG CGTTTCCGTT TTTTGTGTA	2160
TCCCAAGCCG CTCGACCTTT CTAGTGACTT TCATGCGAAG GCCTTGAAGG GGGAGGCACT	2220
GGTTCCTAGC CTTTCAAGG GAAAGGTGAC GCTTTTGAAC TTTTGGGCTA CGTGGTGTCC	2280
GGCCTGTCTG GCGGAGATGC CGTCTATGGA TCGCATGCAG GCTCTTATGA GGGGGAATGA	2340
CTTTCAGATT GTCGCGGTCA ACGTTGGTGA CTCGAGAAAA CAGGTGGAAA GTTTTATCGC	2400
GCGTGGAAG CATACTTTC CTATCTATCT TGACGAGGAG GGGAGTTTG GGAGTGTTTT	2460
TGCTTCCCGT GGTCGTCCAA CTACTTATGT TGTGGACAAG GCAGGGCGCA TCGTGGCAGT	2520
GGTTGTCCGG AGTGTGGAGT ATGACCAACC AGAGCTAGTG GCTCTCTTTA AGGAACGGC	2580
GCGTGAAGT TGTCCCCGGC GTTGTGGGT CTTTTTGGC CGGGTTGCTT TCTTTTCTCA	2640
GTCCCTGCGT CCTGCCGCTT ATTCCGGCGT ACGTCTCTTT CATTTCGGGA GAATCGCTCG	2700
GTTCTATCCG GGCGGGGCG GCGCGGCTCC AGGTTTTTCT CAGCAGTGT TTTTTGTAT	2760
TAGGACTGAC GACGGTTTTT GTGTTGTTTT CAATCGTATT TAGCGGAGGG GTGCAGCTTG	2820
CAGGTGCGGG TGTGCTCACT GTGCTCACGC GTGTAGCGGG CGTGGGGGTG ATACTCCTCG	2880
GCTTAAACAC AATCTTCGAC GTGGTTCCGT TTTTGCCTGT GGAAAGGCGT ATGCACACAA	2940
CGGTGCGACG GGTGGGTGTG TTTCTGCGT ATCTTTTTGG GTTGCTGTTC GCAACGGGAT	3000
GGACTCCGTG CGTGGGGCCG ATTCTCTCTT CTCTGTTGTT CTATGCGGCG AGTTCTGGGC	3060
AGCTGCTCCA CGCAGCAGGG CTCTGACCG TGTATGCACT GGGATTGGGA CTTCCCTTCG	3120
TGTTTGCAGG GATCTTTTTT GGACGTGCGG AGCGGGTGT TCGTGGGTA AAGAGTCACA	3180
TGCACGCAGT AAAGCTCGCC TCCGGGATGT TGATCGTCTT TTTCCGACTG CTGATGCTAA	3240
CGTCGGGGTT GCAGGCACTC AGTCGGCTTT TTCTACGGGC AGGATTTCGCG TTAGAGGAAT	3300
ACTCGACGCG GGAATAAACC CCTCTTCGGC AAATAGCGGC ACTTCTTGCG CATGGTTTTT	3360
GTACCAGGGG GTTTGAGCGC GAGCGGCTT GGGGCTGTGC GGGTGGGTAG CCATCACGTA	3420
AATAGTTTTT TGATGCGTGT GAAGGCCCGC GTGACCTCTT CCTCGCTTAT TTTTCCTTCC	3480
GGTGCATGGG CGCGCACCAG GTGTTTGGGA ATTTCTGCTCA GAAAGGGGA GCGGTGCGC	3540

771

```

TCTTCCCTTT TTCCGCCGCG TTTCCTTGTG CGGCAGTGTG TCAGGTACAA CTTCCTCTTTT 3600
GCGCGGGTAA TTGCAACGTA GAAAAGGCGT CGTTCCTTCCT CGATGCTGTG AACCTCTTCT 3660
ATACTTCGTT CGTGTGGAAT GGTTCCTCGCT TCCACGCCGG CGATAAACAC TACGGGAAAT 3720
TCCAGCCCCT TCGACGCATG AATTGTCATG AGCGACACAG CGCCTCTGT TTCTTTTGG 3780
ACGTATATCGC GTGCTAGCAA CGTAACGCGG TTTAGGTAGT CGTACAAGCT TCCGTGTTCT 3840
GAACTCTGTT CCCAGTGTTG GATGGATTCG ACTAAGTGTT CGATTGCAA GAATTTAAAA 3900
CGTGCGGCAT GTTCGTTTTT TTGGAATTCT TGGATGAGGT AATTAAAATA CTGAATGTCT 3960
TCAACAAATT TCGGTACCTT GTACGCAAGA TTTTTCCTCCG AAAGTAGATG GGTACGCGCC 4020
TGGGTAATGA GCTGGAGAAA ATTTTCCACA GCGGTACGAT GTGATTCTTT TAAATCGACT 4080
GCATGTGTTT TATTGATAAT TTGATTCAGT GCATTGAACA CGGAACATTG TTGTGTATTA 4140
GCAATGTCGG AGACTAGATG CAGTGTTTTT TTTCCAATTC CTCGCCTCGG GGTATTAATG 4200
ATGCGTAATA GGTGACATC GTCGTCAGGA TTAGAAATTA CCCGCAGATA ACTGAGCACA 4260
TCCTTTATTT CTTCCTCTG AAAAAAGCTC ATGCCGCTG AGACACGGTA TGGAATATTT 4320
TCTTGCAAAA ATACGTCTTC AATTATGCGC ATAAACTAT TCGTGCGGAG TAGGACTCCA 4380
AAACTACTGA AAGAATAGGA TGCGGTATT TGTCTGCGA GAATCGTGTT TGCAATAAAG 4440
ATTG 4444

```

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5695 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

```

GGACGCAAAC GGCCTTCnCC TTCAAAGGCG CGCTCGATAC GCCGCGTTCA ACCCCATAGC 60
GTTGCCGGTT GCCGCTTCn AGACTTcCCC CttACCGTAC AGTgCACGCG CGCGCGAACy 120
TTCCGCAAaG CAGACAGCGA TACTGTCCCA GACGCAGGCT TCCACCCGTT GGGgTATyTA 180
CACAACCGGG CAAAAGATCA ACAACCGGGT GAGGGGTGTC TACCGCAAAT TCTCGAGAGT 240
GTGCACTTGC CAGCAACAGT ACATTGCGCG CAAATTCAAT GACTGCAATC TGCATCCCCA 300
AGCAAATGCC AAGATAGGGC AGGTCTGCA CACGCGCGTG CGAAACTGCA CAGATCATCC 360
CTTCAATCCC CCGCACGCCA AAGCCACCTG GAATTACCAG CGCATCTGCG TCCGCAAGAG 420

```

772

CGTGCCACAGC	GTCCTGCACG	CTGCAGATTT	CCTCTGCGTC	TATCCAGCGC	ATGTCCACTC	480
GCGCACGATG	GCAAATACCC	GCCGCCGTcA	ACGCTTCGCT	CACGCTCAAA	TACGCGTCCG	540
CAAGCGACAC	ATACTTACCC	ACCAGCGCCA	CCGTAAGCTC	CCGCCGCGGA	TAGTACAGTG	600
CACGGACCAT	TGCGCGCCAC	GCCGTAAGAT	CTGGCTCTGC	CCCCTGCCCT	GCTGCAGGAT	660
GCAGACCACC	GTCTGTACGG	ACCGTCCCCC	CCGCTCCCAA	CACAGCCGAC	TGCGCGCCTC	720
CTGCACCGAG	ATTACGCGCC	AcCTGCCCCC	CGCAGCAGGT	ATCAAAAAGA	CGCAAACGCT	780
CACACAAGAG	CGCTCCCAGC	CCTTCTGCTT	CCAAAAGGAG	CGGCACCTCA	TAGATAGAAC	840
GAGCCGTCAC	GTTCCTGACA	ATAGCACGCC	GCTCAACATT	GCAAAAAAGG	CTCAGCTTTT	900
CGCGCACCGC	ATCCGTGATG	TGACGCTCGC	TGCGGCACAG	GATGACATCC	GGCTGCACAC	960
CAAGTCCTAG	CAGCTCCTTT	ACGCTGTGCT	GTAGCGGCTT	GGTTTTcATT	TCACCACAAC	1020
TGGGTAAGTA	GGGAACATAA	CCCAAATGAA	TAAAAAGACA	GCGCTCCTTC	CCCAGAACAC	1080
GCCTGATTTG	ACGAATCGCC	TCGATGAACG	GAAGCGACTC	TATGTCACCG	ACGGTACCAC	1140
CGATTTCCGT	GATAACCACC	CGAGCCCCCG	TGGTAGCAGC	AGCGGcCGGA	ATTCGCGCcT	1200
GgATTTTCATC	CGTAACGTGA	GGAATAACCT	GTACGGTAGC	ACCTCCGTAT	CCTCCCGCGC	1260
GTTCACGGTC	CAAAATAGCC	CGGTACACGC	TCCCCGCAGT	CGTGCTATTG	AATCTACTTG	1320
AAGGCACGTC	CGTGAAGCGC	TCGTAATGGC	CCAGATCCAG	GTCCGTTTCG	CCGCCATCTT	1380
GCGTGACAAA	CACCTCCCCG	TGCTGATAGG	GATTCATGGT	ACCGGGATCC	CCATTCAGGT	1440
AGGGATCAAA	CTTTTGATTG	ACCACGGATA	TACCCCGCcT	CTTAAGCAAA	AGTCCGATGG	1500
CAcTGCGGCA	ATACCTTGC	CCAGCGAGGA	AACTACACCG	CCTGTAATAA	AGATAAAAGC	1560
CGGATCCATA	CGGCACGAGT	GTAGCGTGTC	CATCGCTTTT	TTAAAAGGGA	GCACCCTGCC	1620
TCTCCCCTGC	GCCTGTAGGG	TGGACTGTCC	CATCGGCTTG	CATCGAACAT	TGCTTTCGAA	1680
TACCATGGGC	CCCATGAACG	CGCGCGCTGC	CCTCGCTCTT	GCCATGGTCT	TCACTTTCCA	1740
GAGGTTGTGC	GCAGAAGAAC	GTTTCGTTAT	CTCCACTGAA	TACTTCGACA	TCATCTACAC	1800
CGAGGCCTCG	ACTGAGTCTG	CGCGTATACT	GGCGAAGCAC	GCTGACCGGT	ACGAAGAACA	1860
AATCAGCCTC	ATGCTCAATC	GGGTTCTCTGA	CAAGAAAAAG	CGCACCACCG	TCGTCCTGTA	1920
TGCCACACA	CAGGATGCAG	GCGGGTCTTT	CTCTTCCAAA	CCGTCAAGGA	AAATAATCAT	1980
CAACGATACG	CGCGTTCCCA	ATCTGGGTTT	AGGCAGTTTT	AAGGATTTCG	TGCTGAGCAT	2040
TTTTTACCAC	GAGcTTACGC	ATAAGATTTC	TCTCGATTTC	TTCATGCCGC	TACTCCCTCC	2100
CCTCTTTACC	GAAGGGGTTG	CCGTCGCCCTT	TGAAAGCAAC	GACGGCACGC	AAGGGCGACT	2160

773

GCACGACCCG CTGACAATGC ATTACTTAAT TCAGAACAAA CTGGAAAACG TCTCCCCCTC	2220
CTGGAGGGAG GTTGCCGAGC TCAGATACAA CTACCCCCAC GGTATGCCCT ACGTGTATGG	2280
GGGAAAATTC ACCGAATACC TGCAGAAAAT ATACGGCAAG GAGCGGTGCG CCCGGCTGTG	2340
GCAGAACTCC TGGCGTCTCT TTATTCGACA CCGTTTTTGG GACGTTTTTC AAAAGAATCT	2400
GGGAACTGCG TGGAATGAGT TCATCGACAG CATTCCAATC CCGGAGAAGG TGGCACAGCC	2460
GCAACTCCTT TCTGAACGGG AAGCGCAGGG TCACTACGGT GCACGCAGCG nTGCGCCGAn	2520
CGGctTCGCC TATTATGACC GTGACCGTCA CGCGGTGCGT TTCCGTGACA AAGCAGGTGG	2580
GGTGCGCAGC CTGTTCTCTC ATGACAACAC GCTGCATCAT CTGAACTTCT CCGAGGACGG	2640
ACGCTATTTC GCAGTATCAG ACACCATTTGA CACGTGGAGC GAGCGCACGC ACCGAGTACG	2700
CGTTTTTGAC ACACACTCAG GCTCGTTCTC GCCGGAGGTG TACACTGGCG CGTCCGAAGC	2760
TTGCTTTGTG GGAACGGGC AGAAAATAGT ATTCGTCCGG GTGCAGGGGC AATACTCGCG	2820
CCTCACGCTC AAGGACCGCA CAGACCTTAC cTTCGAGAAG GTGTTATACG AAGCAGGTCC	2880
TGGTTTGCCA TTCGGTGCGC TGTACGCGCC GGcGTACGCg sTGaTGGCAC CGTCGCCATT	2940
ATTGGCGCAC GCGGTATGGA GCGTAACTTG CTTTTTCATCC CGGTGGACGA CAGGCCAATG	3000
ATGCAGGTTC CGCGCGAGCA GATGCCACAC GCAATGCGGG AACTGCAGTC GCAAAAGATC	3060
aAAGGCTCGT GGACGCTCAC CTTTAGCTGG GCAAATATGA ACATGCTCTC TCGCCTAGGT	3120
TTTTACGACG TGTCCCGCCA TACCTTCAGA CTAATGGACC AGGACGTGTC AGGGGGGGTG	3180
TTTGACCCGG TGGTGACGA GGCACGCTT GCTGCGGTGC ACGAAGAGTC TGCAGCAGAG	3240
GCGACCATAC GCGGTGAAGA GCCGGTTGTG CGTGTGGCCT ACACCGGCAG ACACCGCATG	3300
CACATGAGCC AATACCAGCG GGATGACCsC GCCCTGCGCG AGCGGCGGGT GTCGCTGGTT	3360
CCCTTGCAAC CGGCAGAGGC GGAGGAGCAG TCGCGCCCCG CCACGCTCAT GGTAAACGGA	3420
GAGTTCATAG CAGACGTGCA CGAAGCCGAC CGCGGCAGAC GGTACCGCGC AgCTCAGTGG	3480
ATGTGGCCTC CCACGTTCTC ACCCCGCTTT GTGCCGCCAA ACAGCTTCAG CAGCCTCAAA	3540
GACCTTGGAC ACACCGGACT GGGGGTGAAC ATGAAGTTTG CCGATCCGTT TGGGCTCGTG	3600
GAGGTGAATC TCCAGTCGGT TTCTCATTTT TATCCGTTTT TTACCTCGCT GGGGCTGAAA	3660
AGCTCTTTTT ATGTGGGCAA AACCACGTaG CCCTACGTGC GTATCACGAG ATAGACACCG	3720
GAGGGTTCCG GTACACTAAG CTCGGCGGGG CCTTTGAAAC GCTGACAAAC TTTCTATGC	3780
AGGATGACCG AAACGCGTTT TTTGTGCGAA CTGCCGTGGG GGTAAGTACC TACTCCTGCC	3840
TGTGCGCCAA CGGCGGGGGT AACGGGAATT GCTGCGGCAA CAACGGGGGG CAGCAGTGcT	3900

GCGCCTGCAA	TGGACAGGGC	GCAAACGGAC	CACATTATTA	CAAGAGCCTT	GAAAGCCCCT	3960
TCATTCAAGC	ACAGGTGGAA	ATGGGGTATA	GCTTTTCTCA	GCGTGCAGAG	CGCACGGGAA	4020
CAAAC TG GTT	CGTGGCGGAC	GTCACGGGGG	TGAGCCTGAA	GTTACACGTT	GCAAATAGTT	4080
TTGACACCGG	TAAAACAAAA	GACGCGGTGC	TCGTGCAAAC	GAAAGGGTCA	TTCCGCCTGC	4140
CGGTGGTGCC	CCTACGGGTG	GGCGTCagcG	CGTACGTTGG	GTATAACGCC	GGGTGGCGCG	4200
GGGGCAAAGG	AAACATTCTG	GCGGAGCACC	CAGTGTACGG	CTTTCCCGGT	CCTACGTATT	4260
TACCCAAGCT	CGCAGGGGTT	GGTGGTATGG	AGGGCTCGTG	TAAAAAAGC	AAGAGTGCAG	4320
GGTTCGGCGC	TGAAGCAGTG	CTCACCATCT	TGGACTACGA	CATCAGCATA	TATGATCCCT	4380
ATCTGCCCCG	CTTCTACCGA	AATATTGTTT	GGAACGTAAG	CTGCGAGTAC	GTGCTCAATG	4440
CGCCAGACTT	TTCCTCACCC	AAACACCTGT	GCGTTGCAAG	CACATCACTG	GTTTTGGAGT	4500
TTGACCTGGC	GGATGTAAAA	GTACGGGCCG	GGGTT CAGTA	CGGCTTCCAA	CTTG CAGAGA	4560
CGCAGAGCGC	CACAACCCCC	GGTTTCAGCC	CGATTTTTTC	CATGGCCGTG	TAGGAAGGTT	4620
CCCCCGTGGC	GTGTGCAAAG	CGCGCTACGG	GGGCAGCGCT	TCGGCAAAAC	GCGGGAGCTG	4680
GCTGTCTACG	CTCTGGCAAG	GGTTTTTCTA	TGCATGAAAC	GTCTTACAAA	CCTATCCACC	4740
GGCTGTCCCC	TGACACCGCT	AAAAAATCG	CCGCAGgAGA	AGTCATCGAG	CGGCCCGCCT	4800
CCGTCTGTGC	CGAATTGCTC	GAGAACGCAC	TCGATGCAGG	CGCCACCAAA	ATCCATCTGG	4860
AAATTAACGC	AGGCGGcTGC	GCGCTCATCC	GCGTGAGcgA	TaACGGCCAC	GGCATGTCCC	4920
CCCAGGATTT	GTTGCTATGC	GCTGAAGCAC	ACACCACGAG	CAAAATATCG	TCTGCAGACG	4980
ACTTATTGCA	GcTGCGCACG	TTAGGCTTCC	GGGGAGAAGC	ACTCGCCTCC	ATCGCCGCAG	5040
TCAGCCGCCT	GCACCTTACG	AGCACCCGAT	CAGGGCCCCCT	CGCGTGGCAC	TACCAGCCAA	5100
AGGCTGCAGG	CACTGCACGg	CACGTACCGC	CGGTGCCGCA	GGgCACCGAA	GCAGGCGTGC	5160
TAGAGCCTGC	AAGTCTTGAG	CGAGGCACCG	TCGTACGCGT	CGAGCAGCTT	TTTGAAA ACT	5220
TTCTTGCGCG	CAAACGCTTT	CTCGGACGCC	AAAGCGCAGA	GACCACCCTG	TGCCGCAGCG	5280
CACTCATCGA	CGTCTCCCTC	GCACATCACC	CCGTGGAGTT	TCGCTTCACC	GTCGACGGAA	5340
CGCACAAGCT	CACCCTGCTC	AGTCAGCAAA	CCCGGAAGGA	TCGGTGTCTT	GAAACGCAAA	5400
TGCTCAAAGG	AGATCCTGCG	CTCTCCACA	CCATAGAAGG	AGGTGACTGC	TCGTTTCACT	5460
TTACCTTGT	ACTTTCAGAA	CCCGCCATCT	GCCGCAGAGA	ACGCCGCGGT	ATTTTTACCT	5520
TCGTCAACGG	ACGACGCATT	TTTGATTACG	GTCTTGTCCA	GGCACTTGTG	TTAGGAAGCG	5580
AGGGATACTT	CCCCAATGGC	ACCTTTCCGG	TCGCCTGCCT	TTTCTCACC	GTTAACAGCG	5640

5695

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 659 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

AACTACTCTn	AGTAGGATCC	CCCTACACTn	TATCGCACAC	GGCGCACAGA	CGGAACGGAG	60
CGCCTGTGTT	TCACACATTG	AATTTAAAAA	AGATAACGTC	CCCGTCTTGC	ACCTCGTATT	120
CCTTCCCTC	CTGCCGAACG	CGGTTTGCCT	CCCTCACCTT	TGCCCACTC	CCACAGGACG	180
CAAGATCATC	GAAAGAATAC	GTTTCTGCAC	GAATAAAACC	ACGCTCAAGG	TCGCTGTGGA	240
TCACTCCTGC	CGCGTGCGGT	GCAAnAGnCCC	TGCCCGAATG	GTCCACGCGC	GACACTCCTC	300
AGGCCCCGCG	GTAAAAAAGG	TACGCAACCC	CATCAGGGAA	TACTACTGCGC	GCGCAAnGCG	360
CACGTCCTGA	TTCGCGCAAC	CCTAATTCTT	GCAAAAAGGC	GTTTGTCTCT	GCCACATCAG	420
AAAGCTGCGC	AAGTCTGCTT	CAAATTTTCC	ACACATAACA	ATTGCCTGCG	TGTTATGCAC	480
ACGTGCGTGC	TCTTGCACCG	CGCGCACGAA	ATCATTTCCG	TAnTGCATGC	CGCTTTCGTC	540
TGTATTGCAC	ACGTAnAGGT	GCGGCTTCAT	TGTCAACAAG	CGCATATCGC	GCACCGGTTG	600
CGCTCCTCAT	CCGACACGGG	CGCCATAnAT	GnCGCTTTCC	CATTTCTAAA	TATTCGCGC	659

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

AGnTTCCTCC	GCCTCCTTGC	gCCGGGCTtC	CTCCGCCTCC	TTGCGCCGGG	CTTCCTCCgC	60
CTCCTTGCGC	CGGGCTTCCT	CCGCCTCCTT	GCGCCGGGCT	TCCTCCGCCT	CCTTGCGCCG	120
GGCTTCCTCC	GCCTCCTTGC	GCCGGGCTTC	CTCCGCCTCC	TTGCGCCGGG	CTTCCTCCGC	180
CTCCTTGCGC	CGGGCTTCCT	CCGCCTCCTT	GCGCCGGGCT	TCCTCCGCCT	CCTTGCGCCG	240
GGCTTCCTCC	GCCyCCTTGC	GCTGCAGCCA	CTGCTCAAGC	GCCGCTATCA	TACGCTGCAT	300

776

TCGTAGTGTT GTGAAGCAGT CGGGTTTTGG GACACGTACT TTTTATAGTC AGCCAGTGCG	360
TGTGCATAGG CTTGTCGCTT CATGGCAGTG TTTGCGCGAT TGAGCAAGGC AGGAGGGTAA	420
TCGTGCTTGA GGGCGAGGGC CTGCTCATAC GCATGTTGGG CTTCCCTCGTA GCGATGTTGC	480
ACGAAGTATA CGTTCCCAG ATTGTAGGCG TATAGGTGCG CATATTCCCTG ACTGTGTACT	540
GGTGGGTTTT GCAGCCACTG GATTGCCcTGC GTGTAGCGTC CTGTCGTAG GTACGCCATT	600
CCCAAGTAGA GTGCTGCTTT CGGGTGGGCG GGTTTTTTGCT GTGCTGCTTT GTGAAGTGGA	660
CCGATGGCCT GCTGTGCCTG CTGTAAGGAA AGGAGGCGCT CTCCTTCACG AAAGTGGtCA	720
AAGGCATCCT CTGCCCAG GAAGGACGCA AATGCGAGCG CAAGAAAGGA GAATAAGCGA	780
ACGGATGGAA GGGAGCGTAC GcKtGCGTAG GTGCACGGTG AGGATTTTTG GCACATTTGA	840
CATTCCTTCT AGGGTGCCT ACCATGGGCG GCATGTCCGC GTACATGGCA CTGCTGGCAG	900
CGGCGTTCTC GTCAAGTATC GTCTTTTTGC TCGTTTTTTT GATGAGAGGT TTTTCCATCC	960
CGCGCAGACA ACTTTTGGTG GAAAAAGTT TTCGAGACGG CAAGTACGCG CTGCTATCA	1020
AGCATGCCCA TGCGGTTTTG GCTAAGGATC CCCATAACTG GGCAGTGCGT GTATTGCTCG	1080
GTCGTGCGCA TCTtGCGGAA GGgAAGcGCG ACGTCGCGCT TATGGAGCTG CGCGcTGCCA	1140
GCAGCAGAGC TkCGTTTCGG AAAgTGGtAr ATGAaGtTgA gTTTcGCAAG ACTATTGCAC	1200
AGCTTATCTC CAGTTTGACC AATCGAnGA	1229

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

TTGGGACTAG CGCGTACTCT TACCGTCGGG GTTGTtTCTG CTCTCGCGCG TCCCATTCAA	60
AATAAGGGCA GTATCATCAG AAATATGATT CAGACGGACG CGGCGATCAA TCCTGGGAAT	120
TCTGGTGGTC CGCTTCTGGA TACCCAGGGG CGCATGATAG GCATTAATAC CGTTATTTAC	180
TCTACATCTG GAAGTTCTTC TGGTGTGGC TTTGCGGTGC CAGTAGATAC CgCAAAGCGC	240
ATAGTGTC CG AGCTAATTCTG CTACGGCCGT GTGCGTCGCG GCAAAATCGA TGCCGAACTC	300
GTGCAAGTCA ACGCATCTAT TGCTCACTAC GCGCAsTTaC AGTAGGCAAG GGATTGCTGG	360
TATCACAGGT CAAGCGGGGA AGCCCCGCTG CACAGGCAGG ACTGCGCGGT GGCACGACGG	420

777

CCGTACGCTA TGGACTGGGA CGGAGAGCAG CGGTTATCTA CTTGGGGGGA GACGTCATTA	480
CCGCCATCGA CAACCAGCCT GTAGCGAATC TGAGCGATTA TTACTCGGTG TTGGAGGATA	540
AGAAGCCTGA CGACGAATTC GCGTTACAGT ACTCCGCGGC AGACGGCAGC ATGTGGTAGC	600
CGTGCGGCTC ACAGAACGCT CAGATGAGTA GCGAGGTCCG GCGCCCCGTG CAGGCTGCCT	660
TTTTCACTGG TTACTTCATG ATGCTGCGTG GTCCTCTTTC CTCCTTTTTC CCCTTCTTTT	720
CCTTTCCCTT GTAGGCGGCG TTTTATCTG TCTCTGGTGT CTTCTTTGGA TCCTGTTGCG	780
TGTCAAACGT TTCAAACGAT TGCGCCATTT CCTCTAGCAG CGCGTCAAGA TTTCCTGAT	840
CGAGATACTG CATAACCTGT GAACATTGAG CAGGAGATAG TGCAATGCGC ACCGCAGGgC	900
AGTTGTAACC ATTTGCACCC GGAATCGTGC GGTTTGCAAT GATAAAATAA GGGCGATCAT	960
CAGTGATAAA CTGATACTCA AAGCGCATAG TGGGGGTGGC ATTGTGCGCA GAGCCAAGAA	1020
TACCCAGGT CATCAGCGGA GTAGTTGTCC CAAGTACGC CCGCTACTA CTCTTTTCCC	1080
GCGTGAGyky TTGTGCTTCA TATTCGCCTA AGTACTTCTC AATAGcTTCG CGCAGTGCTG	1140
TACGGTCCTT ACGCTCAAGG TAGAGCGTAA TGCCGTCCAG TAGGAATTTG AACTGCATAA	1200
GCACAGTGTC GATCGGCGGG TCAAACACAA AGGTAAAGTC GCGTGGAGAA ATCGCAGTAC	1260
GCAAGCGGtC GACCGTGTAG GCATTCAGGA CTCCTAATTC CTTAGGAGGG TAGTCGTTG	1320
AAACAGTCAT GTTCGTGCTT GAAGCACAGC AAACCAAGAC CCCCCTACCC AGCAGTGCAC	1380
CCAGAGCGCG ATAnCCTGCG CGACATAACC TGATTCCCCA CTTCCGTAAA GGnAGAGTGG	1440
AGGGAGAAAG CATACAAAT CCTnAGCGTT TCCATGGGGA CGTCAGCGTA CACACAAGCG	1500
nTGTCa	1506

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

TCAGCCTATG GTCTACGGGA ATTATGGGGG AGGCAGCTAC TCGGGTCGGT TTTTCAGTAG	60
GAATATTATA ACTGGAGAGA AGAACTTCA GGGTCAGTAT TTTGAGGAGC GGTTCGACGA	120
ATGCGATGCC GAAGGcAGTG aTGTAATGC GATAAAGCCG GCTTATCTTA AGCAGTTGCA	180
GGATATTGCG TGGAACTGG AGGATCACAG CCGAGAGATT CGGGAGGTTC GCTTTACTAT	240

778

CGAGGCGGGC AGTTTATGGC TTATTGAGCA AAAACCTGTC GAAGCGAAGA GCACAATCTC	300
TTTGGTACGG TTGCTGCTCG ACCTGTACGA GCGCGAGGTG GTGGATGCTG AATACGTGGT	360
CAAGTCGGTA AAACCGGGTC AGCTGAACGA GATTTTGAC CCGGTCATTG ATATGACGAG	420
TGTGACAGGT TTGAAATCCT CGCAGGGGGG GATTATTGGT GTTCCTGGTG CGGCGGTTGG	480
GCGAGTGATC TTTACCCTG ATTCCTCAT CGAGGCGTGG CGTGTGGCGA AGATGGGCGG	540
ACAAGATACA CGGTGSTATCT TGTGTATGCC TGCAACGTAC GCGGGGGACG TTAAGGCAAT	600
TGAGGTGGCA ACTGGTGTTT TTTCTAACGA GGGGGGGTAC TCCGCCACG CTTCGGTTGT	660
TGCCCGTCAG TATGGGAAGA TCTCTTGGT CCGTCCAGAT ATGAAGATTT ATTCGGACAA	720
AGCGGTCGTT GACGGTATGA CTATCAACGA GGGCGATTTT GTAACGCTTA ATGTTCTTCTTA	780
CTACGGGGAA TCCACCCTGT ATATGGGAGC TCGCGAGcTC ATTGAGCCTG ATCCAGAGAC	840
GTCTGGCCTA GTGAGCTTCA TCGAGCTTGC GAAGGGTTTT GTGCGTTTCGT TTCACGTGCG	900
GGCGAACGCG GACAGTCCAC ACGATGCAGA gCTCGCGCTC GCCTTTGGTG CGCAGGGTAT	960
CGGACTGTGT CGTACAGAGC ATATGTTCTT CAAAGAAGAT CGGATAAATG TGTTCGCCCG	1020
TATGATCTTC TCGGAGAATG CTGAGGAGCG GACGGGCAGT CTCAAGCAGT TGCAAAAGAT	1080
GCAGGGAGAG GATTTCTACG GCATCTTCAA GGTAATGCAG GGACATGAAG TGACTATTCTG	1140
CCTTCTGGAT GCTCCTTTGC ACGAGTTTTT GCCGCACGGG GAGAGTGAAG TTAGCAAGTT	1200
TTTGAGATAT CTCGAGAAGG TTTGTGGTAA AGGTCTGTCC CGGGAGGAGT TGCAGGAGCG	1260
GATCTCCATG CTATCTGAGG TGAATCCCAT GCTGGGTAC CGTGGGTGCC GTATTGCGAT	1320
TTCATACCCG GAAATCTACG CCATGCAGGT GCGCGCCGTG TTCGAGGCAG TGTACCGGTT	1380
GCAGAAAGAG AAGATCTCGG TGTACCCAGA GATAATGATC CCCATTGTCA TGAATTGCCG	1440
TGAGTTAAAG CAGATTGTGT ATGGTAAAAA GATTGAGGGG CACGCATACC AGGGTATCGG	1500
CTCGATAGAG GAAGAGGTAC GTCTTGCGCT CAAGGCAAAG GAGGTTGACT ATAAGGTGGG	1560
TGCTATGATT GAGCTGCCTG CAGCTGCGTT GAGTGCAGAC GAGATTGyGC gcTACGngcA	1620
GTTTTTCTCG TTTGGGACTA ATGACTTGAC GCAGACAACG CTTGGACTCT CCAGAGACGA	1680
TTTCAATACG TTTATGCCGG ACTACACGAT GTATGATTTG GTTGACGGAA ACCCCTTTGC	1740
GATACTCGaT GCGCgCGTGC scgAGTTAAT TGAGGTTGCT ATGCaGCGTG GACGCTGGC	1800
ACGGCCGGAT ATTCAGCTAG GTTTGTGTGG GGAGCACGGT TCACGGTCAG AAAATATTCG	1860
TTTTTGTATG GAAGTAGGAC TAGATTACGT TTCGTGTTCT TCTTACTCGG TGCTATCGC	1920
TTTACTTGCA ATTGCACAGG CGGAGATTGA AAACGCAGAA AAGGAAGGCA GGAAGCCTGC	1980

779

ATGGCGGGGA AGGTCTTCCG CGAAGTCAGG CGGTAGGCGC GCTAGGTAAG GTGTCGTTCG	2040
TGCTTGGTGA GCGTCTCTGT GCGTTCCACT AACGGTGCGA GGGATGGCTG CGTCTGCGTG	2100
GTTAGAGGTG TAGCTGGGTG TTTTTTGGAG GTTTTGTGTA CGCGCTGATT GAATACAAGG	2160
GCAAGCAGTA TAAGGTGGAA CGGGGTAGTA GTATCGTTGT AGATAATATC TCCGAAGTTG	2220
CGCCGGGCGG GTGCATCGAT GTGCGTGAGG TGTTGATGAT TGGTGGCGAG GGTTTGACGC	2280
GGATTGGTTC TCCTTATCTT GAAGGAGTGG GTGTGCGCGC GGTGGTGGGG GAATGTTTTTC	2340
GCAGTCGGAA GATTACCGTG TACAAGTATA AGAGCAAGAA GGATTACCAC CGAACTATCG	2400
GTCTACGGCA GTGGTACACT CGCTTGACCG TTAGTGACAT CTTGGGGGTG TAGGCTCTGG	2460
TCCGAGTGTT GCTTGAAGTC GGTGACCGAG GGCAGTTTTT ATCTGCAGTT GCCTCTGGTC	2520
ATGCTGCGCG TGGAACACGA GGCGGTGATG TTGTGTGTGC GGCAGTTAGT GTGCTTTTGC	2580
GCACTGCGGT GCTTGGGCTT GAGCGTTTGG GTCCTCAGAT AGAGGCGGCG GATCGGGGTT	2640
TTCTCTCCTT TCGCGTGGGG GGGTGTCCGG ATTCCGCGTT GGCTCTCTTG TGTTTCACTG	2700
CGGAGTTTCT AGAACGTGGT TTACGTACGT TGATGCAGGA GTATCCCAGT TCGGTGCATC	2760
TTTGCCTGCG GAGGGGAGTG GTGTGTGCGT AgcGTCGCG TTAAGACAAA ACGGGGGGTA	2820
GTATGGCTCG AAAGAGAGGT GGCagTGGAT CTAAGAACGG GCGCGATTCT AATCCGAAGT	2880
ATTTGGGAGT AAAGTTGTTC GGTGGTCAGC ACGCTCGTGC TGGTTCGATT TTGGTGCGCC	2940
AgCGGGGTAC CCGAATTAC CCGGGAGAAA ATGTGGGAAG GGGGAAGGAC GATACGTTGT	3000
TTGCTCTTGC TCCTGGGGTT GTGACCTATC TTCAAAGGAA GGGGAGGCGC CTCGTTTCTG	3060
TGTGCGTGGA AAACCGGCCT TCTTGAGCTT TTATAGAGGG AACCAGGTGC CTCTGTGCT	3120
TTGTGTCTGT GGTGTAAGAA GGGTCAGGGG GTATTTGCGT GTCTGTGGGA TCGTAGGGGG	3180
CGTGACACAGG TTTTGTAGAG AGCATGGCCA GTTTTGTGTA TGAGGTGCTG ATTCGTGTTT	3240
CCTCTGGTCG GGGTGGAAAT GGCTGTGTGG CGTTTCGGCG GGAAAAGTAT GTCCCgCGCG	3300
GCGGCCCCGC GGGGGGCGAT GGAGGGCGCG GCGGGGACGT TGTGTTCCAG GTACGGCGCA	3360
ACATGCGCAC GCTTGTGCAC CTGAGGTATG GACGCGTGT TCGTGCAAAG AATGGGCAGG	3420
ATGGAGAGGG GGCACGCCGC TTTGGTGCAA AGGGGCACGA TTGTGTTATA CCGCTGCCTC	3480
CGGGTTGTCT TTTAAGGGAT GCGCAGACTC ATGAGGTTTT GCACGATTTT GGTGATGCCC	3540
ATGAAGGTTG CGTGACGCTC CTTTCGGGTG GAAGGGGTGG TTGGGGGAAT TATCATTTCC	3600
GTGGCCAGT GCAGCAGGCT CCGCAACGCG CGCATTCTGG GCAGCCGGGG CAGGAACGTG	3660
TGGTGACGCT TGAAGTGCCT ATTGTGGCAG ACGTTGGCTT TGTGGGGCTC CCCAACGCGG	3720

780

GCAAATCTTC	TTTGCTGAAT	TTTTTTACCC	ACGcGCGGTC	GnTtwGcCCC	TTATCCTTTC	3780
ACTACCCGGA	TTCCTTACTT	GGGGGTGCTG	CGTACGGGGG	ATGGGCGCGA	CGTGATCCTG	3840
GCAGATGTCC	CTGGGATTCT	CGAACGCGCC	TCGCAGGGTG	TCGGCTTGGG	GTTGCGCTTT	3900
CTCAAGCACT	TGACCCGCTG	TGCGGGGCTT	GCATTTCTCA	TTGATCTTGC	AGATGAGCGT	3960
GCGCTGCATA	CATACGATTT	GCTTTGCAAG	GAATTGTACG	CTTCTCCTCC	TGTCTTTGAG	4020
ACAAAGGCGC	GCGTGCTCGT	AGGTACCAAG	CTTGATTTGC	CGAATGCGCG	TGAGTGTTTG	4080
CAGCAGCTTc	tGCACAGCAC	CCATCCACTG	AGGTTTGTGG	AGTCTCGGTG	CACAATCGCT	4140
GGGGTTTAGA	TGAATTGCAG	GAGGCTTTTG	TGCGTCTCTC	TGACGCAGGT	GCGGGCgcGT	4200
TGCGTTCCCC	TGTGTGGCGG	AACCAAGCTC	CCAGTTTAT	GTACGCTCAG	CTTGAGGATC	4260
CGGTGTGTCA	GGTGCGTGAT	GATTTTGGGG	CAACGGTGAG	CTTGAGCAGA	AAACGAAAAG	4320
TGCGCGGATG	AAGTTAGCCC	TGTTTGGCGG	TTCTGACGAT	CCTGTTTCATC	TGGGCCACTT	4380
GCTCTTGGCT	GATGCAGTAC	ACCGGCACGC	CGGGTATGAC	CGCGTGCTGT	TTGTGCCTAC	4440
CTTCGTTTCC	CCCTTCAAAG	AAAAGGAAGG	AAGTGCAAGT	GCGCACGATC	GGGTGCGGAT	4500
GCTCCATTTA	GCAATTGGGA	CAACGCCGTA	TTTTTCTGTT	GAAGAGTGTG	AGATTAGGCG	4560
TGGGGGTATT	TCGTATACTG	CCGAGACGGT	GCAGCATGTG	CGGGAAAAGT	ATGGCGCACA	4620
GCTTGAGGGC	AAGCTCGCGC	TGGTATTGGG	GGAAGATGCA	GCGCGCAGTG	TACCGCACTG	4680
GCACGCGTTC	GATTCGTGGA	GTACACACGT	TGATTTtGTC	GTGGGTGCGC	GCCCTGTGAC	4740
GTCAGGCGAT	GGGGGGAACG	TAGAACGCGC	CACACGCACT	CTACAATCGT	TTCCCTTCCC	4800
ATGGGTTTCG	GCGGAGAAAt	TGGcGCTTCC	TATTTCGTCA	ACGTACATAC	GCACCGCAAt	4860
TCAACGGGGG	CgTAgTTGGG	GTTaTCTTgT	ACCTtCCCCA	GTTCGTGAGT	ATATTATCGC	4920
GCGTGGAATC	TACCGkTCGT	GAGCCTCTGC	CTTCTTTCTC	CGGAGTGGAC	GATTCTTCCT	4980
GTTCTTCTCG	TTTTCTTTCT	TTCTTGGAC	AGGCGCAGAT	GCCAGCGTTC	TCTTTTGTGT	5040
CTGCAGATAT	GACGGCGCTG	ATTGCGCGTG	TGGmAcCGTA	CGCGCGCGCA	GTGC'TTTCGC	5100
CACCTAGGTA	TGAGCATTCG	CGTCGTGTAG	CGGAGTTTGG	GTGCATGCTG	GTACGGCGGT	5160
ATGCGTTGGA	AGCGCAGCTT	GAGCCGCACG	TTTATTGCGC	GGGTATTGCG	CACGATATGT	5220
GCCGGGAGCA	TTCGGAAGTG	TTCTTGTTCG	GTGCTGCcTG	CGTGCGATGG	TTTTCCCATT	5280
GATGTAAC TG	AGCGTGGTAC	GCCATTGCTC	TTGCACGGGC	GCGCAGCCGC	GTGTGTGTTA	5340
GCACAGGAAT	TTGGCGTGCA	GGATGAGGTG	TTGTGTCTCG			5380

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13954 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

CACGCTCAAC CGGGAACGAT TCGTGGTGAT TTTGCTTACG CACCACTACT AATATTGTCC	60
ATGCTTCTGA TTCTCCCGAG AGCsCTGCAC GAGAACTAGC GCTCTACTTT TCTGCGCAAG	120
ATTTTGTGTA ATGGCGTGAC GGAATTACG ATTTTTTCTA AAAAGTTTAG GGTCTGCGGT	180
GCGTGTCTT TTTGATACG GTGATCATGT TTCCTCTTGC TGAAGAAAGG TGAGGATCAG	240
GGGAGGGGTT AGGAATCATG GCTTCGATTG CAaTACTCGG TGGAGGGGCA TGGGGCACGG	300
CGCTTGCTGC GTCTCTCACC GTAAACGGTC ACACCGTAAT GCTGTGGGCC CGTCGTAGGC	360
AGACGTGCGA TGCTATCAAT GCACGAAACG AAAATGTTCA GTATCTGCCG GGCATTACGT	420
TGCCCCGAGC CTTGTGTGCC TCTCCCGATA TGGCATATGT CTGTGCCGGC GCGGATCTTA	480
TTGTATTAGC GGTTCCTTCG TGCTATTTGG CTGAAGTAGC TGCGCTTATG AATACCACTC	540
CTCGTTTTCA GAGGTTGCGT ACTGCTGCCG TAGgACAGGA ATATCCCCCT ATTGGTATTT	600
TGACAAAAGG ATTTATTCCG GATCAGGAAG GGATGCCTCA TCTAATTACC GATGCGCTGG	660
GTGCGTTGTT GCCGTCTGGG GCGCACGGGC AGCTCGTGTA TATTTCCGGT CCAAGCCATG	720
CACAGGAGGT AGCGCAGGGA AAGGTGACCG GACTTATTGC AGCGAGCCAA AATCCTATGG	780
CGGCCATTTC GGTGCGGGAA TTGCTGCGCT CGAAGAGGgT GCAGGTGTAT TCCAGTCTTG	840
ATGTTGTGTT GGTGCAAGTG TGTGCAGCGG TAAAAACGT GATTGCCATT GCATTTGGTC	900
TTTTGGATGC GATGGCTGAG CATTCTGAAG CTTTTGGGGA CAATACAGAG TCGATGCTGC	960
TCGAGCGGG CTTGAATGAA ATTCAAACCA TTGGAAAACA GTTGGGTTCT ACACATCCTG	1020
AAACATTAC ATCGCTTGCA GGAATAGGAG ATTTGGATGT GACGTGTCGC AGCGCTATG	1080
GACGCAACCG ACGTTTCGGA CGCGACATAG TGCATAAGGG GATCCTTGAT TCCTTTTCTG	1140
GAATACAGGA TCTCGTGAGT CGTTTGCCCC AAGTAGGGTA TCTGGCGGAA GGGGTAGTTG	1200
CCTGTATGCA TGTGCAGCGC CTGGCTGAGC GGGATCGGTT GAAGGTTCCA ATTTGCGCGG	1260
GACTGTACGC TATTTTAAAT CGGGAAAAGG GTGCTGACAC CTTTATGCAA GAGATTCTTG	1320
GTTGGTAGCA CGGGGGTGTT TTCTTCCGCG CGTCTCTGTG GGGGAAGCGT AAAGAACGAG	1380
TCTAGGAGTG GAAGTGAGAA CTCTTACCCA AATGTTATTT TTGGCCCATATA ATCCGCGTTC	1440

GGACGGAGAG ATATATGCAT ATCATCAAGC GAAATGGCGA ACCGCAACCT TACATGCGCG	1500
AGAAAATAAT TGTGCTATC AGTGCTGCTT TTAGAAGTGT CCAGAATCCT CTGCTCCTG	1560
AAGTTCCTGC TATCATCACA GATCTTGCCG CGGAGGTTGA GCGACAGCTT TTTGAGATGA	1620
ACCGTGCGGG CGTTCCTGTT CACGTGGAAA AGATTCAGGA CTTTGTCGAA AAGACTCTTA	1680
CCAAATACAA TCACAGCGAT GAAGTGAAGA GTTTTATCCT GTACCGTGAC GATCGCACAA	1740
AAAAGCGTAT TGCAAGAGAA CAGATTGCGT GCTGTTTTAC TGACTCTTCA GTGCTCGGTG	1800
TACTGAAAGA AATCCAACAA GACTTTCCGT TTCCTGAGTA CAGTCTCGAT GCACTCGCCA	1860
GTAAGTTCCT GCTCTTTAAA AAAGAAGTTA CGGACGAGCG TCGGAGTATG CAACTGCTTA	1920
TTAAGGCAGC GGTGGAAGT ACTGCCAAG AGGCTCCCA GTGGGAGCTT AtTGcTGCGC	1980
GCTTGCTTAT GCTCGACTTT TCACTCGCGC TAGGAACATC TTTGGAAAAG TTAAATATTC	2040
ACTCCTTCTA CGAGAAAATA ACTTATCTTG AAGAGGCCGG TCTATATGGG GTGTACATCC	2100
GCACGCACTA TAGTCGGGCA GAAATTGAGG AAGCTGCCAC GTATCTTGAG TGTAGTCGCG	2160
ATAAATTGTT TACGTACAGC AGTCTGGATA TGATTCTGCG TCGCTATGTG ATCAGAACGC	2220
GTGCGCATGT ACCTCTTGAA ACTCCTCAGG AGATGTTTCT CGGTATTGCA CTGCATCTAG	2280
CGATGAATGA AACCCAAGAT CGTATGCAAT GGGTAAAACG CTTTATACA GTCCTCAGCA	2340
AGTTGCAGGT TACGGTCGCA ACACCTACGC TTTCAAACGC GCGCAAACCT TTTTCATCAAC	2400
TTTCCTCGTG TTTTCGTTGAT ACGGTGCCAG ATTGCTCGA CGGTATCTAC CGCAGCATCG	2460
ACAATTTTTT CCAGGTATCT AAGTTTGGGG GAGGGATGGG GCTGTACTTT GGAAAAGTGC	2520
GTGCGGTAGG CGTCCCAT TCGGGGTTCC AGGGTGCTGC AGGTGGTATT CTCCGTGGA	2580
TTAAGCTCGC CAATGATACT GCAGTTGCAG TAGATCAACT AGGAGTACGC CAAGGCTCGG	2640
TGGCAGTGTA TTTGGATGTA TGGCACAAGG ATATTCCGGA ATTTTGTCAA TTACGGACTA	2700
ATAATGGGGA TGACCGCATG AAAGCACATG ACGTATTTCC TGCGGTCTGT TATCCAGATT	2760
TGTTCTGGAA GACAGTACGC GATAATTTGG GGGCGTCGTG GTATTTAATG TGTCCGCATG	2820
AGATTCTTAC GGTGAAAGGC TATGCTTTGG AGGATTTTTA TGCGGAGGAA TGGGAGAAGC	2880
GCTACTGGGA TTGTGTAAAG GATGCGCGTA TCTCTAAGAG GACCATTCCG ATTAAGGAGT	2940
TGGTGCGCTT GGTGCTAAAA TCTGTGGTGG AAACCGGTAC TCCCTTTGCG TTTTACCGAG	3000
ATCATGCAAA CCGTGCAAAT CCCAATGGGC ATCGGGGAAT TATTTACTGT TCTAATTTGT	3060
GTAATGAAAT TGCGCAGAAC ATGAGCGCTA TTAATTTAGT AAGCGTAAAA ATCACCAGG	3120
TTGATGGACA AAAGGTAGTG GTGCAGACAA CGCGCCGGG GGATTTTGTT GTATGTAACC	3180

783

TCGCGTCGTT	GGTGCTGAGC	AATATTGACC	TTTCAGATGA	TAAGGAGTTG	CGCGAGGTAG	3240
TGCGTGTGGC	GGTACGTGCA	TTAGACAACG	TGATCGATT	GACATATTAT	CCGGTTCCCT	3300
ATGCACAGGT	AACCAATGCG	TATTATCGTG	CTATTGGTTT	AGGTGTTTCA	GGCTACCATC	3360
ACGTGCTTGC	CCAGCAAGGA	ATCGATTGGG	AAAGTGATGA	ACATCTTGCA	TTTGCGGACA	3420
GAATATTTGA	GCGCATTAAC	CGTGCCGCAA	TTGAAGCGAG	TATGACAATC	GCGCGCGAGA	3480
AGGGTGCGTA	TGGGTGTTTC	ACTGGGAGCG	ATTGGTGTAC	CGGTGCGTAT	TTTCGCAAAC	3540
GCGGCTATGT	CTCTGAAGAC	TGGCAACGTT	TGCAGCGTGA	GGTAGCAACA	CATGGGATGC	3600
GCAACGGTTA	CTTACTTGCA	GTCGCGCCAA	CTAGTTCTAC	GTCTATCATT	GCAGGGACCA	3660
CTGCGGGTGT	AGATCCTATT	ATGAAGCAGT	ATTTCTCTGA	GGAAAAGAAA	GGCATGCTAA	3720
TGCCACGCGT	AgCTCCTTCT	CTTTCGCAGA	AGACCTGTCC	ACTGTATAAA	AGTGCACACG	3780
CAGTGGAGCA	GCGTTGGAGT	ATCCGTGCTG	CGGGTCTGCG	GCAACGACAT	ATTGACCAGG	3840
CACAGTCAGT	GAATCTGTAC	ATTACAACGG	ACTTTACACT	GAAGCAGGTT	CTAGATTTGT	3900
ACGTGTATGC	GTGGGAAGTA	GGAATGAAGT	CACTATATAC	GTACGAAGCC	AGTCGCTCGA	3960
AATAGATTTG	TGTGGGTATT	GTGCCTCGTA	GGAGCGTGCT	TGCATAACAC	TGTCCACTGT	4020
GTAGGCTTTC	TTTGTGACGT	TGCGTACGCT	TCAAGCCGGT	GTGGCGGTCA	GTATCGCTCT	4080
GGATCGTGTG	TGCTTTTCT	GTTATAACGG	GGCGGTGGCA	CACTGTgTAG	TAGAAGCTGC	4140
CGAAGATATT	TTGGACCGGC	GTTTTTCTGT	ATTGGATAAG	GGTTTCGTGC	GTTTGATAGA	4200
TTACCTGGGA	GGGGATGCAC	GCATTGTGCA	GGCAGCGCGT	GTTTCTTACG	GTGCGGGGAC	4260
TAGGACTGCG	CGTGACGATG	CGGCGCTTAT	CGATTTTCTT	TTACGCAATA	AGCATACGTC	4320
TCCTTTTGAG	CAGGTGGTCC	TTACCTTCCA	TGTACGTGCA	CCGATTTTTG	TCGCGCGTCA	4380
GTGGATGCGG	CATCGCACTG	CTCGCATCAG	TGAGGTGTCT	AGTCGTTATT	CGCTTCTTAG	4440
TCATGACTGT	TATGTTCCGC	AGGAAACTTC	AGTTGCAGTT	CAGTCCACGC	GTAACAAGCA	4500
GGGCCGCGCG	TCCGAAGGTA	TCTCTCCTGA	ACAGCAGCAG	GAAGTGCGGG	CAGCGTTTGA	4560
AGCTCAGCAG	AAAGCGGCGT	GTGCCGCTTA	CGACGCATTG	ATTCAAAAGA	ACATCGCGCG	4620
GGAnCTAGCG	CGTATTAAACG	TGCCgCTTTC	GCTTTACACC	GAGTGGTATT	GGCAGATTGA	4680
TTTACACAAT	CTTTTTCATT	TTTTGCGTTT	ACGTGCGAGC	GCTCATGCGC	AAGCAGAGAT	4740
TCGTGCGTAT	GCAGAGGTAA	TCATTGAAAT	TACCCGTGCA	GTTGCGCCGT	GCGCTACCGC	4800
CTCTTTTGAA	AATCATGAAA	AAGATGGGGT	GCAGTTTTCA	GGGCGGGAGT	TTGctGCGCT	4860
TAAGGCCTTA	CTGGCTGGAG	AGGGTCTCTC	CCTTGAGGGG	AAGGAACGTG	CGCGCTTTGA	4920

AGAAAAATTA CGCTCTGGCC TGCAGCAGTA GAAGTCTATA GTGCGCTCGT CTGTGTGAGC	4980
AGCAAGAGTA TTGCCTTTCT GTGTCTTAAA AAGGTGAATG TGGTCATAGG TATGCTGAKG	5040
AAAAGGAGAG CGGTCAGTTA TGGGGATTGA GTACTCAGCG AGTAGCATT A CTGTATTGGA	5100
AGGTCTTGAA GCGGTACCAA GCGTCCGGGG ATGTATATCG GCTCTACCGG TCCTAATGGA	5160
TTGCACCATC TGGTGTACGA GGTGGTGGAT AACTGTATCG ATGAAGCCAT GGCTGGGTAC	5220
TGTGATCGTA TCACCGTGGT GCTCGAACAA GGAAACGTCG TGGTGTGTTGA AGACAACGGG	5280
CGAGGTATTc CTGTTGACGT GCACCCTCAT GAGGGGGTTA GTGCGCTTGA GGTGTACTT	5340
ACTAAGTTAC ATGCGGGGGG GAAGTTTGAC AAGAAATCGT ATAAGGTGTC GGGTGGACTC	5400
CACGGAGTTG GAGTTTctGT GGTCAACGCG CTGTGCTTGT GGGTAGAAGT GACAGTGTAT	5460
CGTGATGGTG CTGAGTATTA TCAGAAGTTT AATGTGGGGA TGCCGCTTGC TCCAGTAGAG	5520
AAGCGGGGAG TGTCGGAAAA ACGTGGcACT ATTATCCGCT GGCAGGCGGA CCCATCCATT	5580
TTCAAAGAAA CGGTGGCCTA TGATTTTGAC GTACTCCTGA CGCGTTTGC TGAAC TTGCT	5640
TTTTTGAATA GCACGGTAGT TATTCAGTTG CGTGATGAGC GGTGGCGAC CGCTAAACAG	5700
GTTGAATTTG CGTTCGAAGG AGGTATTCGT CATTTTGTCA GTTATTTAAA CCGCGGTAAA	5760
TCAGTTGTGC CCgAACGTCC TCTGTACATT GAGGGATCGA AGTCGGATGT TTTAGTGGA	5820
GTTCGCTTGC AATATCACGA TGGTTATACG GAAAACGTGC AGTCATTTGT CAATGATATT	5880
AATACCCGTG AGGGGGGCAC GCATCTTGAA GGATTTAAGT CGGCAC TTAC GCGTGTGGCG	5940
AACGATTTTT TGAAAAAAG TCCAAAGCTT GCAAAGAAGA TAGAAAGGGA AGAAAAGCTC	6000
GTTGGGGAAG ATGTGCGTGC TGGATTGACA GTGGTGCTTT CTGTGAAAAT TCCTGAACCC	6060
CAGTTTGAAG GGCAGACAAA GACGAAGTTG GGAAACACTG AGGTGCGGGG TATTGTTGAT	6120
TCTTTGGTGG GGGAGCGTCT GACGCTCTAT TTTGAGCAAA ATCCAGGTGT GCTTACAAAG	6180
ATTCTTGAAA AGAGCATTGC AGAGGCGCAG GCGCGTCTTG CAGCACGTCG TgCAAAGGAA	6240
rcTGCGCGCA GAAAAAGTGG AATGGATAGT TTTGGGTTGC CGGGAAAGTT GGCCGACTGT	6300
TCGCTCAAGG ATCCGGCGAA GTGCGAAgTA TATATTGTGG AAGGGGATTC TGCAGGAGGT	6360
TCGGCGAAAA AAGGACGGGA CAGCAAGACA CAGGCCATTT TGCCTTTGTG GGGGAAGATG	6420
CTGAACGTGG AAAAGACACG TTTGGATAAG GTCTTGCATA ACGAAAAATT ACAGCCAATT	6480
ATCGCAACGC TCGGTACAGG TGTGGCAAG GATTTTGATT TAACAAGGAT TCGCTATCAT	6540
AAAGTGATCA TCATGGCGGA TGCGGACGTG GATGGCTCTC ACATCCGTAC GCTTCTTTTA	6600
ACGTTCTTCT TTCGATACCT GCCGCAAATA ATTGAAGCTG GTTACGTATA TCTTGCGATG	6660

CCGCCTTTGT ATCGCATTGC GTGGAGTAAA AAGGAACGTGT ATGTGTATAG CGACACAGAG 6720
CGTGACGAAG CGCTAGAAAG TATCGGTAAA AAAAGTGGTG TCGCTGTGCA GCGTTATAAA 6780
GGTCTGGGGG AAATGGATGG CACTCAGCTT TGGGAGACAA CTATGAATCC AGTGCCTCGC 6840
AAGATGATGC aGGTGGTGCT CTCAGATGCG GTGGAAGCAG ACCGGGTGTT TAGTACTCTC 6900
ATGGGTGAAG ATGTGCAACC GCGCCGTAAG TTTATTGAAG AGAATGCAAT ATATGCGCGT 6960
TTGGACGTAT GAATGTTTTG TGCATTTGTA TTCCATGTG AGTGGTGCCG TCTGACAGGG 7020
GGAAGGATCA GTGGCGTATC AAGTGACGGC AACACGGTAT CGGCCGCAAC GTTTTCAGCA 7080
CGTGTTGGGT CAGAAGTTTG TAGTGGCAAC ACTGCAAAA TCTCTTGAGG AGAACAAAGT 7140
TTCTCCTGCG TATTTGTTTT CCGGCCACA TGGGTGTGGT AAGACCAGCT GTGCGCGTAT 7200
CCTTGCAAAG GCATTGAATT GTGTGCAAAG AGAAGCGTCT GAACCGTGTG GAGAGTGTCC 7260
GTCTTGTAGA GAGATTGCCA CCGGTACTAA TTTAAATGTT ATCGAAATTG ACGGTGCGTC 7320
ACACACAGGG GTGGGCGACG TACGTCAGAT TAAGGAAGAG ATTCTCTTTC CACCTCATGG 7380
GACGCGTTAC AAGGTTTTTA TTATTGATGA GGTGCATATG CTTTCAAACA GTGCCTTTAA 7440
TGCACGTGTG AAGACAATCG AAGAGCCTCC GCCGTATGTG GTATTTATCT TTGCAACAAC 7500
GGAGGTGCAC AGGATTCTCG CAACGGTAAA AAGTCGCTGT CAACAATTTC ATTTTCGTTT 7560
GGTAGATACT CAGACGCTTG TTTGTGCGTT GGCGCAAGCT GCCCAGCAGA TGCAGATTGC 7620
AGTTGAAGAC GGAGTACTGT CTTGGATTGC GCGTGAGTCA GCCGGTAGCA TGCAGACGC 7680
ATATACTTTG TTCGATCAAA CCGTGGTGTC TTGCGCAGGG CCGGTAACAC TTGAGAACAT 7740
TCAAAAAAAA CTCGGGCTAA TGA CTGACGA CTCACTTGCA GCACTGTTTT CACATTGCTG 7800
CCGCAAAGAT GCTCGCGCCG CCTTGGAATT GGTAGATGCT TTGGTAAGTT CTGGTGTCTC 7860
CGTTGAACAG TGCCTAATCG ACTGTGTCCG CTATGCGCGT GCACTGTTGC TTTTCACGCA 7920
GGgAATTACA AATGAGTCAC TGGTAGGAAT AGCGGCAAAC CAAGTGCTG AGTACGTGCG 7980
TACCACATGG AATGCGTCGC AGATTGAGCG GGCGCTTGGa CTGTTACTGC AACTGTTTCG 8040
CGACATTCTG TTTTCAGTAG ATCCGCGGTA TGAATTGGAG CTCGCAATTT CGCGTTTAGs 8100
tGGTTGAGTG AGTATGTCTC AATTCAAGAA GTACGCGTTG CATTGGATAG TGTGCAGCAG 8160
ATACTGGACA CGCATGCAGT TCCCGGGGTG TGTCTGCGT CTGTAGGTTT GGACGATGGG 8220
GAAACAGGTG TCGTCTCCCC ACACGGTATA CGTCCCCCTA TGTCAACATC AGTATGTACC 8280
GTGCGTGCGT TACAAGATGC CTTGGTAGAA AAGTTGCGCG CGTCACACCA GATGTTGGca 8340
ACAGCGCTTG GTTCTTCATA TTCTTGGCGC GAGGAAGATA CTTCTGTGTG CATGTGCGTA 8400

786

CGCAgCATTa	TGAGCGCAGg	TTATCTCTCA	GCACGCGTCG	CTGCTCAAGG	AGTATGCGTC	8460
AGAATTACTG	GGACGGGAGG	TATGCGTTTCG	CGTACTTCTG	GATTCCGGTGC	CTTCGTCAAA	8520
AGTCGCGCCC	TCCCATCTTC	CTCAGAGTCC	TGcCCCATCT	GCTCTCTTTA	CAACTTCTTg	8580
CTTAcTCTGG	GgCAGGAGTG	TGATAgGGTG	AtGGAGATCT	GCCTGCACAG	tGaAGCTTCT	8640
CTGTGATTGT	GTGCAAGGGC	ACGTGGTGCG	TGTGTATGAA	GGTACTGCAC	GGTGTGTACC	8700
TGGGGAGGGG	AAAATAGCAG	GGGCTGTGCG	TACTCCGTAT	TGAgTAGCGA	CAGACGGGTA	8760
GGAAGAGTGC	GAAAGCTGTC	AGTTCAATAT	GGGGATTTTG	TACCAGGGGA	TGTGTGATGA	8820
TACCGGCGAT	TGAAGAAGTA	GTGGAGCATT	TATCTCGTCT	CCCGGGTATT	GGAGTAAAGC	8880
TGGCGACGCG	CCTTGCCTAT	CACCTTTTGA	AACGTGACCC	CGCTGAAGCG	CAGGTTCTTG	8940
CGCGCGGGAT	TGCGTGTTTG	CATGAGCGCG	TATATCGGTG	TGTGTGCTGC	GGTGCTTTCT	9000
GTGAGGGGAG	GACCTGCGCG	TTGTGCACGG	ATGCGTCTCG	GGACCGAGGC	ATCATTTGTG	9060
TAGTGGAGCG	TGCGCAGGAC	GTGGAAATGA	TGGCGGGTGT	GGGGGAGTAT	CGGGGTTTAT	9120
TCCACGTGTT	AGGAGGAGTC	ATTGCACCGC	TTGAGGGGGT	CGGTCCTGAC	CAGCTCCGTA	9180
TTGCGGCGTT	GCTGAAACGG	TTGCAAGAGA	GTTCAGTACG	GGAAGTTATT	CTGGCGTTGA	9240
ATCCCACCGT	GGAAGGGGAT	ACCACCGCCT	TGTATGTGCA	AAAAATCCTT	GCAAACTTTC	9300
CGGTAATAGT	AACGCGTCTA	GcgTCTGGTA	TCCCCGTAGG	nGGGGACTTA	GAATATATCG	9360
ACCGAACGAC	ATTGGCGCAC	AGCCTGCGTG	GGCGCCGGCC	ACTTGATTGC	TCGGAGGCTT	9420
AGAGCATGAT	CTCTACCGCA	GTGACTACTG	CCATATGTGT	ACCCGGTGGA	CGCTGCGGAT	9480
AAAGAACACG	CTTGCGGTGT	TCAGCAAGAA	GAGTCCAACG	ATACAGGCGC	TCCACGTGAG	9540
TCCGTGTGTG	AGCAATCGGT	AACCTGCAAT	CACAAAAGGT	AATGCTGCCG	CCGCGATGTA	9600
GTAATGGGAG	ATTTGCAACG	TGTGGCCGAG	CACCCCGTAA	GAAAGTGCGC	TGAGGACTGC	9660
CGTTGTCCAG	AAAAACCACC	GGTGCCACGC	GTGACTCCCG	TAGTAGAACG	TGAAGTTCCCT	9720
CTGTGGGGTC	ACCAGGATCC	GTGTTTTTCT	GTGGGCGGAs	TGCGCACTTT	GAGCGTTTTT	9780
TCTTCACCAG	TACTATCTAT	GATAGATCCG	GATTCTGAGA	TCGGcTGTGC	CAGCAGTATA	9840
GCTCCCTGTG	TGCTCTGTGA	GGGACGATAT	GCGTGATATAG	TGTGTATCGT	AGTGTATCGG	9900
CTAATAAGAA	ACGCCACCGT	GCACAGCACA	AAGACAACGG	CCCCTTCTCTG	TCGTGTGAGT	9960
GTCTTTTTTCG	CAAAAATGCC	ACTTGCAAAG	AGAGCAAGCA	GTGCCAGACT	CCGGAAGAAC	10020
ATGACGATTT	GCATGGGAAC	ATTCCCTGCG	TATGTGGTAA	GCGTGCCTGT	GTAGAGTATG	10080
GGGAGGAAAA	GACGGACTCC	TTCGAAGTTG	AGTGCGCACA	GAAAAAGAGA	AAAATAGGAT	10140

ATCTCGACCG	CATGTGTTTT	TTCGAAGCGA	CGAAGGAGGT	AAGTAAGCAA	GAGTGGTGCA	10200
GAAAGACCCn	TACCGAGGAT	TGCCACCAAG	GTACTGCTAT	TTGAGGGTGC	GGTGGACACC	10260
GCAGCAAGCG	AGCGAGCAGC	TGCTTCCGGT	AGCAAGAAAG	TGAGCACATG	CATGAACGCA	10320
CGGCCAGTGG	TGTGTAACAG	GGGAGGAACG	CGCGCAACGG	CAAGTTGTGG	GAGTGAACCA	10380
CCAGATAGCA	CGAACGCGGC	CTGTAAAAGG	GAAATGCTGC	ACAGCAGGGC	GGAAAGTACG	10440
ATGGAGAACG	CGACGACTTT	GTTCGTCCA	GCGATGGTCA	CCGGGCCATT	GTAGGCGGTG	10500
CATGCGTGTT	ATGTAAAGTT	GTGCTGCGAT	CAGGAGTCTT	CTTAAGGAGA	TTGGCGAAAG	10560
GTGCCGAAGC	TGCGGGCGCG	GAGGACGTAT	GGGTAGAACA	GGATGTGTGG	GTAATCGATG	10620
CAAACGGATA	GGTACTGTGC	GTGCGCGTGG	CGAGAAGCAA	AGGAGAATAG	CATGGGTGTG	10680
CTATCTGGCA	GCGGTGTTTT	TGACGTTATG	TACGAAGTCT	GCCATGGCGG	GAGATATCGC	10740
GACCTTTGTG	AATTTGGGAT	TTTCTGCGCA	CGGAAAGACA	TTTGCCTTTG	GACAGCACGG	10800
GGTAACTGAT	GGTTGTATC	aGGCGTATGC	GGATATCTAT	GTGGTGGACG	TAGAATCAAA	10860
CCGTTTTGTG	CAGGGAGGGG	TAGTGCGCAC	AACGCCGACG	CGAGAAACAA	AAGGCAAACG	10920
AAGCATGGAT	GTCTTTCTTG	CGTTGCAGAA	CCGCGCGCAA	TCTCTCTTGC	AACGTGCAGA	10980
TATTTCTGCG	CTGCGTTTGG	GGCGTACTCT	GTACGTGCAG	GCTGAGGATC	GGATGGGGGA	11040
AGAGACGCTA	CTGTTTCGAG	ATTTTAAAAC	GAATGTAGAA	TATGTGGTGG	TTATGCATGT	11100
AGAACGGACA	ACAGAGCTGG	GTGTGTCGTT	CTATTTGACG	GTGAAATGA	CAAGACCGAA	11160
TGGAAGCAAA	GTTTCGCGTG	TGGTGGGGCA	GCGCGGCTAT	GTGCGACCGG	GGGTGAAAAA	11220
TTACGCCTTA	AAAAAAGTAC	TTATTAATGA	GCAGCAGGAC	GCTTTGATTT	TTGTTGTTGA	11280
AAAGCACGGA	TATGCCCCtG	ATGGAGCATC	AGTTCGGTAC	ATGGTAGAGG	CGTGTCTCT	11340
GTAACGGTTA	TGGGTTCTTG	CAATCGTACG	AGGGTGGGGT	ATGGCTTACG	TGTGATATAA	11400
TGGGCGTTAG	CCTATTTTTG	GTGAGGGAGC	ATGTCGTCAT	GTGGGATCTG	CATCGTGCTT	11460
TATGCGCAGG	GTTGTTGAGT	GTGCTGCTCT	ACGCGGGCTG	TTCTTCTGCG	CGGGACTTTG	11520
TACACGTTAT	GAAAAC TGCG	GGCAATGAAG	TGGCGCTTGT	GCATTACGCG	TTGCAAGGTG	11580
ATTGCATTGT	GTTTGGTTTT	CGCGGTGAGG	TATCTGATGT	AGTTGCGCGC	GTATATCGCG	11640
CAGAGGGTGT	TGTTTCAGAG	GAAATGAGCG	ATGAGCTGTT	GCAGTCCTTT	ACAGACGAAA	11700
TCCCCCTCTGC	ACTTTCACGC	ATTGCGGTGC	CTGCAGCGTA	TCAGGAGTCT	GTGGATGCAG	11760
CCCGTGAGCG	CCTTTCGTTT	TTGCGAGTGC	GCTTTTTTACA	AAAGCCGCAC	GTGGGGCAGC	11820
AGGTGGTATT	GCGTGGTAGT	GCGCAGGACG	TGGCGCACCA	GAAGCATGAT	TTTGTGCTTC	11880

CTTTTGAGGG GATAAATACA CAGCCTGCGC GTTTAGAAAT CAGCGAAGTC CGTCCCCTTT	11940
ATGGGAATAA ACGCTCGGAA TTTGTGGAAT TGCTTGTCGT GGAATCCGGT AATTTGCTGG	12000
GAATTACTAT CACAAATGTA GGTGGCAAGG GGAATCGCTG CGACTATCAT TTTCTGCAG	12060
CCCAGGTGCG GGTAGGAGAG CGTGTGGTAT TACATTGGCG TAACAGGATC CTGCTTCGTG	12120
TGATGAAC TGCTGCTGAAA CGGTATCGGC AGGTTTCGCG GCCTGTGCGC GTGCACGCGA	12180
TTTTTGGGGG CAGGAACGCT CAATCCCAGG GCGTAACCCA AACGCAATCG TAGTGAAAGA	12240
ATCTGCCAAC GGAAAGATAC AGGATGCGCT GCTATTCTTT AATACCCACG TAAAAAAGGG	12300
AAAGGCGCCG ACGTTTCGCT GGGCTTTTCC AGAAATTGAA GCTGCCTCGC GGCTTGCAAT	12360
GGAGCAAGGG GCGTGGCTGA GCACGCACGA GCACTTCCCT CTAAGAGAGA GTCACTTTTT	12420
TCAGkGCGAT TTGACGCCAG CGAAGAGTAT CGCGTTAAAG CGCAAACGGG GCGCAGGCCG	12480
ATCTGCGGCA GATTGTTTTG TGCTAAAAAA AGCAACGATG GGGTTGCCAA ATCAATAGCT	12540
CTTCagGGTG CTGCTAACTT CAGCAAATTG ATCGTGTGCG cACCCTGcTT AGGTCTTGGC	12600
GCTTGCTCTG AAACCAAAAG CTGTGCGGGT TCTACAGCGG CCGCTTTTGC GTGTCCACAT	12660
CCCTTCTCCT ACGCTGaTCA TTCGAGTTCC TCAAGAATTC CTGCCATTTT TGCCCCACAG	12720
GATACTCCCC ATCTGTCCAA CACCTCGTTC ATCCGTCGcA GATCCTCACT TGaAAGCACG	12780
aAGCACCCTG cACTCCACGC ATAATTCGTG TCGCGCCCTA ACTTTTCTGA CCACCGGTG	12840
TGTATTAACC ACCGACCGGT CTGATATCCT TCTGTAGATA TTTGCATCGC TTCCCGATCA	12900
ATCCACTCTC CATCCATATC CCATGTGCGT GTGATTGCGT GTATCCGTCC ATGAAACGCG	12960
CGGGCAGGCA CAAAGCAACG CACTACAAAT GCGCCCGCG CAACCGATTG CCCATGTGCC	13020
ACCCAGACC CCGGTGCCAT CCGCCCGAAA CAATAATTCG CCACGGTTTG TACCATCGCG	13080
CCATACAGCA CCGTCCCGC TTTATCCTGT AGTTGCATTG TATCACAACT GTTGTTTGCC	13140
CAGTTGTTCT CGAAACTATC GCCTTTGAGT GGATCTACGC GGTAATGGAA ACTTATCCTT	13200
CTTCTCAATA CGTGCAATCG TACGTCCTCT CTCATCATTG TCTCTCCCCG CTGTACATCC	13260
GCGCGGTGCG CCGCACTGCA GACACCCTTC CTCCTGTGAG GCTGGTAATC GGCGTTGGAA	13320
TAAAAGGGCA GGGTATCGCC TGCTTGCAAT CTGCCGCCCT TCCTGAGAAG AAGGCgCGCA	13380
TCGCGCAGTC ACTGACTACC CTTCCGGCAG CCTCCGGTGC ATCGTGCCCTC ACCTTTTTTA	13440
CCCGTGGACA CATACCCCAA TTGCGCAGTT TCAAAAAGTC CGTTGAACAA TCGTTGCTCG	13500
TTTTCTTACA CGCAGATGTG CAACAACTAC GAACGCAAAA CATCACGTGG CTTGGATCCA	13560
TTCGGCGGAC CGACCACCCC CCTTGCTTCC ATTTCTTCGA TTAGGcGCGC GGCGCGATTG	13620

789

TAGCCTATCT TCAATTTACG TTGCACATAC GATGTGGACG CTTTACCCGC GTATTGCACT	13680
ACCTGCACTG CCTGCTCGTA TAAAGGATCG CTTTCATCCA CAAAATTTCC AGATATACTC	13740
GCGTCGTCAT CGTCAAAGAA AATTTCTTCA TCAAGATACT CAGGCGTTCC CCACGCGCGT	13800
ACATGGGCGA TCACGCGCGC TAATTCTCGC TCGGAAACAT ACGCACCTTG AATCCGCGTA	13860
GGAAAAGACT GACTCGGGTT CATGTACAGC ATATCCCCTC GTCCCAGCAA TTTTCTGCG	13920
CCCATCTCAT CAAAATAAT ACGGCTATCC ATTT	13954

(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

AGGGTGCCGT ACACCGGCAA CCACTCTAAC AACTCCACGC CAGAAAACCC ATACGACTTC	60
ACCCGTTCAA TGAGACTGAA AATAAGATCA GACTCAAGTA AATTGAGCTC GAGCTTTGAA	120
GCACCCTTGA ACAAGGCCTC GCGAAAATAC AACTTCGACC AGCGCTCATC TCCCGCAAGA	180
GCGTATGCAT CAGCAAGTTC AGCAAGAATT GCAGAAGAGT CTGGCTCCAA AGAGACTGCA	240
AACTCAAGGC ATTCACGCGC AgcATCGTAA TTGCCCAATG CTTTATAGCA CAGCCCAGTC	300
TTACGATAGA CTTCCGCGGG ATGCTCGCGC GCATCACCGG TGATAAGACT CCCATAAAAC	360
CGCAATGCGT AAGTGAACAC ACAACAGCGC AATGCATACA TAACAGGTTC GACAACGCCA	420
CCACGTTTTT GCATATATGC AACGAACGCA CCCCATTGTC CAACAAGATA CTCACCCTGa	480
CTAAGACCGC CAGAGATAGT ATGTACACGC TGCATCCGAT CCTCCCAAAA GCGAATACCG	540
GTAAGCGCGT ACAAACATC CCGATTGTCT AGCTCTTTTT GAAGCAAATC CTGCAAATCC	600
TGGTGTGCCT GGCGCAGATC CCCCTGCTTC AGTAAATCCA GTGCTGACTC AAGCTCTACA	660
CGAATCGATC GTGCAACCAT AGCGGGATAT TGTATCGGTA TCAAAGCGCC ACGTCAACGA	720
AAGTACTTTT TCAAAAACAA AACCAACGCT ATGTAAATAA ACACGAGCTA CTCGCAGTGT	780
CCTTTCCTG TGACATAAAA ATCCCGCAAA CGCGCACGCA CACACTGGTA GAGCTGAGCA	840
CTTCCCTGCT CTTTCAAATC GTCCGGCACC ATCAATTCCA GCGCATCATC AATTGTGCAT	900
ACCGCCCA CA GTGAAAGTA CCAGCACGCA CCGCATCTG CACACGTTCA GGCAAAAACA	960
ATTGTGCACA ACTACTCTTT GGGATCAAAA CTCCCTGCAT TCCCGTCAGT CCGTTCAGAG	1020

790

CACAGACGTC ATAAAAGCCA CTGATCTTCT CGCTCACTCC TCCAATAGCT TGCACCTGTC	1080
CCAACTGGTT CACACTTCCT GTTATTGCGC GGTCTTGCCG AAGAGGAAAC CGGCCAATCG	1140
CAGAAAGCAA TACTAAAAAT TCTGCAGCAG ACGCCGAATC CCCATCAATC CCGTGATACG	1200
ACTGTTCAAA ACAAAGCGCT GCAGAAAGAC ACAGTGGAAG ACTATCCTGC CCCTTTCCAA	1260
GGTCATCCAC AGCTGGATCA AATGCAGCAT CTGCAAAAGC AGACAAGCAC TTCTCACGCA	1320
ATAGCGAAGT GATGATTAAA TGC GCCTTAT CATAAATTTC CCCCAGAAAG CCTGCCTCCC	1380
GcTcaATATT CATCACTCCT TCCTTACCCG CGGATGCCTG TGCCGTAAAC GAAATTACTA	1440
TGCCAAAGCT ATGGCCGCAA TGTTCTTCGA TTGCCAGCGC GTTAATTCTC CCTATTGAT	1500
ATCCCTGTAC CTCTACCAAT AACTCTCCAC AGGCTATCAT GCGCTGAAAA CGCTCCCCGCG	1560
CGCGGGAACA CACGTACTGC CTGCGATTCA GCGCTTCCTG CACCACATGC GCAGTAATCA	1620
CCGACACATC TGGATGCATA TCCACGGCCA CTGCATGAGA CTCCAATACT AAATCTGCAA	1680
TTTGTAACAA AGAAGTACTG AGCCGTGTAT GACTCTCTGC CAGTTCTTCC GCATATGCTA	1740
ACAATCGCGC GTACGCTGAG GAATCAAGTG AGAAGGTGCC ATAACGCGCC ACAACTCTAT	1800
CAAGGTAGGC TATCAAAGCA ACTTGATTCT TATCAGAATT CGGCATGCTC GTATCAAATT	1860
CTGCACACAC CTTAAATAGT TCTCGGAACG AGGAATCTTC CTGAGATAGA CGTTCGAAAG	1920
AGCATGGCTC GCCAACCAAA ACAAGCTTGC ATGTGAGCGG AACTCCTTCA GGCCGCAACA	1980
TACCTTGGA CTGGGAACTA CCCGCTGGA GTAACACCTG CTTGGTACGC AGCGCACGCT	2040
TCAAATGTGT CCATGCTTCT TCCTCCGCCA GTAGATCTTC GAGCTGCACG ATGAGTACAC	2100
CTGCATGCGC TCGATGCAGC GCACCTGCAC GAATGCGTAA ATGCCCATT CACAGCGTAT	2160
CCCCCTCATT CCCCTTGCTT TCAATCGATC CACATAAATT CGCCAAATTC GGCTGATGCT	2220
CCGTAAACAC ATACCCCGCA TGTCTGTGT GCACACACAC GAAATTTAAG GTATAGCGAT	2280
CGAAAAACCG CTTTTTTACT AGTGCAGAAA TACGCATTGA CATTAAACAC TGTACCCGCA	2340
CCTGCACATC GgTTTGTATC CGCTCTATGT ACGATATGAT GCGCGCACGC ATTTCTTCAA	2400
ATTCTATGCGG CACCTCAATG AGGCGAGAAG AGGAAGTCTT CTCCCTTTCC GTCTGTTCG	2460
CCGCACACGA AACAGGTGGA GGGGAAAAA CCGGTGCATA ACACGCCACG CGTTTTTTAA	2520
TACAGGCCAT CTGCTCGAGG ATAATTAAAC GCAAACGCGC ACGGTAGTAC TGCGCAAGAC	2580
GCCTAcGCGC GGCCCGyCGC gCAGTGCAGC ACGTATGGAG CAGCGAAGAA ACCTCATCAC	2640
AGGAAAGACG ATATCGCGCA TGGAGTTCGT GTACTACACA TCTAGAAAGC TTCGCGCGGG	2700
AAGCTAAATC GTGCAGCGCT TCAAAGCTAC TGTCTTTTCC CTTTAATAGG GGAACATAAT	2760

791

CAAAGGAGTA CGTACCACGT TTCCTATGCC ATCTCACACG AAACCCACGC GTATACAACT	2820
CCGCTTCAAT ACGTGAAAGC TCAGCACACT CACGTGTTTC AATATCAGCC AGCAATGTGC	2880
GCCGCTCAG TAAGAAGGCA TCACTTTTCA CAATATCCTG TGCTGTATTG AGAATAGCGT	2940
TAACCGATCT CCTCAACGCC GTAGCAAAAG GCATCCCTTC TCCCGCCGGA AACTGCAGCA	3000
CcTGCGGTTC GTGCGGATGC ACAAAATTGT ATGCATACGC TATATCCCAC ATTTGCTCGG	3060
GACGAGGTAC AAAATCTTTT AATAGATATT GGAGCGTAGT GCGCTTCCCG GTGCCTGACG	3120
CGCCAATCAC ACAGATATTG TAGCCGTCAC CGTACATTCT CATCCCAAGA CGTATCGCAG	3180
CGCAGGCACG TTCATGCGCT AGCAAAAAGG GGTGATCCTG CGCACGGGCT TTCAGATACG	3240
CAATAGTGTC AGGAGCAACG ATACCCGTAA CTTCTTGCCA GGAAAGCTCT CGCCAGAGCG	3300
AGCTACGGCA ATAGGGCCCC AACATCAAGT TCCCCAGCAA AGCACGGCAT GCGGATATCC	3360
CAATTACTCA GCACtGCGGA TGTATCTCCC CAAATATACC CACACGAGAA CCATGCACGC	3420
AGATACTCGC TTGTCTGCCT AAGACAAACC GCGGATCCTG CGCTTCCTCT ACCTGATACG	3480
GAAGTTTCAA ACAATACAAA AGTCCTGAAA CTAGGCTCGC CACCTCATTG TAACTTGCCT	3540
CCTGCGAGGC ATTGAGGAAT CCAAGTGATT GTTGCGTGCA TGTACCGTGT TCACCATGAG	3600
GGGAGCAAAA GGCAACCTTT CCAATTTGCA AAATACGATG TGGATACAAC GCATGTGCTG	3660
ACTTTAGCTC AGCTGACAGA AGACACGGAA TGATAGACCT GCGCACGAAT CGGTAGCTTT	3720
CAGTAAGAGG ATTTTCTATC TCGATTAAAT CATCTGCCGT GCATgCATAC GCGTGCAAAA	3780
CTCCCTGGCA GAGCCAAGAT AATGAAAAAT CATCTCCTGA TAACCAAATC CAACTAGAAG	3840
GTGCTTAATT TTGCGCGTCA AAAGGGTCAG ATCACTCAGT CTGCCCCACTG TAAAAGAACA	3900
TGGAAC TGCG GAGAAAAACG GTCAAGCGTT CTACCCAGCA TCACTTCTTC AATCAGATCT	3960
ACCGCATGGA GAAAATCATT ACGGTACGCT GCAGGCTCGA CGACATAGGT TCCCTGCTTA	4020
ACTTGACGG CACAGTCCAT CCTTGCAAAG GCTTCGGTTA TATCTGCAAC AGGCAAGGGC	4080
ATCCCCAAAA GACGATCTAT CTGCTCGTGC GCAACCTCCC TTTTTTCTTG AAAATAAAAG	4140
GGGGTAGTAA CAGACCTCCC CCATGGGGTG tCAAACTAT AGGTAATTG CACAGGTTCA	4200
ATCTGCATAC CCATATCAGA AAGATCACAC GCAAGGCTAT TCACCGCTAC TAGCACTGCG	4260
CACATATCCG TACCACTACA CTCGATAAAT AGTTCTGTAT CCCC GGTCAC TACTGCACCC	4320
AGCGACGCGC TATTAGTGAT CGGAATAAGC GAAAGCACCT CACCACGAGC ATCGACTAAT	4380
AAGGGAACGA AAGAATAATC CTTGAGGAGA TGACCATATT CACGCCCTTT CGGATGTTGC	4440
GTCAGAATCT GCTCACCAGA CAGCGGCATG GACATACCGA GAGGCGTGAA ACTTACCTCT	4500

CCGAGTAGGA CAGCGCGGTA TGCGAGTGGC CAACATATAT CCTGTGCACG GTAACACCCC 4560
AGCGAAAGGG TACACCTCCT ACGTCCAAAA TTACTGGCGA GTCTTTCCCTG TGTTTGTATT 4620
AGATCCCACA GTCTTACTTC GCTCAGTCCA GTACCCCGAG CCACAAAGCC AGCAATAAAA 4680
GGGCGTATAG TTTGCAAACG CGCATCCACT ACTACGCATC GCCCATACGA GTCGCGCACC 4740
GTACAGCGAT CTGAAAGAAA TGCACGATAC TGCGCTGCGC gsGAAgCCCC CCCTGCGTGA 4800
ACACGCAAGA GGCGCGCAAG CCCTGCTGTA GACCACAAAT CCGGACGATT TGTGTCGTTA 4860
AGTTTCGATTT TTAAAAGACG CGCATCAAAC GCACCCCTCAC GTACACAGCT GGcCTGaCCC 4920
CTCGTCTCTT GcACAGGaTy GcACACCTcC CCTcCTGGcG AAAGGCTCCC TCCCTcTTTA 4980
TCTTCCCTCA CGGAAAAAGA GCTGCACTCC AATTACAGCCT TAGCAtTCGC AAACGTCGCT 5040
CCAACGTATC ATCGTCGCAC CGTTCACCGA GCAGCTCAAA AAACAACGCC TCATGAATGC 5100
TAATTTTCGG CATGAGCCCT CCGACCGTGC TCAGTATACG GTCAAAAAAA GGACACCACA 5160
AGGGCCAGCC ACCACACCGT CTTTGcAGAG GATGCCACTA CACGGCACAC GTGCTCTACA 5220
CTTTAGTCAT AATACGCGTA ACACCTTAA ACTGAGCGCT CATATGCGCA CGGCATAAGT 5280
ACCGTGCgCm CAAAGGCATG AGCTCACTGA CGACCGAAAC GAATACTCCG ATACTTTTCC 5340
GGAAATTCCT GGTCTGTTAC CGGTAAAGAA AACTTACCCA AAATATGTAT GTCAGAGAAC 5400
ACTGACACAT GGTGGATAC TTCCTTCCCT GTGAGAAGAT CCGTGTACGG CGCAACCCTC 5460
CATCGTGTTT CTTTGGAAAA CAAACTAAAG GCATCAGAGA GAGCTACACG CATATCCTTT 5520
TCTCGGAGTT CATTTTGCAA TATCCTGCGC GCATATTAG TTAACCCAAG TGTGCTGACA 5580
AAAATATGCG AACTTACATT CACCCGAAA CGACCTACCA ACCTCTTCTC TTCTACCGCC 5640
GaCTCGACGC GcTCCAGGAT CCCCACACA TCCTCATCGT CAGCATACTC CACCCCGAGT 5700
GCTTCAGCAC AGTCAAACAC ATTCGCCCCC AGAAGCATGC CATCTTTGCT TACCAGTTCT 5760
CTCATCAGGG AAACACGGTG CGTATCATTA GTGCAAAAGA ACATAGTGTT CTTCCCATAC 5820
TTACCGATCC ATTGCTTCGT GTGTGTGCCG ATAAACGCAC GCGCCCTTC AACACCTGAC 5880
TyCCTGCGGG ATCTGGAGCC TCCTCAGACG CAAACTCTAT ACCGATATCT GCACACACTG 5940
CCTCCATTAC CTGACGCCTC GTCCTAAGCT CAGCCTTTGA AAGGTGACGA GGAAAAGAAA 6000
CGTGACCAA CGTACGCGCG CCCATTTTCT TTGCAGCCCA GGAATAGCA TACCACCAA 6060
ATGCATAATC ATCACTAACC ACGATATCAG CAGATTTTGT GATAAGCTCA GGATACTCAT 6120
GCGGATCCCC TACAAAGAGC ATGATGTCGG AACGtTCGCC CTAATTTTGT TAAAAGCCTC 6180
TGCAGTTCCA TGAATTCCTT CGCTGACAAC AATAGCACCC ATGAGAGGAT CATCAGCAA 6240

793

TGCAAGGAGC	CGGGACACCG	TTTCATCTTG	CCGATTTACA	AAATCTTCAG	GATACGTGAC	6300
ATGCAAGATA	CATCCTCGGT	GACCGTCACC	TACCGCACCG	TACATGGCGC	ATGCTCTTTT	6360
TGCCGCAACT	ACATCATGGC	TAGAGTGACT	ACCCGGACCG	GTCATAACCC	CGATGTGATA	6420
ATCCTCCACC	GCTTTTCGTG	CCCCGGTATT	TTGTGGAGCA	CGCGCGCCCC	CACAGCGACA	6480
CAACAGTGCA	CCGACACATA	CCACCCATAC	CTTCAATAGA	AACTGACTTT	TCATAGTCTC	6540
CCCTTAACGA	TCTGCACACA	CCATCTCTCC	AAAACGCTTA	GGCGTATGGT	CCACCCCCCC	6600
CCCACGGGAA	AATCAATTGT	GTATTTATGA	TACAGCATCA	AAAAATCATC	GTGTGCAAAC	6660
CAAAAAGGTA	TCCCTTCCCT	CCCCCTTATT	GAAGGCTCCC	TCACCACAGA	ACCTTACACG	6720
AACACACGAG	cTyGtCCGCT	TATCCGGCCA	AGAACCATGC	TCCAAACTTA	TGTAGGGACG	6780
ACGCGCAAGC	ATTCCCTGCG	ACCACTCAAT	GAGCAACTCA	CATCTTTCAA	ACGGACTCAC	6840
CGCCACCCCT	ACCTGATAAT	ACAGATTTTT	ACCTGCGCGG	AACGTGCGGT	TCCTCTTTAn	6900
CGTTCCGGCA	GCACCACCTG	GTCCGTAAGA	AAAACCCtGC	GCACCATATG	TAGCGCCATA	6960
CAGCGAAACC	ATCGGTCTTA	TCCATGCGTG	AGcAGnCAAG	AGTAATCCGG	TAGTTAAGCC	7020
ACAGTTTCCC	CACAACAGGC	AACGCGCTGT	GTGCACCCGG	ATGGACAACA	CCGGGTGGAG	7080
GAAGCACAAA	CGCCTGAGGC	TTCTTTCCCC	GTGTGGAATT	CGGCGTACAG	GAGCCAGGTT	7140
CCAGGTACAA	GCCATGAGTG	AAAGGAATAT	ATAAAcGCGC	CTcGAcACyT	CCGCTCAGAC	7200
CGGACACAag	CTTAGAAAGA	GAATCGTACC	ACTTACTTTC	CACCCCG		7247

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2898 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

AACCGnTTCC	CGTTGTGCTT	CTGCAATTTT	TCTGCTGTGC	TCGCTGCTCC	TGAACTGGCC	60
TTACGCGCGG	AGGCTCTCGG	CCTGTTGCGT	TGCCTTCTGC	GCAGTGTGAG	CCGCCTGCTG	120
AAGCTTCCCT	GTGCGCACGC	TCGGCGAACG	CGCTCCTTCT	CTTTTGCTTC	CTGCGTACGC	180
GnCCGGGTCC	GGTGAAGTTC	TGCGCCGCGT	GCTGAGCTTG	CTGAGCTTCT	CGGCGTGTCT	240
TGTCCGCGTG	TGCCTGGGCG	CGCTGAGCCT	GAgTGGAaCA	cTCCGCCGCG	CGCTCCTGCG	300
CCTGCTGTGA	CTGCTGTGCT	AGTTGTTGGG	CCCGGCGCGT	TCCTTCCTGC	GCCTCCCGCT	360

CTTTAAGGTC AATCATGTcC CTGCGCAGAT CAACGTTCTT GTCCGGATCT TCACGCAGCC	420
GCTCCACCAC CCGCTTGTC GAAATGGCGC CGGTGTCCAC TGCCTGAGT GCGTCAGAGT	480
CCCCGGAAG GGAATGACG AGCTGCGTTT TTCCCGCCA CTGATCGAAA CGGCGCGCAA	540
TACCGACGTG CTCGGGGGAG AGATGCGCCG TTACCACCCC CTTGTAGCGC GCCTTGAATG	600
TGGGAAGGTC TGCACGATAC ACCGCGTTGT ACACCGTTGT GAAGGTTGCT ATCGTGCCTG	660
CGTCCTGCAG GCGATAGCaT AGGCGGCAGA AAGATAGGCG GCGACGATCT CGCGTATGTT	720
GTCGATATGG TCCACCCGTG CCTGTGCGCC AATGATGAGG ATGTCTGCAT CAAAGCCATT	780
GGTCGTGTGG GGACCTAcTG CGTGAATAAG cGCGTAACGC gcACGATCCC CCGCAACACC	840
GCCGCGCAGT GCAGAGGCCA AGCCCTCCCC GATGCGCCTG ATAGCGGCGG CGCTATCTAC	900
GTCCGTGTGG GTTCCTGCAA AATTTTCAA CTCTACCGTG GCGTTTGCAC GCTCAAGCTC	960
ACGCGATCC ACCTCGAGTG CAAAAAGACA GCCTGCGCCC AACACGGCAC ACATGGGCAG	1020
CACGTTCTTC ATGACCCTCT CCCCTTCTA CACCTTTGTT TTTGAATACC GCACGCCTAG	1080
ACACCTGAGA TCCCAACCTT CCTGCGTCAT CAAAGCCCCA TCAGCGTACA TnACTCTGAA	1140
CGAGAGTTCT TGCATAGGCC CGTATGGTGT ACGGAAAGC CCCCCTGGAG ATGCGGGAGA	1200
GTTCTGAGAC TGCCTTTTCA GAAAGGGTGC GCGGTGCACT GCGCGCGCAT GCAGCGAGTG	1260
CATCGCACGC TGCACGCATC AGCGACTCGG CGCGTGCCTC CTTAGCACGC GTGACTCGGT	1320
ACAGCGCAAG TAGTGCCCGC TCATCGAGGC CGAACGTGCA GCGGTGAGC CCTTTGAGGA	1380
TACCTTCGAG CACGGTGTAG TCCTGcTCTT TGAGAAGCTC AAGGAGCGCG TCTCGGTATT	1440
CGTGTGCGCC TAAGGCTCCT AACAGCGTTG CTGCCTGCGC TCTCCTGGCA GAGGTCACTG	1500
CAGGCGCCCG TGCGCGGGgT GATGCGGTGA AGTAAGAAGC GCGTGAACG AGCGGGGCAT	1560
AGGCCGGTTC TCGAGGTcmT ACATTcCTTC CTTCAGGGAT GTTTGCACTG CCTGAAGGAG	1620
AAGCTCAGGG GTGGCGTACG GTCCGGGCGG CGACGTTGTG TCGTCTCTT GCGCGTTGTC	1680
TGTCTTTCCG CTGTTTTTTG CAGGAgCGGG GGAAGAGAAG AACGGTCCG AaGAgATTGA	1740
GTCATAAGGC GACCGCTTAG CAGGGGCAGC AGGGCGAGAA GGGGAGCCT CTTGCACGTG	1800
TGCACGGCGT GAAGAACCGA GCACGTGAAA ATACTATCGC GGTGTATAT GGGCGTGTGG	1860
TCAATGAGTC TTGTTTCTGC ACGGTATGCG TTGAGTACCC AACCGCCTGC AGATACTACG	1920
AGCCCGTCCG TGGTGATAAG CGGAGTAAAC GGTGTTTCGT ACAGCGAAAT GTTCCACTTC	1980
AGCGCGCCTC CTGCGCTGAG GGTAATCGCC CGCGCTGTAT CGCTGAGCaT ATTTCTGCCC	2040
CCTGTACGCG GCACTGGGCA GCCGAGGAAA AGGTACACGG AAGTGTGAGC GAGAAAAGCT	2100

795

CATTTTCCCC ATCTGCGTCG TAGGCACGCA CCGCACCGTC TGCAAAAAGG GCGATGAGCA 2160
 TGTTTTCAGT AGCAAAAAGA GCGACACAAG AGCGCTGTGT GCTGATGCGC ACCGGCACCG 2220
 GCGCCTGGTG nCTGTTTCGCG GTCTTTCCCG CCTGAGTCTT ATCAGGCGTA CTGTTTAGCG 2280
 TGTCAGTGCG CACGCGCCAC AGGCCCTGAT CCGTGGCAAC GACGTACCCG CGTGGGGTGC 2340
 TCCTACGCGC ACGTACGGAC CCTGATGCGc GCAGGGCGCC TTTTTTTTCT CCAAATATGG 2400
 ACCAGTACTC CACGGTTCCT GCGGGCCCGT GATGAAAAT TCGCGCGTTT TTGCATCTGT 2460
 CGGAGGAAGG AGGGGCTTTG CGCCAAGCTT CTGACTCCAC AGGCGCTGGC CGGTACTGCT 2520
 GAAGCACAGC AGGGCGTGTG CgGTGGTGTA CAGCAGCCGT CCGTCTCTTA AAATTACAGG 2580
 CGCGGTGCAC AGCCCCCGT TCGCCGCGTT CACCGCACGC TTTGCACCGC GCGTGGCAGC 2640
 AGGCAGGACA GCAAATTCTC GGACGGGTAT GCCCTGGCTG GAGAAAACCC ATACGCGTCC 2700
 GCTAACCTCG CTTACGTACA CGAGTCCATC GTCAGAAACG CTGAGAAAGG GAGTGCCGAC 2760
 TACGGGGCAG TTTCTGCGCC ACACGAAGGA TCCTTTGGAG TTTACGCAGT TGAGGGCGCG 2820
 ATCTGCGCTA AATGTATAGA TGAGCGAATC GTAACGCACC GGCTGTGTTA CGTTCTGCCC 2880
 TGCAAGGACC ACACTCCA 2898

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3956 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

CACGATGTAC TGCATTCCGn GGCATGCCCA GGA CTCCGnG GATGCGCGCG TCAGAGGTGA 60
 TAGCGGATAT CTACCCCGGC GGTGACAAAC TGCGCATGGC GCGTGTAGT CTGcTctCTC 120
 TCtTCTTCAA CCACTTTTTT GCACGACCGG GGTACGCCG TATATGCAGC ACTGGCACCC 180
 AAGGACCAGC GCTCTGTCAG CTGAAGgTAA CAGCCGGCCC CTGCTTTGAG CAAAAGACCG 240
 TAGTACGTAG ACGTGTAGTA GTGCTGGTAG CTGAAGCCGG CCCCCACCGT CAGCGGCAGA 300
 CGGATGCGCC AGAAGGCGAG CGTGTAAC TT GCATTACGCG TTACAGGAAC GGCAAGgTAG 360
 GAACACAGCC GCTCCTTCTC GTAATAGAAC GGATAACTGC AGGAGTGCTG CGCGCTCGCA 420
 TCAATCCCGA GCGACAAGCC GCGATACACA AAATACTCGT ATCCAAAAGA CACCCCAAAC 480
 GCGGGGTA AA CTTCcTTATT CCCGTTGGCT GCAACGCCCC CAGATCCCCG CGGGCGGTAT 540

TGCACCAGTC CACCTGGAAA AGGGGCACCG CGCCAATAAA CGAAACGCGC GCGATCCCCC	600
GCCCCGCGnC GGTTaCATCC CACGATGCGG CAGGCGCCAC CTCTGCGCA TACGCTGCAC	660
CCGCGGcAAC ACCCACCCCG CAGcGcAGAC CTGCAGAAAG CGTATCCCGT GTGCCGCGCA	720
CTGTTTTAGC TGTTTCATAC GTTTTTTCGC TCCACACCTT TCAAAAAGCT GCGGGCAACC	780
CACACAGCCT TCCAAAATTC TACCCCCCCC CGGCCAACAT TTGTCGAGTT CTTTTTTTGC	840
AGGAGGGTCG CGCCCCGCGC ACCACCGCTG cATACCCAGT GCGCGCCTGT AACATTCTGA	900
CCGGGGAGGT GTTTTCTCAC ACCGGGGAGG TTTTATGTGC AAACCGCGCG TGTGGCGCAT	960
CGCCCACACC ATCGTCCATG TAGGCGCGTT GCTGCTCGGC ACCAGCCAGC TGACAACCTG	1020
TGATTTCTCC GGCATTTTGT CCACCATTCa GCAGGAAGTT GCCATTAAGT CGCCGTCTAT	1080
TCCGGGGGCG ATTTATGGCC TGGTCAAGGC CGGGGATAAG CTCTATGCCA CCAACGGTCG	1140
GCTTTGGGAA AAGGAGCTGA ACGGCATTAA GTGGAAGCCG GTGCCTTTTC TTGACGGCCA	1200
AGATAAGCGA ATTGATAGCC TTGCAGCCAG CAACACGTGC GTATTTCCTT GTGTTTCAGG	1260
AGACGGTGTG TACAAATACA CCGCCGGCAC CACCTCTTCG CAGAAGGAGA GTAATACGGA	1320
TAAAGCGCAG GCGGTGGTAC AGATGTCGGA CGGAAAAGTG GTCCTGCAGT GTGCCTTGGG	1380
GGATGAAAAG ACGACCCCGA GCGACGCAGA CGAAAGGTTG CTGGGGGGCG GCCAGGGCTA	1440
CCTCGTCACA TCCAAGGGAT TTTACACCCT CCCAGGGTCA GCCTCCTGCG AGGTTATCTC	1500
CGAAACAAAG GACGTCACCT GTAAGGCAGA GCGCCGATC CTCGCCAGCG CCTGCGATGG	1560
CAGCAATACC TATATCCTTA CCAAGGACAA GGTGTACTGC CCGTATACGA ACGGCTCAGG	1620
GAGCACCCCC aCTACGTGGT GCGACGTGGA ACACAAGGTA TCAGAGCCgc TTGCGCTTGC	1680
AGTGTTCAAA AATAAGGGTG AGACGTTCTT GCTCGTTGGG GGACAGCAGG GATACGGGGA	1740
AATAAAAATA GCCACGGCAA GCGGCAGcTC CTCTTCTTCC TCATGCGTTC cCCTCACGGC	1800
GGAAAACGTG CACGCCACCA CCGGGTGGGG CGCCAACCTG TCCACCCCGG AAGGCAGCGC	1860
CGAGCAGTAT CGTAGTACGA TCGGCCGCTG GGCAGTGAGC GGTATTTACG TAATCAAAAA	1920
AGACACTAGC GGTGGGCGGA AAAAGCGGag CACCTCAACA GACTGCGAAA GACCAGACCT	1980
CTACGTGGCG GTGGGGGATG CGAGCGACAC CTACACCGGG CTCTGGAAGT TCGACACCGC	2040
TACGAATACC TGAATCGCG AGTGATGGCG CGCagCAGAT GcGTGCACCG CGTGGTGCAC	2100
CAGGCAGCGT GCATCGGGGT GATAGGCCTG AGCACCAGCG CGCTGACCAC GTGCGATTTC	2160
ACTGGCATCT TTGTGGCCAT CCAGTCGGAA GTGCCCATTA AAACGCCGTC TATTCCGGGG	2220
GCGATTTATG GCCTGGTCAA GGCCGGGAGC AAGCTCTATG CCACCAACGG CCAGCTTTGG	2280

797

AAAAAGAACG TAGCAGAAGA AGGTAAAGAC TGGGAGCGGG AGTCCTGTTT CGACTCGGTG 2340
ATAGGCGACA GCCGCATCAC GAgcTTGCGG CAGACAACGG CGAGAATGGC GTGCTCGTTG 2400
CCTGCATTCCT TGGCAAGGGG GCGTACAAGT GGTCCGAGGG TAGCGCCGAC CAGACAAGCG 2460
GAAATCCGTC TGCCCTGAGT GGCACAGAAA AAGCACTCAG CGTGGTAGGG ACCGGGACAT 2520
CATGCGTGTA CCTTAACCAC ACGGATGATA AGGTGCGGGA AACCAGTAGT TCGGAAAGTG 2580
GTGGAaTGcT GCGTCAGGAG AAACGAATGA GTTCTGCCTG CACGCCGGTA ACGGtTTTTA 2640
GTTACCACCA AAAAGGTGTG TGTCGGTAGT GATGGTTCTC CCGTGGCAAA GAGTGATGGC 2700
GAAGAACCAG TTCCGCCGAT TCTTGCGGCA ACTGAÇGACG GGAGCGGGCA CGTTTATATC 2760
CTCAGGAAAG ACAAGGTGTA CTGCAAAAAA GTTAATCAAA GCGAAGGGAA AATTCAGGAT 2820
TGCCACAGT CTGCCGAGC AGCGCCGGAG CCAACCGGGG CACACAGTGT TGCCATAAG 2880
GTAGCAGACG CGCACTCCAT AGCGTTCTTC AAAAACGGCA GCGACGAGTT CTGCTCATC 2940
GGGGGCCGGC AGGcTACGGA GAGATAAAGC TGGAAAGAGG TTCAGGAAGC AACGGGAACG 3000
GAGCACAGTG CGTCCACCTG AAGGAAGAGA ATGTACACGA TCAAACCGGC TGGCATGAGA 3060
AgGGCTCCAC CCCGAAAGGC AGCGCCGAGC AGTATCGTAG TACGATCGGC CGCTGGGCAG 3120
TGAGCGGTAT TTACGTAATC AAAAAAGCA CTAGCGGTGG GCGGGGAAAG CGGAGCACCT 3180
CAACAGACTG CGAAAGACCA GACCTCTACG TGGCGGTGGG AGACACGAAC GATACGTACA 3240
CCGGCTGTG GAGGTTTGAC TCCGCCGCGC AAAAGTGGAA CCGCGAATGA GTGGCTCTAA 3300
CCtACGCTTC CCCTACTCCC GCGCGTACGG CGGGGCAGGC GTAGGGCGTA ATTTTGAAAA 3360
ATCAGCAGA TTCTCAGTAC AAAAAGAGGG TATAGGTGCG CCGGTTCTcG cGChGTACCG 3420
CTTTGCAGTT CAAATGTTTT TTGCTTTCCC GCCTCTTTTT TATTTTACG TCACATATTC 3480
CCtAGACGGG TGGGGGGGGG TGAGGTAGAA GTGAGAGGAG GGGGAGTGAG TGGGCAGGCA 3540
GGTGATGCAA GCGGGGkyAC TTGCGGGCAT GGTATGTGCT GCTTCTGGTT ATGCAGGCGT 3600
ACTCACTCCG CAGgTCAGTG GCACAGCCCA GCTCCAGTGG GGCATTGCGT TCCAGAAGAA 3660
TCCACGCACT GGCCCGGGCA AGCACACCCA TGGGTTTCGC ACTACCAATA GTCTGACTAT 3720
TTCCCTGCCG TTGGTGTCAA AGCACACCCA CACCCGCCGA GGGGAGGCAC GCTCAGGGGT 3780
GTGGGCACAG CTGCAGCTGA AGGACCTGGC AGTAGAGCTT GCGTCTTcTA AAAGCTCAAC 3840
GGnCCTGTCC TTTACCAAAa CTACCGCTTC CTTCCAGGCA ACCCTGCACT GTTATGGGGC 3900
CTACCTGACA GTGGGTaAG TCCTTCCTGT GTGGTTAACT TTGCCAGCT GTGGAA 3956

(2) INFORMATION FOR SEQ ID NO: 146:

798

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

GGAAAGCACT GCGTACTAGT GAAGCTAACG CGGAGACTCC CGCGAAAGTC AAGAAAAAGC	60
GCGCCTTTGC TCGCTGGGAT ACCAGAGAGG ATAGCTTGGC GGGCGAAACC TTTTTTTTCC	120
GCTTCTGGAT TGGGGTAAAG TCCTTTTTTC GGTCTTCGTC GGTGGAAGCG TTGTACGAGG	180
AAACACTTCT CCAGCGTCTG GGCAATGATC TTAAGGCGCA TTACGCGCAG TACATTGACG	240
TAAAGGAAAA AACCTTCACA AAGGTTTTTT ACGACAAGAT GGGCGAGTTG CGCAAAACAC	300
AGGTATTTTT TGATTCAATTG CTCGCCTGCT ACAATAGCGA TAAGGGGGAC TTCTACCTCC	360
TGTTGAGCTC TTTTATCACT CCCGTTGTGT ATGAGCAGCT GATGGCGTGC AGCGATCCGT	420
TTGCTGCGCA GGGAGATGGT ACTCCTTCTG GTTTGCGTGC GTCCCTCCTT AAAAGAATGG	480
ACGTCGCCCT TGCCACCCTG AGTGGTCCTC ATAAACTGA GTTGATCAG GCGGCGCGCG	540
CTATCGAGTG GATGAAGGTT TTTGTGAAG TGCCTGTCGA TCGTATTCTG CTGCGTTTTA	600
CCGTCATCTC CCCGGCGAGT GCCGTGTGTC CCATTACTAT TTTGCAATCT GAATTGAAAA	660
AGCTTGCGTG TGTATCCAT GACAGCAAGC ATATTCCCGA CGCGGTATTG CAGGGGCTTT	720
TTGTGCTGAA GAGTAAACA TCGCTGCATG ACGCGCAGGT GGATAACGCT GCGCACGCTG	780
CTGCCTTTCT TAAGGAGGCG AGTGCAGCGC TCGTTGTTAT CAAGGATTTA TCGCACAGCA	840
TTCTATTGA GGATTTTGTC CGTTTGCAG GTAGGAACAT TCGTTGGCAA CCTCGGGCAA	900
TTGCCGGTGG TGAGGATTGG TTTGTCCTTT TTAAGAAAGC GTGGAAAAAA CGTTTCAATG	960
AAAAATGGGC GCTGTGGTCT ACCGCACAGA AGCGTTTAGT GCTTAAGGAG CAAATGCTTT	1020
CTCTTCTCGG AAGGGAGCAG TTCTCAGAGT TGAATCATCG GCCATGGGAA GGGTTTTGGT	1080
ATCAGCTTGT GTTTAGGCGA GAGATGTCTT TTGTCTTTTT AAAAAATTTG TTCGAAGgTG	1140
CGTATGCGCG CGTCGTTTCA CCGCCGCTGA ACGTTATTCT TGCTGAGGGC AGTTTCTATC	1200
GTCGAGATGA GTTGATAGAG TACACTGACG CGGTAAATGT ACTGGAGCAG ATGGGAGCAA	1260
AGATTAGGAA TTTCGAGGTA AGACTTTCGC CGGTGGGGGA ATGGGGAGTC GCCT	1314

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1058 base pairs

799

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

GTCGAGTATT TCGTTTGAGT AGGTAATTCC TCCTTGTGTG TTGTCCTGTC TTGTCGGGGT	60
GCGAAACATC AGATTACAGA ACTGTGTTTC AAGCGGCGAT ATGCGCAGTA TTTTCTGTTC	120
GAAGTGTTTA GAAAGATATG TCCCTCGTGC ATATGGCTTT CCGTTGGTGT AGGAAAAGTC	180
TGTTCCAACA GAAGTGATAC GGGTAAACCC TAGAAAGGAA GCCACCGAAT AGGCGGCGCC	240
AGCAACCGTT nCCCCGAAC TA GTTTCTAAAA AAGGTAGGGA AGAAAAACGA CTGCGTATA	300
CACTAAAAGG GTGACCTCCT CCGGTGAAAA TAAGTGAATT ACCATTCAAA TAAAAACTGC	360
GTACTGCGCA TGGACACGCG CATATGTCGA ATATTGCAGT TACCTGTGAA GGAATGAACA	420
CATAGTGTGT GGCATACGAG ATGTATTGCG GATCAATGCT GATAAAAAAA TCTGGCATAA	480
GACCGCCTGT GCAaCACACG GGAAAAGCAG TATCGCATGC AAAAATAGTG TACACATCCC	540
TATGTGAACG TATTTTTTCA ATACCTTTTT CAAGACTTGG CCCTGCACCT AATATGATCG	600
CCTCAGTTTG TGTATTGATG TTCGGTAGCT TTGGTGTGAA TATCTGTGCA TATCTTAGAT	660
TGAGTAATGC GTTTCTCATC CAAAGCTTTC CAAAGTGCAC TTGGACTGAA AAGTCGGCAC	720
GAATGATTTT CATTGCTTGG CTGGTAAGCT CAGCGATCTT TTGTTGCTT GTGGGAAAAA	780
ATGCCTTCCA GGGTTGTAGA TAGTGAACAA AAAAATTGCC GTGGATGATG GGCATATAAC	840
ACTGTGCAAT TTCTTGTGAT GCACTACCGT GGGTGAGCGG ATGAAGAAAG TGGACGCGTT	900
CTTGGACGAT AATATGCGTG AGGTCCACCT GGCTCCAGGA GTGCACGGAA ACTCGCGTAA	960
TCAAATTCAC ATACCGCGCA cATGCGTGGA CGAAATTTTT CTAAGAAAAC ACTGATGTGG	1020
GATACCTGCC CCGATGCCAC AAAAAAGAAT GGAAGCAT	1058

(2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

TGACCGGCCA GCAAAAGGCT CATGCTCAGG CCGGCnCCGT TGCAGGACCG GGCTCGTACC	60
---	----

800

CCGnTGGGTG CCGGTTTATC CCCCACCAG GGTTTTTTGG ATGAAGTCTG CCGCTGGCCA 120
 TTGCGTGTG ATGGACAgTT TctGGCGATT GCGAGCctT TTTTACGCAa GArTgCgGTG 180
 CaCGATGTGA CAGCGTTCaT TGATGCrCAC AATGCgCGCA AAAGGGCGCC gCGTGCCCCg 240
 CTGTTGGTTC CgGAcTTTtTA GCTGTCaTGG GGAAAgCGAA TTTATATGCg CGTATTCGTG 300
 TCTTGGCATA AGCaAAAGGA TAAGGGGGaG CGCGAAcGCg CAGGTGCGCT GCaGGGAGCG 360
 TGCATAGGTA CGCCTGAGCA CCGCCAGtTT TTGCGCTGGT AGGAAGAAGT GGCAGCGGAA 420
 AGAGTTTTCG TGCGCAGATA GTGATGCGGC GTTTTGATAT AGCGTTCGTT ATAGACGATG 480
 GATTGCTTAT TCGTGAGGAT AAGATTATTG CAGtCGCTCG GCAAAGCAGG AAAGGACGCT 540
 GCTtGCGGCC ATACGGGTG CGCTCTTCGA GAACACGATG CACCGTCGCG TAtTGCCCGT 600
 GTGTTGACGT ATTTTCTGTG TGGGTCACAG AACAAAAAGG TGCTCATTCT GGGGACTTCA 660
 GAGAGGATGG TGCGCAGAAT AGCCCTTCGT GTGGGGCTTC CTGAACCTGG GCATATCATC 720
 CGCATTGAGG ATATTGCCTC GAGCGAAGAA ATTGCCTcCG CgCgCaCACG GCACGTGaGG 780
 GCACGCACGT CATTCCAGTT CCCTCTGGGG AGGTACGCAa GAGCTATCCT AAGATCTTTT 840
 ATGAAAGGAT AAAACTCTTG cTGCgTAGAG AGGCAGGTGC GGAACGAATa GGACGGTGGG 900
 CGCACGCCAT ATGGCATGAG GGGCTCAAGC GTGcGTGCAG CGGCGCGCAC cGCATGtATT 960
 TGAAAAATCA ATAGTGCgTC CACCTTTCTC ATGCAATCTG CGCGTGGTGG CGGCGACAGA 1020
 GGGCACACAG GATGCGTCGC CTGTTGTGGT GCCGCTCAC GAGGAGCTCG CTCTCCAGCA 1080
 GTAGGAGAGC GATGACAGGA GAGGCAGTAG TTTGTCCCGT AGCGTGTGGA GCCGGAnGGT 1140
 CGAAG 1145

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 860 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

TAGGAGTTTG TTTTCTAGAA nTTGTTTTTC AATAAAGGGC CGGTTCTAAG TCACGCTCTC 60
 CCTTCTGCCG ATAGAGGGnG CGGAGGTGGG GATGCTATGG TGATGGCCGC GGCgCCTTTA 120
 CAGAATTTGT GTTACGACGG ACTTTTACAG GTAACCTCAG GGGGCAATAT CTCGCTCCCT 180
 GtACCCTCGA ATCAGGTGAT ATACGCTCAT TTCGAACATG TTGATGCGAC TCCTGCGGAg 240

801

```

cGGAGrCAGG CAGGGGTGTC GGTGTCTGAG CTGCAGATTT TGGACGCGTT GGTCGAGCGG      300
CTGATAGTGC AGCGTCGGGT AGCGGCAGAA GCGGCAGACA TGGCGGTGCA GAAGCGGCAG      360
GAGACACTGC TCCGCGCCGC AGAGCTTTTT TCTCAGAAGC AACTGGACGA GACCAAACGG      420
CGGGGAGAGT CTCTTCCTTA CACCTCAGTA GAAGTACAGG GGCCTGAGCT TTTTGACTTG      480
CGCGCGTAGG GCACGTGCAG GCAGAAGTAC TTGACTTTTT TGAGGATAGG GGGGAGACCC      540
CGCCTGGCCG GAGTTCTGAG GCTGGGTATG GACTCTTTTG GAGAGTGGGG GTTGTGTGGG      600
TATGAGAAGA TTGCTGGCAT GTTCGGCGGG GGTGCTGTGT TTTTCCCAGC TTGGCGCGCT      660
TGAGTTGTTT CTTTCTCCTA AGATTGGGAT CACGAGTGTG TATCAGTTTG GGAGTAACGG      720
TGTTTCGGAC GGTACgTCGT CGGTAAGGG TGTGTCTTTT GATAGACTGA TTGGAAGGGT      780
TGACCTGGGG CTAATTTTGG TGAACGGCCT AACGATTTCA GCTTCGGCGG AAAGTTCGTT      840
GACCAATGTC TTTGTGCGTG                                     860

```

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

```

TAAAAAAGGT ATGGATGACT TGTGACTAGG AGTGAAAGGC TAAACAAACC TGGAGATAGC      60
TGGTTCTCCC CGAAATGCCT TTAGGGACAG CCTTATACAA AACTGTCGGA GGTAAGCAC      120
TGGATGGGCT AGGGGGTTTC ATCGCCTACC AAACCCAATC AACTCTGAA TGCCGGCAGT      180
CAACGTGTGG GAGTGAGACT GCGTGCGACA AGTTTCGTAG TCGAGAGGGA AACAGCCCAG      240
ACCGTCAGCT AAGGTCCCGA AATACCGCTT GAGTGTGAAA TGAAGTGTGG GTACCTGGAC      300
AGCCAGGAGG TTGGCTTAGA AGCAGCCATT CCTTGAAAGA GTGCGTAATA GCTCACTGGT      360
CGAGTACGCA TGCGCAGATA ATGTATCGGG GCTAAGCGGT ATACCGAAGC TACGGGTCTT      420
GCATTTTTTG TGCAAGGCGG TAGGGGAGCA TTCCATGTAC TGATGAAGGA ATATCCGGGA      480
GGAGTTCTGG AGGGGATGGA AGAGAGAATG CAGGTATAAG TACACGAAAA GGAGGGTGAG      540
ATTCCTTCCC GCCGAAAACC TAAGGTTTCC TGGGTGAAGG TCATCTGCTC AGGGTAAGTC      600
GGCCCTAAG GCGAGGACGA GGGTCGTAGT CGATGGGAAT CCGGTTTATA TTCCGGAACC      660
TCTTGCAATT TCGATGGCAG GACGCGTGAG GTGAAGCCCG GCCAAAGATT GGTAGTTTTG      720

```


GTCTAAGTAT CCGAGCCGTT TTAAGAGCGA TAGGCAAATC CGTCGTTTGA GGTAAGGTGC	780
GAGTGCGACT GGAGCGATGA GCGAAGGGAA GCAGGTGTAG TCATGGCGAC GGGAAATACT	840
GTCTAAGGTT AGGTTGCAAG AGACCGTACC GCAAACCGAC ACAGGTAGGT AGGATGAGTA	900
ATCTAAGGCG CTCGAGAGAA CTCGCGTCAA GGAAGTCGGC AAAATACACA CGTAACCTCG	960
GGAGAAGTGT GACCCTTGCC TTTGGTGAGG GTGGCAGAAA GCAGGTCCAG GCGACTGTTT	1020
ATCAAAAACA TAGCCATCTG CAAATCAGTA ATGAGACGTA TAGGTGGTGA CACCTGCCCCG	1080
GTGCTGGAAG GTTAAGAGGA GAGGTTCGTG GTAACACAAC GCTTTGAATT GAAGCCCCAG	1140
TAAACGGCGG CCGTAACTAT AACGGTCCTA AGGTAGCGAA ATTCCTTGTC GGGTAAGTTC	1200
CGACCCGCAC GAATGGTGTA ACGACTCTGG ACGTGTCTC GACGCGAGAC TCGGTGAAAT	1260
TTATGTACCG GTAAAGAAGC CGGTTACCCA TAGTTAGACG GAAAGACCCC GTGAACCTTC	1320
ACCGTAGCTT ACTATTGGAA CTTGGTTTAC CATGTGTAGT ATAGGTGGGA GACAGAGAAG	1380
CTTGGCCGTC AGGTTAGGCG GAGTCAACAG TGAAATACCA CCCTTGGTAC GTCAGGTTTC	1440
TAACCTTTGG CCGTGGATCC GGCAAAGGGA CCGTGGTAGG TGGGCGGTTT GACTGGGGCG	1500
GTGCGCTCCT AAAAGGTAAC GGAGGTGCGC GAAGGTCTCC TCACACCGGT TGGAAATCGG	1560
TGCGCGAGTG TAAAGGCACA AGGAGGCTTA ACTGCGAGAC CGACAGGTCG AGCAGATACG	1620
AAAGTAGGTC TTAGTGATCT GGCGGTAGCG TGTGGAAGCG CCGTCACTTA ACGGATAAAA	1680
GGTACTCCGG GGATAACAGG CTGATTTTCC CCAAGAGTTC ACATCGACGG GAAAGTTTGG	1740
CACCTCGATG TCGGCTCATC GCATCCTGGG GCTGAAGCAG GTCCCAAGGG TTTGGCTGTT	1800
CGCCAATTAA AGCGGTACGT GAGCTGGGTT CAGAACGTCG CGAGACAGTT CGGTCCCTAT	1860
CTGCTATGGG CGTTGGATAT GTGAGAGGAG CTGCTTTTAG TACGAGAGGA CCGAAGTGGA	1920
CGAACCTCTG GTGTACCAGT TATCCTGCCA AGGgTACGTG CTGGGTAGCT ATGTTCGGAA	1980
GGGATAACCG CTGAAGGCAT CTAAGTGGGA AGCCCGCCTC AAGATTACAT ATCCCTGAAG	2040
GTGACCTTC CTGAAGACTC CTTGCACACT ACAAGGTCGA TAGGCTGGAG GTCTACGTAC	2100
CGTAAGGTAT TAAGCCGACC AGTACTAATA AGTCGTGAGG CTTGACCATA TTATTCATCC	2160
TTCTCCTTCA CCCTACCCCT TTGCGTAAAA TATTTGCGCT GGTTGCCATG GTGGAGAGGT	2220
CATACCCGTT CCCATCCCGA ACACGGAAGT CAAGCTCTCC TACGCCGATG ATACTGCTCC	2280
TTTCGCGGAA AGTAGGTAGT AGCCAGGCTC CCCTTTGCCC ATCACTCGCT TGACAAAATA	2340
TTATCCGAAA CCTTAAAGTC CGCAGtGGCT TCGGCGCATT CGTTTGACCT GGTAGATTG	2400
GATGATGAGG ATTACGGTAC TATCCTTGCT GAGGATGTTG AGTTTTCAGG GACGGTTCGC	2460

TTTGAAGAGC CTTTCATGGT ACGTGGTGTT TTTGAAGGGA GCATCGAGTC CTCGGGTGAT	2520
CTTATGGTTG AGGAGCAGGC GCGTGTTCGC GCTGAGATAG TTGCAGATCG TGTGTTCATT	2580
AAGGGAGAAG TAATCGGGAA CGTCACGGCT ATGTCTGTTG TTCGCGTCTT CCCATGTGGG	2640
AGGTTGATAG GGGATGTTAC CGCGCCAGAA GTTGTGCTTG AGAGTGGGTG CTTTTCAGT	2700
GGCGTGTGTA GTATGCCCGA ATCGGGTTGA TCGGTTTCCC TTGCAGACGG GTAGCTCTCT	2760
TGGTCGCTAG GTTCTTTTTC CCCGTTGTGT TCTGTTTCGT GTGTAGGGGG CTCTGTTTCGC	2820
AGCAGTCTGG TCTTGCTTTC TACCGGGCGG GTAGTTACCG TGAGGCGATT AGATGCTGCG	2880
AGGAAGCTAT CGCACAGGGG TCTAAGGACC TTGAGCATTA TCTCGTGCTT GCCTGGGCGC	2940
TTGTTGCGGT TGGGAAGTAC CATGAGGCTG CCCAGTGGGC CCTCGAGGGG CGCGCCGTTG	3000
CCGCCCATGA TCCTCGCCTC ATAGAGGCGC AGGCGGAGGC TTTCTGCCAC TTGGGGAGAA	3060
ATGAAGAAGC GCTTAGGTTG TTTCAAGACT ACATTGCGTG TGCCCCGAAT GGAgCgcGGC	3120
AGACCGCCGC GTATTATCTT ATGGGGGAGA TTTACCTGCG CACTTCGCGC TTCTTGCACG	3180
CAGATATCGC TTTTTCGGTC GCGCTCCAGT TAGATTGCGT TAACGATTTT TGGTGGGCCC	3240
GCTTGGGCTA TGCaCgcGAG CGCGCGGGGG ACTATCGCTA TGCCTTACAG GCCTACGACC	3300
GAGCGCTCCA GCTGAATAGA GATCTGGCTG ATGCTCGCCG GGGCAGGGAG CGGGTGCTGA	3360
GGTACGTGTT CCGTAGGTAG GTTTCTTTCG TGTTTTCCGT TCGCATCGAG ACGCTTGGCT	3420
GTCGTCTGAA TCATGTCGAG TCTGAGTCGC TGGCAGCGCT CTTCTTGCAG GAGGGCTTTG	3480
CGGTATGCCG TGGCAATACC TCCACTGCCC CAGTGGTTCT GTGTGTGATC AACACCTGCA	3540
CGGTCACAAG TAAGGCAGAG CAAAAGGCGC GGCGCCTCGT TCGTCTCCTG TTGCGCACAT	3600
ATCCTACTGC AATAGCGCTT GTCAGTGGAT GTTATGCGCA gcTTGAGCCT GCTTCTCTTG	3660
AAGCCATGGA TGATCGTGTC CTTGCTTTTC CAGGAAAACA AAAAGATGCC CTCAGCCTTC	3720
TGCCCTCGTG TCTCCGTGCG TTACTTGTGC AGCGTGGTCC TGCGCCGATA GATCAGTATG	3780
TATGCGGTAT GCGTGCGCTG CTCGCTTCTT TGAAGAAAAA AATTATTTCT TTGGAACATA	3840
CGTCTGAGTT TCCATCGCAG ACGCATATGC CCACAAGGAA TGCCCTTCCT CAGTTAACCG	3900
GTGTGCCTCA TGCGCCGCGC GTTCTGTAT CTTGTTTTC AGAACCTACA GCCGTTCCCC	3960
GTTTTGCTTT GTATGCCCTT CGTTTTTGT TCCACTCACG CGCAAGCATT AAGGTGCAGG	4020
ACGGTTGTAA CAGTGGATGC GCTTTTGTG GCATTGCTT TGCACGCGGT CGCGCTGTAT	4080
CACTTGAAAC ACACGAGGTA ATTGGGCGGG TGCAGGCCCT TGAAGCTCGT GGTATGAGCG	4140
AGGTTGTACT TACAGGGGTG AACTTGTCTC AGTATAGAAG TGGCAGTATA GATTTTGCGG	4200

TTTTATTAGA	TTGATTGTG	CAGGAAACGC	ATACGATTCA	TATTAGAATT	TCGAGTTTGT	4260
ACCCAGAAAG	CGTAACATCT	GCTTTTTTGC	GTGCTATTGC	GCACACGCGC	GTGTCGCCTC	4320
ATTTTCATTT	ATCGGTTTCT	TCGGGCAGTG	ATCGCGTGT	ACGACGCATG	CGACGCGCTT	4380
ACACACGTGC	GGACATTTAT	CAGGCAGTTT	CCGATTTACG	GAGTGTGCGT	GAAGAACCCT	4440
TTTGTGGTTG	TGACATAATC	GTCGGCTTTC	CAGGGGAAAC	AGAGGAAGAT	TTTGCAGACA	4500
CCCAGCGTAT	GTGCAAAACT	TTGCGTTTTG	CAGGTATTCA	TGTATTTCCG	TTTCTGCAC	4560
GCCCCGGTAC	AGAGGCGTTT	GCTATGGATG	CAAAAGTGCC	TCAGCGTATT	GCAGGAGAAC	4620
GCGTTGCTGC	AATGCAGCAA	CTGGCAGAGA	AAAACCTACG	TGCGTATTTG	GAATATTGGA	4680
ATGGGAGGGA	ACTATGTGCG	GTGGTAGAAC	AGTCCGTCGC	ACGTGTTTTG	ACAGAAAATT	4740
ATTTGAGCCT	CCCAATCATT	GAACGGGGTG	GCGTCGCTGC	CTCAGCAGGA	TCACACGTAA	4800
GGATTAGAGT	TCATAACGAG	GGTGCTATCC	TCTTGAGAGT	TTCTGATTCT	CAGTGGAGAT	4860
TCATTGTTGT	TAGAAAAAAA	CGAGCATGCA	GTAGAGCGTG	AGGAAGGGTC	TGTGCGCGTG	4920
TTTCTGTCT	GTCCCGTGCT	GCGTGAAGTG	AGTGAGCGTT	TCATCCGTGC	AGGATTTTGC	4980
ATTTATGTTG	TCGGGGGTGC	TGTGCGTGAC	TTTCTCCTGA	ACCGCAGTGC	TCATGATTGG	5040
GATCTTGCAA	CTGACGCTCC	CCCTGAGCGT	GTGCGTATGC	TTTTTAGACG	CACGGTTCCT	5100
ACTGGTATTG	AACACGGCAC	TGTTACAATT	CTTTTCAGAG	GGCATTCTAT	TGAGTnGCAC	5160
TACGTTCCGT	GTGAGTCGG	ATTATTCCGA	TAGGAGACAT	CCGATTCTG	TTTGCTTTGC	5220
CGCGCGCATT	GAGGACGATT	TGGCAAGGCG	CGACTTCACT	GTCAATGCTT	TCgCTGCCGC	5280
GCTCCCCTCG	GGGGAAATCA	TCGACGTATG	TGGCGGTAC	GCcGATTTGC	GTAACGGTCT	5340
TATCTGTAGC	GTTGGGGATG	CACATGCTAG	ATTTTCTGAA	GATGCGTTGC	GTCCTTTGCG	5400
TGCTGTGCGT	TTTGCAGCGC	AGTTATCTTT	TTCCATCGAA	GCGCGCACGC	GTGAAGCAAT	5460
TtnAckcTAC	GCGCTCaTAC	TGCACGTATT	TCTCGTGAGC	GGGTGCGTGA	TGAACTTTCT	5520
AAGATGCTTT	GTACTCCCCG	TCCGAGTATT	GCCTCCGCCT	AATGGAAGAG	ACTGGATTGC	5580
TGCACACACT	TTTTCTGCC	TGGCGCAGGT	GTGTGGGAGA	AACGAAGGGG	AGGAGAAGGA	5640
GACGCAGGAC	AGTCTGCAGG	TTTCACCGCA	GCAACGACGT	GACGCTCGCA	CCTTTGCTGC	5700
GTGCGCGTTT	GCTGCGTGCG	ATCGGGTGCC	TGCAGAGCTT	GCGGTCCGCC	TTGCAGCACT	5760
TCTCTTTCCG	CTGGCTCACT	ATCGTACGCT	TCCTGCTTCA	GGAACGGGGG	CAGCGTTGTT	5820
TATATGCCCT	CCTGCACTTG	CTGAAGCGCG	CGAGCTTTTG	CGTGGCCTGA	AGTACCCGAA	5880
TTACcTGACG	GCTCAGGTGT	GTCACCTGGT	TGCACACGCG	CGTTTTACTC	CACACGAATG	5940

TTGGTCTGAA GGAACGCTCC GTCGTTTCGT TGTGACGGTA GGTACTACTC AGCTAGAATC	6000
GCTGTGTGTC CTGCGGCGTG CCTATCTTGC TGATGACGAT TACCGCATAT CTGCTCAGCC	6060
TGGAGTGTCC TGCGAGAATG CGCGGGAAGG AAAAAAATG CAGGAACAGT TTGAAATATT	6120
CGTAACACGC GTGCGCAGGG TCGCCGCACA ATTGCCTGTG CACGGCATA CCGACCTTGC	6180
GGTGAACGGA CGCGACTTGA TAGCGCAGGg CATTCCCCCA GGTCCCACCA TAGGGCACAT	6240
CCTGAACGCA CTGTTTGATA TGGTCCTCAT GCAACCGTCG CGCAACACGC GTCCGCAGCT	6300
TTTGGAACAT GCGCAGGAGA TTGTGCGCAC CATGGCGCAG AATTAGTGCG CCTTGAGCAA	6360
CCCGTAGAGT CTTTCTAATT CTGCTTGCGA GAAATACGTG ATCTCAATTC TCCCCCGTTG	6420
TAAATTTCCA CTGATGCGCA CCTTGGTTCC CAGTTGTTCC AACAAATGCT GTTCAATGTC	6480
TGCGATGTCT GCGTTACGTA TGCGCGCATC TAATTGCGCA TCCGTCGATG GGGAAGAAGG	6540
AGGAAGGCGG GTGATGTCTG TAGCAGAACC GCCGGGTGAA GGGGAAGACG CCGCCGTGTG	6600
CGCGCGAGCT CCAGCGTAAT CGTGCAAAC TCCGCCACGA TTAAGACATG CAACGCACTC	6660
CTCTGCGGCA CGTACAGACA ACGCATGGGT AACTACATAC TGAGCAACGC TTACACACAA	6720
CTGCATGTCT GTGAGTGACA GAAGTGCGCG CGCATGCCCT GCGCTCAGCG TTCGAGACGA	6780
AAGCGACTGC TGAACCTCAG GAGGCAGTTT TAAAAGACGC AGCGCATTTG TAATGGTACT	6840
GCGGTTTTTTT CCAACCCGCT GTGCGAGCTC TTCATGACTT AAATTACCCA GATCCATGAT	6900
ATGTTGATAG GCGCGCGCCT CTTCCAGGGG ATTCAGGTTT TCTCGCTGAA CATTTTCAAT	6960
GAGCGCGATG GCAAGCTTTT TTTTCATGATC GCAGGTGCGC ACGATAACAG GTATCCGATT	7020
CAACCCCGCA AGGATGGCAG CGCGTGTCTC ACGCTCCCCC GCGATAATGA CCCAGCTTCC	7080
GTCCTGGTTT TTTTCCGCAA GGAAGTGGCTG GATTACCCCG TGCTCACGAA TAGACGCGGC	7140
AAGCTCCTCG AGAGATTCCT GCGCAAAGGT GCGACGCGCC TGATGTGGAT TCGCCTGCAG	7200
CAGCGTGGGA TCAAGATAGT GTACAGTCTG CACACCGCCT GAATCACGAA CATCGTATCG	7260
ATCTGAGCTT TCTTGACGCA GCGCGTCAAT GCCTTTGCCT AATTTATCTT TGCCCATCGC	7320
GTGCCACTAT TTCCCGTGCA AGCTTCTCAT AACTCCGTGC CCCTGCGCAC TGTGCATCGT	7380
AAGAACTAAT GGGTAACCCG TGCGAAGGGG CTTGCGATAA CTTTACGTTG CGAGGAATGA	7440
TAGTATTGAA CACCTTGTC CCAAAATAGG TTGTCACTTG CTTAACCCT TCTTGCGCCA	7500
gCTTAGTTCT AGTATCATAC ATGGTAAAGA AGATGCCTCC GATCGAAAGC GCGGTATTCA	7560
GACCACTTTG TACACGCTTT ACCGTCTGCA GTAAGAGTGT GAGGCCTTCA AGTGCAAAAT	7620
ACTCACACTG CAATGGGATG AACACCTCGT TTGCCGCTGC AAGTCCATTC AATGTGAGGA	7680

TACCCAGCGA GGGCGGACAA TCAATCAGGA TAAAGTCGTA CGTGTCTTTT ACTTCTGCCA	7740
ATATCTTTTT AAGGTAGAGC TCGCGGTCTT GTTCATCTAC TAGTTCCACC GTCGCGCCAG	7800
AAAGATCGAT GGAAGCGGGG ATAGCAAAAA GGTATGCAC TGGTGTaGTG CGCAcGctGt	7860
TGATGTGTGC CTTACCTGCA AGAAGATCAT ACACGGTCAA CCCTCTAGCT AAGCCGAGAC	7920
CCGAGGACAT GTTCCCTTGA GGATCAAAAT CAACGAGCAA GGTTTTCTTT CCTGCAAGCG	7980
CTAAATACGC ACCCAAGTTA ATGGCAGAGG TTGTCTTACC CACCCCTCCC TTTTGATTTA	8040
CGAACACCAA GGTTTTACCC ATGGTGCCGG AGTGTA CTCC ACTTTCTAAA TAAATAAAAG	8100
GACTTCGAAA GCGCGTCTGA ATGGGAAGCT ATGCGATGGG GTAAATCCTG GTAAGGAGAT	8160
ACGGTGTGCA AAAGCTAGAG TGATACGATG AACTGTGCTA CCTTACGCGG AGGTGATCCT	8220
TTTTCTTATA AAAAAACATT GCATTGATTG TGGTGAAGCG TTTTTCGGTA TTGTAGTGCT	8280
CAATGCGTTG TGTCTTGCA GGGTAGGGTA CAGTCTGTTA TGGCACCAAG GGCCTGGTCG	8340
GAGCGTGTG TTTGTCTTAG TACTGGCTAC GCTGTACGCA TGTCTGTGCG CGTTCTGTGT	8400
CGTTGCGGGA GAACGGGGAT GTGATACTCT GGCAGATACG AATCTACGCG TCTTCACACA	8460
CGCACTGCGC GAGGTGTGGC TCCAGAGCCT GTGGTGTGCA CTGCTACAGT GTGTGTTGTT	8520
TCGAACTGGA AAATACGTGT GTACATATTA CTTTGCACGC ACGCATTCCTG TATTTACCGC	8580
GTGCGgTATA CTCAGTGCCT GGACATACGC GCTCGCgTGC GGTGCACTCC TGTGGTTTGT	8640
GCCGGTGCCT GCACGCTACA GAACGCATTT TCGCCAATGC GTATATCTCT CGGCACGAGT	8700
ATTTTTTGAG CACCCGTGTA TTACCTTCCT TATGGTTTTG TACAGCATGG GTGTGCTCGC	8760
GCTGAGTGTA CCAATGGCTT TTTTATTTCC AGGACCGTGC GGCATTGTGC TTCTGTGGCA	8820
GgaTgtgCTG CGCACGCTCT GTTTTCGTG TGCATGGCTT GCTGCACACG AGGGGCGCAA	8880
GGCGGCGTGC GCACCGCCTA TTCCCTGGGA GCAGCTCATG TGCCAGATGC GTGCACAATC	8940
CCGCGCGCAC ACCGTCGGCG AGCTCTTCTC TCCGTGGAAA TCGTAATGTT CATTGTGTTT	9000
GAGAGAAATA ACAACCCCGC AGTCTATGAG GGGGTGCCGT ACTCAGCAGG ATTTTGGTAT	9060
ATGTGCTCAA GCGCGATCTG TGCTTGTCGA AACAGCATGA TACTTTCTGT CGCAGTCTGA	9120
TAACGCTTCT CAGCAACGAC ACGCACAATG CCGCAGTTAA TGATGAGCAT TGCACAGGTG	9180
CGGCACGGTG TCATGGTACA GTAGAGTGTT GCGCCCTCTA GACCGATGCC CAAACGCGCT	9240
GCCTGGCAGA GGGCGTTTTG CTCTGCGTGC ACGGTGCGAA CGCAATGCTG CGTGCACGTC	9300
CCGTCTTCAT GCTGCACCGT GCGTAGCTGG TGTCCATGTT CGTCACAATG cAGGAGACCT	9360
CGCGGTGCGC CTGCATACCC AGTTACAAGC AGATGGTGAT CGCGCGCTAT GACGCAGCCT	9420

GCGCGTCCGC	GATCGCAGGT	GGCACGCTTG	GCAATTGCAT	GACACACTTC	CATAAAATAC	9480
TCATCCCAAC	TCGGTCGCGT	AACCAACTCC	TCACGTTGTC	CCATTaTCGT	ATGCTCCCTT	9540
TTTCCCTTAA	AGATGCACAT	GcCCTTGTGC	TGCGGTGCGC	AGCACACTCT	GGCGGGTGAG	9600
TTTAAACATC	GCTcaCTTCG	TGCGGAATAT	ACGGTAGAAA	AGCAAGAGAA	AGATATACCA	9660
TACGTATCGC	ACGCTCCTGT	GCCAGCGCAA	TGGATGCAGT	GTTTGTCCCC	AGGacTGCCT	9720
CCGTGTAACA	GTTCTTTTGC	GCGTGGTCGT	TTGCGCCGTT	TTGAGAAAAT	GTCGATAACC	9780
TCGCTGTCTT	GCACAAAAAT	GCCACCGGCG	AAGTGTGcGC	GATTGCGCGC	AATCCATCGT	9840
ACGCCCTCTG	GTACCCCATTT	GCCGACAATT	ACCAGCGATG	CGTTGGATTT	TACAATTGCC	9900
GTGATAATGT	TGTTTTCTAA	CGTCTTACGA	TAAAAGCCGT	GAAATCGACC	TACCACGCTC	9960
AGTCCGGGAA	AGGTAGAATG	CACGtTACGC	TCCGCCTCGA	GCAGACTCTG	TCCCCGACCG	10020
CCGAACAAGT	AGAGTGATTT	GTAGTGCCTG	TCCATAACGT	TGAGCAAGGT	GATGATGAAT	10080
TGAAACGGGT	GCCGAAAGAT	AGGTGTCGGC	AATCCC AAAA	AGCGTGCACC	GCGCACAATA	10140
CTGTAGGATG	TGGGCAGACA	CAACGCTGCG	cGGCCTACCA	TGGTGC GGAA	CTCGTGATTA	10200
TGCCGTGCCT	TTAGCACGTC	CCAGAGAGAA	AGAAATATAA	TGTGCTGCGG	CTCTTTTTTTT	10260
TCTAACAGGG	AGAGATGAC	GGTGACAGA	TACTCTTCAC	GCACCACATC	AAGGGGTACG	10320
GAAAGGAACT	CAATGCGCGT	TACCAGCTGC	GTTTGTTCCT	TAGTGCTGCC	TCACTAAGAA	10380
GGAGATGTGC	GCCTGCAAGA	GCATAGAGCG	CGGCCGTTTC	TACGCGwCAs	ACATTCGTGC	10440
GAAAGTGAG	GGGTGCAAAG	TGCGCGTCAT	GAAGCGTGCG	CTCTTCTGTA	TCAGAAAAAC	10500
CCCTTCAGCG	CCTACTGCAA	GTATAACCCC	TGCGCGCGCA	CATCCGGCGT	GTTGTGCGGC	10560
GCATTTGGCT	CTGTGGGCGT	ACGGTGCGCG	GTGCAGTGTG	TAGAACGTCC	TGTCCAAAGC	10620
AGTTCTGTAA	AGGAACCTCC	CACGTGTTTT	TCACTGcAAT	AGATACGCAC	TGCAGAAGGA	10680
TAAGGAAATT	CCTGCTCGAG	CATATGCAGT	GCGCCAAGGA	GGCTGTGGAG	CGTGTCCACA	10740
CGGGTGTTCA	CGGcAGAACC	AGACTGTTGA	CGCGCTTCCC	GCACGATGCG	CTGCAAGyGt	10800
GCATGCTGGG	TGTCTTTTTC	ATCGCGGATG	AGCGAACGTT	CTCCTCGAAT	CGGTATGATG	10860
CGCGCAGTTC	CAAGTTCTGT	CGCATGCCGA	ACGAtCGCGT	CAAAGACGnG	CGCACGGGGC	10920
ATCCACTGAA	GCAACACAAG	CGTTACCTGC	GTTTTCTCAT	CCACTGGGGG	CATGGGCGTG	10980
CAGTGGAGGA	TTAGTGAACG	CGTATGTATG	TCGAGAGCGG	ATACTACTGC	GCTGTACTGC	11040
GCACCGGCCCT	GCGTACGCAG	GGTGAATGTA	TCCCCcAgCG	TGCGCGTcGA	ACACGCACCA	11100
TGTAATGAAA	ATCCTTGCCCT	GAAAGCTGCA	CATACCCGCC	GGAATCCGGT	TCTGCGGTTA	11160

TCAGCAATTG	TTTCATAATA	TCnCaCGgCT	GAGcGCGCCG	GACGCTGTGC	GACAACACCA	11220
CCGTAAGGAA	CTTCTCTCAC	CGTAAACCCT	ATACATATCT	GAAAgTAGTG	CGGCGCCGAG	11280
CACGCACAGT	CTGGCTCCCA	TAGCCTGGGC	AGCGGGACCG	ACCTGATAAG	GgCCACACTC	11340
ACCAAGTCTT	TGCAAGGGGT	ATAACAAGGG	CGCAGCGTAc	rAACTGGACG	TTCAAGATAC	11400
CTTCTTTTTT	TCCTGTATTG	CCTCTTGCAA	TTCTTTGACC	GTTTTAGTAC	GCGCCACCAG	11460
CGCKTGaATA	TCCTGTGTGC	GTATCAACTC	CACCGCCTTT	CGCAGCTGTT	CATCATATTG	11520
TAAGTCATAT	ACAAAAGACG	CATTGTGCCG	GTGATACTCC	TGTGCGATGA	GCTTTTCCAC	11580
CAGTATTGAT	CGGAGTTTAA	ATTGCGGTGC	CAGGCCACGT	GCATACTGTT	TTATGCGTTC	11640
GGAGTTCATG	GTACGGTTCT	GCTCTGCAAA	GAGTTTCACT	TTTTCAGACT	TAAATAGACT	11700
GACAAGTGCC	TCTTCTTCCT	CGGGAGTAAA	CTCTGTTTCT	CGTACCTCGA	GGTCCGGCGG	11760
AATGCCGctc	TTATCGATAT	TTGCGTCGCT	TGGGGTGTAG	TAGCGTGAGA	TAGTCATTTT	11820
CAAACCTCTCC	CGTTCATTGA	GGTCAAAGAC	TTGCTGCACG	ACTCCCTTTC	CGTATGTGGT	11880
TTGGCCGACC	AGATATGCGC	GCTTGTGGTC	TTTTAGCGCA	CCTGAAACGA	TTTCTGAAGC	11940
GGACGCAGAA	TCCCTGTTGA	TGAGAACAAT	CACAGGCATA	GACGGAGGTA	GCTTCTGCGC	12000
ACGTGCGTTA	ACGCTGAACG	TTATGGAGTG	TCCCTGCACG	CGTGACTTAG	TGGTTACAAC	12060
GGTTCGGAG	GGAATGAATG	AGCTGGTAAC	GTCCACTGCG	GCGGTGATAA	GGCCGCCTGG	12120
ATTGTTGCGC	AGgTCGAGAA	TGAGACGGTC	GCAACCTTGC	CTACGCAkTT	CGGTAACGGT	12180
TTCTACCATG	CGGGTAGCGG	TGACTGGGTT	GAACCTCTATG	AGGCGCACGT	ACGCGATGTT	12240
TGGATCGATT	TTTGCGTACT	TAACAGTGGG	AATTTCaATT	TTCCGACGGG	TGAGGGTGAA	12300
TGGTCGAAAA	ATCTTTGTAC	CCCGTTTGAC	AACAAGAGTC	ACCTTGGTGC	CTATCGGCCC	12360
CCGTAGTTTC	TTTAAAACCT	CGTCCATAGT	CATGGTGTCA	GTGCTCATGG	TGCCGATTTT	12420
GACGATGAGG	TCCCTCGGTC	TGATTCCCTCC	TTTCCAGGAA	GGAGTGTCCT	CAATGGCGGC	12480
GGTCACTTCC	ACGTAGGCGG	GTTTGCCCGG	AGTGGATGTT	CTGGACTTAG	AAATGACAAC	12540
GCCGATGCCG	CCAAAGAAAC	CCTTGGTAGT	GTCTTGGAGA	TTAACGCCGC	TGATGCTGTC	12600
GCTTTCGACG	AAGGTTGTGT	AAGGGTCCTG	AAGAGAGTTA	ATCATGCCTT	CTAGTGCCCC	12660
CTTGTAAGAG	ATGTGGGGGT	CTACCTCGTC	GACGTAtATT	TGCGGAGGAA	TTCGTAGACA	12720
TCCTGCACCG	TCTGCATGCG	CTCGTCTTCC	TCGGAAGACT	GTGGCAAATA	AGCGGCAGTC	12780
CATGTGGGGA	AGGGAGCTGC	GCTGGTGATC	AGACAACAGA	CGAGGAGCGC	AAACAGTCTC	12840
AGAACACTCA	TGGGCGGATG	ATGGAATGCG	TGCCCCGTCTG	TGTCAAGAAT	CTGCGTTGGA	12900

CAGTTTCCTT TCCATGCGAC TAGACGGAGG AGGGCACTGG GGGAGGTGCA GGCGCGCCCC 12960
 AGACCCGCTC TGGGAGGAGC AGGATATAGC GTGACTTCCG TTTTCTGCCC TGTACTTCCC 13020
 TTCTTCGTTT TTCACCCCTG TGCATGGGGG GGGGGAGAGA GAGAGAAGTT TCGTTCATCC 13080
 TCGCACCCGT TCGGTTGCGG TCGGTGCAAG GACTGTGCTA CAGTGCCGGC CGATGGGGAC 13140
 CGTGATCATC GCTCTTGATG GACCTGCAGG CTCTGGGAAG AGCAGCGTCT GTCGTCTGCT 13200
 CGCGTCTCGC CTTGGCGCGC AATGTTTGAA CACGGGTCTT TTCTACCGTG CATTTACCCCT 13260
 CGcCGCATTG CGTAGGGTAT CGGAGTTGGC CGTGCAAGCG TGCTCTCCTT CTCCGGACCC 13320
 TGATGCGGCG GTCGGGTGCG CGGCTGTTCC ACACGCAACA AATCTGGACA CATCATATGC 13380
 TCCTCTGACG GCCCAGAAGA AGGTTGCACT TTTTGATGAA GCGTATTGGG TTTCGTTTGC 13440
 GCGCACAGTT GCGCTTTCTT ATCGTGCGGG TGTGATGTAC GTGGGCGAAG AGAACGTGGA 13500
 GTCACTGCTG CGTTCGGATG AGGTGGAGTC GGCAGTCTCG TACTTCGCGG CAATGCCGGC 13560
 TATTCGGGCA ATTATGACGG GGAAGATCCG GTCGGCCGTT TGTGGTGCGC GGGTAGTTTG 13620
 TGAAGGGCGT GATCTAACGA CGGTTGTGTT TGTGGATGCG GACTTGAAGT GCTACCTTGA 13680
 CGCTTCTATT GAGGCGCtGT GCGCGTCTGT TGGGCGCaGG GAACGAGCCG GTTATCGAAg 13740
 CAGGAACTCG AGCAGGCGCA TGCGCGCGAC GTGACGCACA CGACAGCGAC GCnCACCGTG 13800
 GGGGGGCTCA G 13811

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

TTTCATACG CTCGCTCCAC ACCTTTGCTT TCTTTTTTAC CTCCTCTGCA TCTTGTCGCT 60
 CGTTGAGCAA CAGGTGGACC CTGCGCAGCG CGTGCAGGTA GCAGACAGCC AATTTAAAAT 120
 CTTCAAAACT GGAGGACGTC ATCTCATACT TTTCCCGGTA ACGCTCAGCT GCCTGCAGGA 180
 GTAATTTCTT TACCAAACGC AGGTGATAGA CCACTGTCTC GTACTCGTCA GCCTGTGGAT 240
 TCAATCCAAT CTCAGAAGAA TTCGCTAAAT CCAGAATATT CTTGCGCCACC GTTGCGTAgc 300
 GCGCCTGGAG CTCTACAAAA GACCAATACC ATTTAGTATT CGTCCCATAG GCGCTAATAA 360
 TGGAATCAAT GCGGAGTCCC ATCTTACGGA TAAGATAATA ACGCTGCTGC TGACTTACGT 420

810

TCGCTATCTG CGCCACCTGT TCCTGGTAAT CGGAAAACGG CGTGTC AATT AAATTGGTAA	480
CAATTTCTTC AAGATAGATG AGCGCCTTAT AAAGCGTTTT CCGCGCCTCA TTCAGCAGAT	540
CCTCCTGCTT ACCACCTACT ACTACAACCT GTGTCTGATA TTTAGCAGCG TACAGCGTAC	600
TGAGGTAAAT CATGTCATCT ACCAACCGGA GCTTCTTGTA CGCCGCGCCC GTCCCATCCC	660
GCCTGATCAG TTCTAAAATG TTTTTCAC GCGTAAAGAT TTGATCAATA GTCCCTTGGT	720
ATACGTTCAA CTTTTCTGG TACAGAGCAT TCTGCTCTTC CTCAGTCACC GCACTCCCCC	780
CTTCTTGCC GCGCACCTGC GGCAACAACCT CCTGCGCATG CGCTAGGGAG GTTGCACTGT	840
GCGTGTCCCC TGCTAGCATG CGCGCAACTT CTTGAACCCG TCGTTCCCCC ACTACATGCG	900
CCGCGCTCGT ATTCGTGTGT TCTCCACTCG ACTCTTTTTT CACACACAG TGCGCATCCG	960
CTGCGCCGC TATCATAGCC AAATGCGTAA TGCACACAAC CTGCTTGTGC TCAGACAACG	1020
CTTGCAAATG CTCTGCAACC GCACGCGCG TTTCACCTCC AATTCCCACA TCAATCTCAT	1080
CAAAAATCAA CGTGCCCACT TCATCGACCG ATGAAAGCAC AGTCTTTAAA GCAAGCATCA	1140
CGCGGAGAG TTCCCCCCT GAAGCAATCT TTGCTAGCGG ACGCGCAGGC TCTCCTGCGT	1200
TGGCGCTAAT TAAAAACTCA ACGTCATCAA AGC	1233

(2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2946 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

GTAAAGCAAA ATCACTCAGG ACAAGACTCA CTTCTTACTT TCGCTGCAGG CACGACCCAA	60
AGACACGCGT GCTGATGTCG CGCGCCGCTG CACTTGAATA TCTACAAACA CAACACGAAT	120
ACGAGGCGCT GCTCCTTGAG AACACACTCA TAAAAAACA TACTCCGCGC TACAATATCT	180
GCCTCAAAGA CGGGAAACC TATCCTTTGC TCAAGCTAAC CTGCGAGCCA TTTCCGCGTA	240
TTTTTCGCAC ACGCCAATTC TGTCAAGACG GTGCACGGTA CTTTGGTCCC TTCCcTGACG	300
TGCAAATCCT CGATTCTTTT CTAAACTCA TTTTACGCAC CTATAAAATC CGTACGTGCA	360
CCACcTTGCG GAAGAGAAAA AATCCTTGCC TCTACTATCA CCTGAAGCGC TGCGATGCCC	420
CGTGTGTGG ATGGGTCTCT CCACGCACAT ATCAAAAGGA CATACATGAG ATTACCCTGC	480
TGCTCGAGGG GAATATTGAC GCGACTGTAG CGCGTCTAGA AAAGCGCATG AAACGAGCAG	540

TCCGCCAAGA AGCATTCGAA GCTGCCGCGC GCATACGCGA TGATATCCAG GCAATCCGCT 600
GTATTACACA CAAAAGTCTT GTTCAAGACA TGGACGAACG TGCACGCGAT TACATCGCCT 660
GGTCGAGCAC GGGAGCAATC GTCACCTTCG CCGTTCTACG CATGCGGGGA GGAAAATTAA 720
ACGGTAGAGA ACTTTTTCGC ACACGTTTCAT TAAAAAATGA AGAGGAAATC CTTTCAGAAT 780
TTCTCATCAC TTACTACTCT GACCATACCA TACCCCCACA TCTATTTGTA CACTCGTCTG 840
CAGGGTTAGC AGAACACTGG CTCAGCCATA AAGCAGGTAC ACAATGTACC GTCACGCTCA 900
TCCCTTTGCA TACCTTTCTT ACGCCGCGA CCCCTTCTTC CACTGTCACC ACAAACGCTC 960
CTACCTTTCG AGCTTCGCAA AATAGCAATG CAGTACAAGA TTCAGGGTTA CGTTCTTGCA 1020
GCGAAACGTC CACCATGCAT ACGCTTCAAA AAGCACACGA CGCCTGCACT GCAAGCGAAG 1080
GCACACGAGA AAACACACCG CACGAGAGCG CGCACACTCC TCATCACC GCATTTTAG 1140
CCATGGCGCA GTTAAACGCT CATGAAGATA TTACTCGGTA TCTGAAAAAT CGCGGCGCTG 1200
ACGATGCACT CAAGGAATTG CAAAAGCAAC TGCATCTTGC ACGCATTCCT ACGCTCATTG 1260
AAGGATTTGA CATTTCCCAT TTGGGTGGAA AGTACACTGT CGCAAGTCTC ATTTGCTTCA 1320
AAAATGGGGC CCCCAGACACA AAGAACTACC GATTGTTTAA TTTACGTGCG CACGACACCC 1380
GTaTTGACGA TTTTGCATCG ATGCGCGAaA AATTgCCCCG CGTTATACCC ACACACCAGA 1440
GGGCTACACT CTGCCCCGATC TTATCCTTGT CGATGGGGGG AATCGGTCAC GTTCTGCTG 1500
CACAGCACGT CCTCGACGCT CTTGGTCTTA GTATCCCGCT TGTAAGTCTT GCAAAACGCG 1560
CAGAAGAGCT ATTTATCCCC AATTCTCCTA CACCACTAGT TCTGGATCGT CGCAACCyTG 1620
CACTGCATAT GCTgCAACGC ATCCGAGATG AAGCACACCG cTTTGCAATC ACACGGAATC 1680
GGCATCTACG CACAAAGAAA GAGCTAGTCT TAAGCTTTGA GCGTCTCCCC CATGTGGGCA 1740
AAGTGCGCGC ACACAGACTG CTGCTCACT TCGGTTCGTT CCGCAGCCTG CAGAGCGCAA 1800
CTCCCCAGGA CATAGCGACA GCCATTCATA TACCGCTCAC CCAAGCACAC ACCATCCTGC 1860
ACGCGGCAAC CCGCTCAACA ACCGCCCCTG TACGAGAAGA ATATAAAGAA CACGAGCACG 1920
ACCCCCAGGG AGAATCACCT GGACCAGGTC GGAAAACAGA CTAACGCGCA CCCGGCCTAC 1980
GACGACGCAT CCAGGAGTCG CTCAAGCTCA TTCTTTCCCA GAAGCTCGAG CGGACGATTT 2040
TCTGCAAACG AAAGCGCAGC GcgTGAAAAC GAAGAAGACG TCACCACCAC CCCACGCGCT 2100
ATACCACGCT CCTTCATGCG CTCCAAAATA GCGCGCAGGA AGCTGTCATC GAGCACC CGC 2160
GCTTCCCGGT AAAAAACAAC GACTTTTGGC TGCGTACGCA CGTTGCTCCA ACCCTTCTCG 2220
TCCCTTTCTG TGGCCACTAT TTCACAACAC CCGCGCACGT CCTGCACCGA GTCTATGGAT 2280

812

AAGCGAAGCG CcTTACTCAC AATTCGCTGA CACAGATCGA AAAAGGAATC GCCATCGAGG	2340
GTCAAATACT CCTTCATCCG GTCGTTCAAA CGTATATCCT GATATTGCGC GAGcTTATGG	2400
TCACATCCTT AAAACCCGCA GACCGTGCGT TGATAGCCTC CCACTGCTCA ATTGCCTTTT	2460
CCACATCCCG CTTTTTTTCG TAACAGGAGG CTAAGAGATA ACGTATCTGC AAATCCTCAT	2520
TTTCACCCGA CTGCGACTTG CAGCGCAGCg cAcGGTCAAA CTCAACAATG GCCCGATCCA	2580
CATCCTTCGC ATCCATGTAG CAACAGCCAC GCTCGGTAAA ACACTTCTGC CGCAGCACAG	2640
GACTCCTCGA CGCCTGCTCA AAGGAGCGAA GTGCCGCCGC ATACTCCCTT TCTTTCCGCA	2700
AGAGCTGCCC CTGGCAAAAAG AGAGCCTCCG CATTTGCAGG TTCCAAGGCT AGCACAGTAT	2760
CGAGCTCTGC CCTTGCTTCT GCAAGATGAC CAGACCGAAG AAGCAACGAA CCGAaGCGmr	2820
CATGCGCTGC AGGATGCGCA GygTCCATAC CGaTGCACTG GcGATAGTAT GCCGCAGCCC	2880
GATCGGTAC ATTCTTGCGT TCAAACAGCT GCCCAATACG GTAGTGATAA TCTGCACACG	2940
TAGGGT	2946

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1905 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

TACTGAAAAA CCGACCCGAG TAGCTGCCTC CCCATAATT CCcGTAGACC aTAGGCTGAa	60
TAAGGATGGC AACTCCaTCT TCCCCaTCCT CCTCAAACGA CaGCAGTTTA CTAACAaGCC	120
TTACCGCTTC TTCAAGCTGA ACGTAGGCAT CATCGAAAAA GCCGTC TGGA aGCAAGGCTC	180
GATACCGATT CATCGCCTCG CGCCCAGAGG GAGAAGATTT TCCTCCCTGC AAAAAAACCT	240
CTATTTCTT CAGGGTTTCG ACAAACCTCCG AAGCACCTT GGTGTTCTCC TCACTTTCTG	300
CGATACCAAG CAATACCCCA AATACACCTT TCAAAAGGAA GAACACCTCG TCGGTTGCAA	360
AATGCTCCCC GACACGCTCG GCAAACCCCG CGAAAGTATC CCGTGTCAAA CCAAAGTTAT	420
GTAATACCGG ATAATTGCAA ATGGCCAAAT TGGGGGATAA AACCACCTTG AGGAGCATAG	480
GATTCTTTGC ATCCGCATAC TCTTTTCTGT TTAAAAGCGT AAACCTTCTT AAATACGGAC	540
TTAGCGCGGA CCGAAGCTTC TCCCCATACA GACTACGAGA GACTGTCGCA TCAATAACCA	600
CGCTCGGAAG CACGGGCAAC CCCAGACTTG ACAACTCATC CGCCTGACGA CCCCGAATCC	660

813

CCAAAAGCCC TCGGTCAAGC CTCTTATCGA GAGCCTCTTT ATTGCTCAGA AAATGAATGG	720
ATTTGGCAAT GTTCATTGTG CACTCCTAAA ACAAATTCAA CACCGTGTCT GGGGAACCGT	780
GCAAAAACAC CTCAAAACGA GAACTCGCCC CCTCCTTGAA ATACTTAGAG AGCTTGACAA	840
AATCCTTAAT TTCCTCACCT GAACTGCAA ACTGAATCAC ACTCCCGTGC TTCACCTTTC	900
CCCATTGAA GAGAGTGTTA ATATCCACAA TACGCTCACC ATCGTAGAAC ACAATGACCT	960
CTGAAGAAGG GTACCGCGCG TTGTAAGTCC TGATAATACG CTTCCACGCT TCCACATTCC	1020
CGTTATGAAA CAACTCGTTA GAAACAGGCA CCGATATTAA CTGAGACATC CGAATCGGAC	1080
CTGcAGAGGC TTGAGCAGGA GGACGCGCGG TAGGAGACAC AGACTCAGAC GAAGCCCGAT	1140
CACAGGTAGC CCCTTCAGAC GCCCTGGCAG CGTCCGCACC CGACTTCTTT GCCGATCGAA	1200
CCCTCTTGCC AGAACCTCA GACTTTTTCG TAGACACAAA TGCAAAAACC CCCGAAAGGA	1260
TTTCTTTGGG AACCACGAAC TTACGATTCT CTATCAGAGC AATCAAACCC TTGGCGrCtT	1320
CGTCTGCAAT CCGTTCATCA AGCGGTCCCC TATCCTGCTT TCCCACGTAC ACCAACAAGA	1380
GCTCATTTTT CCGAAAACCC TCGACAAGGG AGGCGTTTCA AGGATTCTTC GGGTTTATTG	1440
CCAAAAATCC AAGATCGGGG TGATGATAAC CAAGTACAAT ATCCACTCCC TTCCACCGCG	1500
CAGTTTCCTG AGCAAACCCG AGACCTCGA CGGAAACCTT CCTTAGATTG TAAGAAAACA	1560
GCCGATACCC CCACGTGTCG ATGAGTAGCA CCGACAGGAG CGCTGCAACC TGCTCGCTTT	1620
GCATCTCcTT CGCACAGAGC AGCAGGTTGA CCTGGTCTGC GACGTTATTC TTCGGATCAC	1680
ACTCATCCAA CACGCTCAAA ACGCCCTTCA CATGACGCAC TAGAGCATTA AAGTTCTTCT	1740
TCACCGCTGC AGGCACGTAA AAAGTAGATG CACTCACCAC GTAACACTCC TTTGATGATT	1800
AAAAAGCTCC CCGAAACAGA AAAGTTCCAG GGAGCTTCGG ATCACGACAA AGTCTATCTA	1860
CAATCTCGCT AGAGTTCGCG AATGGCAGAc CGTCTACCAC GTCGA	1905

(2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

AGGATCTTTT CCTCAGTCAA CTCCAAACGA TCTCCATCTA CATCCAGATA CAGCGTCGTC	60
CCCTCGAGTA TCTCCTGAAT TTCTGCAGAA GACAACCGCT CAATGCTGAG CGCTGCACGC	120

814

TTTGTCTTCG ATCCAAGCTC TTTTCCGAGC ACTCTAAAAT TCGCTTTTGC ACGGTACTCT	180
ACTATCTCGT CTTCTTTCTC ATGAAACACG AGCTCTTTTA CATTAAGCTC ATCAAGCACA	240
TCTTCTTCCA TTTCAAGAAG TGCTGAGCGC TCCATCGGGT TACGCGTAAT AACCTGCATA	300
GCTTTAAGTG GCTGGCGTAC TTTGAGGTTA CACTGCGCTC GGATCGCACG CGCCATAGAA	360
ACAACTCGCT GCACTGTTTC CATTTTAAAC TCGAGTGCAT CGTCTCGCAC CATTGGTGTA	420
CAAACAGGAT AGTCTGCAAG ATGCACAGAc TGCACATCAT CCGCGGCGCG ATTATTCTGC	480
CATATACTCT CGGTGATGAA TGGCACCACG GGAGCAATAG CGAGCACACA TCTTTTCAGC	540
ACGCAATACA ACGTGTGTGA CGCACATCGT TTATCTTCAT CGTTGATGCT TTTCCAAAAT	600
CTCCTTCGAG ATCGGCGGAT GTACCAGTTG TTCAGCTGAT CTACATACGA AACGATAGGA	660
TCCGCAACTT TCGATACATC GTAAGCATCA AGTGCACAGG CAATGTCTTG CACCAATTTT	720
TCGTGCAGCG ACAAGATCCA ACGATCTAAC GGGTTATTCA AATGCGTCGC TAAACGCGTG	780
ACCGCCTGaC CCATTcCGTc AACTTTTGCA CATAcAGGcA GGATCGATAC CATCGATGTT	840
CGCATACGTA ACGTAAAAAC TGTAACtATT CCACAATGGG ATAATCACAG TCTTCAAAAT	900
ATCTTTcACC CCTTCGTCAG AATATTTTAA ATCATCCGCA CGGACAACCG CAGAACGAAC	960
AAGAAAGAGG CGGACGCGTC ACACCGTAGC GATCCATGAC TTCATTGGA TCCGCATAAT	1020
TGCGCAGGcC TTGGACATCT TCTTTCCATC AGACGCAAGT ACCAACCCCG TAACGATACA	1080
GTTTTCAAAC GCAGGACGCT CAAAGAGTGC CACAGCCAAG ATGGTAAGGG TGTAaaACCA	1140
CCCTCGCGTT TGATCTAACC CTTcAGAGAT AAAATGAGCA GGGAAATACC GcTCAAAGTC	1200
AGTTGcATGT TCAAACGGAT AGTgTgTgTG CGcATAAGGc ATTGcACCAG ATTCAAACCA	1260
ACAATcTAGC ACCTCAGGkA acGCGTCGCA TcACACTCCC AcAGGsGcAA GGaATTGTTA	1320
CCATATCTAC AACGTGcTTA TGCAAACTCTT CAAGCAACAT GCCGGrAgTT	1370

(2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1073 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

ATGAGCGATC TCTTTTTTAG AAAGAACCTG TCAAAAGGAC AAACGGAGCA TAATGCACAT	60
CGTAAGAGGA AAATAAAATT TCTGTAGAA TCGGATTGAC AACTCTCTAT GAGGCTTTGA	120

815

CGCATATTTT AACGTATGAA GCGTCTCTTT TATTTTCTGG ATGGACATmC CTTTGTGTTAA	180
AAAATCCTGA TGATCAAATA ATTCAAGCGG TTCTCTCAAC TCGAAAGAAT CAAGATATTC	240
AGAAACCATA AGTTTCATTT CATGAGTGAT AGTATATACA ACCGGTTTTA TArGAACCCA	300
CCTGTCTTTC TGCCAATGTG CAGTGTGTGC TTCGATAaGC TTCTGAATAG TACCGTTACT	360
ATTTTTCATA ATAACATAA TATCAACGAG CACCTTTTGT CCTCTGTGAT ACGCACCCGC	420
AATGGAGATT ATCTTACCAT CAAAAGAAGA AGCAACAACG TCATTTTCAC TATTCCCCTG	480
AGCATAGCTC ACAGTACGTG CAATGATTTT ATCCTTTTTT GACTGAGAAA CAACTACCAC	540
ACTATTGTCA AATGCAAATA TTCCAATTGC TAAGAAACAC ATAAAACCAA ACCACGGGCC	600
TACGATACTA AAAAAAGATA ACCCACCGAA ATGGATGGCA AGAAATTCAT TTTGGACATA	660
CAAGATTGCG ACAGTATACG TTGCAGCAAA AAGCACAGAC AAAGGACAGC ACAGCAGTAC	720
ATAATGTGGG ATAGATACAT ACCATATCTT CACCAAAGAA GAAAAACGAT ACCCATTCGA	780
AATAnAmTGC GTAAGATTAA CCAGAATATC AATAGCATCG AGAATCATAC TCGCACACAC	840
GAGCActAGA AAAAAAATTG GTAAGAACAT GTCCAACATA TACACCTGCA GTATTTTCAT	900
ACTGCAGATT TTCTCATTGA CAAATCAAT GCAGTAAAAA ACAATGCGGC GTTTGGAATC	960
CACAGTGCAA GGGAAAGAAC AATACTAAGC CTCAACGCAA GTTCTTGTC TCCGATAGAG	1020
ATAATCCAAT ACCCTAGTAC AACAAATAAGC CCTCTACAA ATCCTTTCCC CTG	1073

(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 884 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

TTTAAAnTC AGGGAGCCCG AGAATTGTCA AAAATATCCT CAAAAATATn GAGCGTTTGA	60
TCAAGAAAAA TTCCAGGCAT TTCTGCAACA AATCCTCAGA aACGTaAAAA CGCAGGAAGA	120
CCCCCGcGTG CTCGACGCCT ATCGGCGCCT TTTTCGCAAG AGCGTCCCCT TCTCCATGCG	180
CTCATACGTG GCCGCACACC TGGCGCACAC GCACTGCCGC GCCGGCGCCA CCGCCGcAGC	240
ACGCGGCGCA CCGAGCGCG GGAAGGTATA CGTACCGGCA GCGCGCACGC GCTTTCCTGC	300
GCCACGCGCC TGCCAGCGCC GCCCGCGCGC GCGACTTTGA GCGCAAAGcG cGCgGACTAC	360
CCCCGCCTCT GCCCGGGGA CACCACGAGC ATCTTCATCA GTATTGGAAA AAATCGGCAC	420

816

ATCTATCCGC GCGACATCAT CGCCCTGCTC ATGCAGCGCG CCGATGTTGC ACGCGAGCAC	480
ATCGGCACCA TCCGCATCCT CGACCACTAT TCCTTTATCC AAGTCCTTTC GGGTGAGGCA	540
GAAGCGGTTA TCGCCCGTTT AAATGGCCTC TTTTACCGGG GGCGCACCCCT GAcGGTGAGT	600
CACTCACGCA GGGCGGACGA GCATCCCGCT CCTTCTACAG AGCCGCACGC CGCTGCCGTT	660
GCACCAGAGC CTGgACTTTA TGGgCAGAGC CcATCCCCGg CCCTGGgAAG AATAAGGgAA	720
CATGgCCGTt CAGTGcAGGG gCGCCGgCCc GGGGCGCGGT GGGCAnTTCG GTGCGGTGCG	780
GCAGTTTTTCG GTTGACAGGG CTGCGCGTGG GAATCCTACC TgNAGCGGCG CTCAATGGAG	840
GCGCACGThc AGGGCCGTTT GCCATTATGG GCAGCCCGCT TTCT	884

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

GGGGAGGTTT ACATGCGTAA TACCGGATCC GCCACCTACG CCCGCATCGG CGGTGTGTTC	60
CTCTCTTTCT TTGTGCTGTT ACCCGTCTTC TGCCATGGCA GCAAAGAGAA GGGAAAGGAA	120
GAAGAACCGG TTCGCCTCTC AGTCCTCATA CGAGAGAAGC ATTACTCTTC GGGCCTGCAG	180
AATGTGTTTA CGAAGTTGGA ATTGGAAGAA GGAATCGCCG TCACCGTCGA AACCATCCAG	240
GACGATCAGT ATCCTACGGT GCTTCACGCG CGCCTTGCGG ACGGGACCGC TCCGGATGTT	300
GTAGAGGTGT CTCTTCCCTC GCTCCATGCC CTTGACCCAT ACCTTTACTT TGTAGATCTG	360
AGCAAAGAAG CCTGGATACC GGATCTACTG ATTCTCCCA CAGATCCGTA CGGCAAGACA	420
TTTGCGCTTC CCTTAAACTG CGCCGTGTCT ATCAATGCAC TTTTCTACAA CAAGGACCTT	480
TTTGATCGCT ACGGGATATC CGAGCCCAA AGCTGGAATG AACTCCTAGA AAGCTGCGCT	540
CTCATTGTAA AAAGTGGCAT TTCTATCGTA CCCCTCGCGC TCAGCACAAC GGAAAGCTTT	600
CCACATACGT TGCTTGCTGA CGCGATTACG AAAGTGCTCG GTGAGCAGGG CGCTCGAGAT	660
TTAGTCAAAC GTGCCACAGA CGACTCCATC GATTGGACGC ACGAGCGTGg CtCTATCCTG	720
TACTCGGAGC CTATCTGGAA CTGTTCAAGC GGGGATACGT AAACAAACAC CACCGGACTG	780
CGCGCGTGCg GAAaTCATTc ATGATTTTAC ACGCGATCGC ATCGCTATGT ACTTTGGCAG	840
TCACCTGGTT GCAGATGCAA TCATAAAAGA ACGTCCTGGA ATCAACTTGG GCGCGTGCGT	900

CCTCCCTATA ACCGAAAATG CACAAGACGT ACTGACTGGA AGTTTGGAAG TGCAAGGACT	960
CGCAGTGCAC AAAAAAAGCG CGCGTGTGGC AACCGCGTGT CGTGCACTCT CTGTGCTTGC	1020
GTCTGCCGCG TACCAAAACA GTTCTTTTGA AGAACACAAA GGGCTTCCTG CGTTTCGAAA	1080
CACCACCAGC GCAGTTATTC CTGCGTGCCT CAGTGcCCTG TTTAAAAGCC ATATAGAGAA	1140
AGGAAAAGTA ATACAGGCAA TCGACGCGTA CGrCAGGCGC AAAACACACC CCACAGAGCC	1200
TCTGTTTTTC CAGATTTCGC CGCGTATGTA ACCGACCCGG CACCAACTGC GCACACCATG	1260
CTGCACCGCG CCCAACTGA AGCGCGGAGG AGAAGAGAGC CGGTACAAA AAAAGAATGA	1320
GAGCTCCTGC GCGGGCAATA CGTGCCACGA GCGCGGAGC TTAACCTACC GCGCGACAAG	1380
ACAATCTTGC CACAGCCGGT CGAGGTGATA AAaGGCGCG ksCgCGyTcA TAAGATGAAC	1440
CAGGATAGAC CCAAAGTCCA GCACCCGCCA TTGCTCTTCG CAAAGGCCTC GTTTTTTTTCG	1500
ATGTACTTCT CTTAGGCCAA AGCGAGCCGC CTGCTCGCAC ACCAGACGAT GAGTGCCGTG	1560
CAAGAGGCCA GGCACAGTGG CAACTACCGC AAAGTCCGCC CAGCCGCAGC GCGCGCTTAC	1620
ATCAAACACA CATACTCCT CCGCGCGCGC ATCACACAGA GCCTCTGCTA CCGCGGAAGC	1680
AGCTCCGTTA GCACTCACGT TCCCTCCTTT ACCAGATATC CATTAAAATC CTTCCCCAGG	1740
ATAAGCGTAA AATCGATGCC CGTTTCCACC CCATACTCAT CAAGCGAGGC GCTAGTTGTC	1800
TCAATATTCT GACAACGAAT CACcTgCGCC ACCACTTTAG CCACTGCAGG ATTCCCAATG	1860
CGATCGACGA GCACCGTCTT TTGCACACTT TGCTCCAATG CATTATCAAC GCGAACTACG	1920
TCGTAACCAA ATCCTTGGA AATATTCGCC GTCGTGCGCG CAAGACCGTG CGATTCAATT	1980
CCGTTAAGAA TTTCCAACGC ATACACACGC TCAAAGGCCG TACCATTCTC TGACGCAAGC	2040
ACCGCAAGCG TCTGGCGCAC GATTTCTTTA ATTTGCTGTC CATCaCGAGA TGGAAAAAGG	2100
AGTACCTTGC CGTCTACCAC TCGTTTAGTC CCTGAAAAAC GCTGCGGCAC TAGGCGTTCT	2160
GAATCCAAC TAGATAATTC ACCTATAAGC TTTTAAAGT CAGCACGCCG AACGTTAGAA	2220
CGTATTAGCC TGTTCAAGGA AAAAGCACGA GTTGAATGAA CAAAAAATC ACTGTGATCA	2280
TTAACACTAC GCAACAAAGC TAAAATAGCT TTCTGTTTCC TCGATGCTGA CTCCCCTTCT	2340
CCCTCATCCT CGTCTTCGTA TAAAAGATAA TCACGCATCT TATCCCCATC CAAAGACACT	2400
GATCctGACG GTAACAGGAC ATGCCCTGCA CGTTCTGTGT GCACGTCGAT GGGCGTAGGG	2460
ATAAACACCG ACAGACCAGA GAGTAAATCT GTCAATTTAG AAAAGTTATC CAGCGAGCAC	2520
ACTACAGAAA AAGGAACGTT AATTCCCCTT AACTTTTCTA CCTCCCTTTT ATACTCCTCA	2580
ATACCACGCT CGCTGTAAAG cGAACCGATG CCATCCGTAC GGCCAAGACT CTGCAGAATA	2640

818

AGTCCCATAT TATGGGGAAT ATCAACATT GCCGCGCGCC TCGTTGCAGG ATAATACGCA	2700
ACAACATTGCG TGGAGATTGG AACGTTCTCG TGTTCATGA CAAACAACAC CTTGAGAATA	2760
TTGTGCTAG AAAGTGAGGA TTCAAGCGGA TCGCGCTTCA TACCAAAGAA GACTGCAAAG	2820
ACGGTGATAA CCAGCATAAA AAAAATGAGG AGTAAAAAA GCCCATGTCT TCCCATATCC	2880
AACACTTTCA TTGCACACTC CCTGGCCTCT CGTCGAACTG CGGCAGATAC ACACACTGCC	2940
CTACTTTTGC CCGACTGCCA CCCGTTACGC GGGTTGACTT ACATCCTTTC CCAGTGCACG	3000
CAACATCGCA CACGTACGCG GATGGGGCGT GGTACGTTTT CGTCTGCGC ACACAATACT	3060
CGCACTCACT ACTTTTGCAG CAAGCGCATC TAACGTTAAC GTTGACACTG CACCGCGCAA	3120
gGACGCCGCC CAAGCACGAG CTGGcTCAAt TTTGTCTGAT ATAAAAAGAA TCTTTCCTAA	3180
CACACCAAAG TCTTCACACC CAAAGGnATG CCAGCGCACC GCAGACAACA ACACCTCATC	3240
CTGnACG	3247

(2) INFORMATION FOR SEQ ID NO: 158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1691 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

CGAGTGCTAA AAGCTCATGA CACAGATCCG AGCGATCCTT TTTTaTGGCA AGCACCAATG	60
CCGAaATCCC ATCCGATCCC GTTTGTCGAT TGGATATCCC TTTGCCAGTA AAAGCCGAAA	120
TGTCTGCACG GGCACATTTT CCATAACCGC AAGATGCAGT GGCGTCTGCC CGTCAGAATT	180
TGCCAGGAGC GGATCCTTCC CCACGACTGC ACCGACAAAC GTATCTCCTt CAACAGGGCA	240
AGTGACAGCG GCGTAGTCCC GTACGAATCG CGCGCAAAGG GGTGCGCTCC TGCAGCGCGC	300
AACGCCGCAA TAACTGAcTG CGAATTGCAC AGTACCGCCT CGTGCAAGGG AGTGCGTCCA	360
TACATATCCT GCTGCACAGG ATTTGCACCC GCAGAAAGGA GCATGTGCAC CGACTCTTCC	420
TGATCTGCCA AAACCGCATC CGTGAGCGCA GACTTACCCG TCTCATCCCC CATGTGCAGC	480
GCCACCCGAT GACTCAACAG CAACCGGATA AAGTCGACAT TCCCCGCACG AGCTGCAAGA	540
TGCAACGGGG GTTTCCCAGA AAGATTCCGA GCATTTAAAA GAGATACATG CCGCGtCATC	600
tTCGCGGATA AGCACGTCAG CCGAACGGAG CGCAGACCAA CGCACACACG CATGCAACAC	660
CGTATTTCCA AtGCGTCCCG TGCCTCCACA AGCGCAGGAT TACCTGCCTG AGGATGCAGC	720

819

```

AAAATTGAAA TAACCTCCGC TGCATCTGAC TTTACCGCAC TGAAAAGAGG CGTTTCTTGA      780
TTCAAATTGC GTGCCTCTAT CTCTGCCCCC TTGCGCAAAA TACCATTAAT CGCCTGCGTA      840
AGTTTCCACT CGCACGCCAG ATGCAGCGGC GTGTTTCCTC CTGTATCCTG AGCGTGCACG      900
TTTGCCGCAG TCAGAATCCA ATCCTCGCGA CCGCCACTAG TTGTCAACGC TGTTTTCAGC      960
GGTGACACGC CATGCACGTT TGTACTGAAG ATATCAGCTC CTTCCCTCAT CAAAACTCA     1020
CCGACAGCAC GGTCATCGTT TGCAACCGCA TAGTGCAGCA GCGTGTTTCC CATCGTGTCA     1080
CGTGCAATCA TCTGTTTTGG TTCGCGAAAT AAGAATTTAA CTATGTCAAG GTGCGCACGC     1140
CTTGATACTG CAACGTGCAA AGGATCGCGC CCCACCACAT CTTGTTTATA CAAGTTGCTA     1200
TCGGTGACGA CAATTTTTTAC TGTCTCCAAA CCGCGCGCAA GTGCCTTGGT AAGCGGCGTT     1260
TCTCCGCGCA TATCTTCTGC ATGGATATCT GCCCCAAGAC TGACAAAGTA CGCATCAAAT     1320
CCCGATGATC ACGGTCAATC GTGAGGACAA GCGGCGTTTC GCCCTTTTTG TTCCGTTTCA     1380
AAATATCTGC GCCTGCGCCT AcTAGACGCT CTACAAACGC CCTGTCCATA CCTAAACGGG     1440
CCGCGACGTG CAAAGGAGTC TCGCCATAGT CATCCTTTAT GCGGACAGAA GCGCCTGCAT     1500
CAAGCAGTGC GCCAACCAAA CGGACACGGA AGGGAGCAGG AGCGACAAGG TGTAACAGG     1560
TGTTCCTCGA CGCGTCACGC ACGTTTGGAT CGGCCCCACT GCGCAcNCAA AGACCGCaGC     1620
ATCCACCTGC CCTGCACGCA CTGCTTCGTG cAAAGGGGTG GcGCTGGaTA GTTTTTTGA     1680
TTGAGATTGA C                                                                1691

```

(2) INFORMATION FOR SEQ ID NO: 159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

```

TGCGCATCGy GTGaGAGGaT TGACATTTTT ACTTGCTGAC GAGGCAGGCG TATTCAAGAC      60
GGTGTATTCT GATTTTGAAG AGATGGCAAC GCATGAGATG GAACATCAGT CGTTACAGTA     120
TTTTTTCAAT CAAGATGTTC TTATGATCAG AAAATCGGAT CCAGTTATTG ACCATGCACG     180
TCAGGCAATT CGGACAGATA TCCTGCATTT TTTTGATATA ACGCACGCCC AGATGATTGT     240
CTTGATTCCG GAAGCTCAAA AACTTATTGG ATGTCTATGT TTTGGTATGA AAAACAACGG     300
CGTAGAATAT AGCAATCATG ATCAGCAtGT TTTAGAAAAG TTGTATtCAC ACTTtGTATT     360

```

820

```

GGTTTCCTAT TACTTACAGA aTATtGCAAA GCAAGACGTG GTTATCACGg TGGACAAAGA      420
ACTTAAATG TCCCATCAGA TTATTGAGTC AATACAACGG aAAAGGGATT TTATTCAGGA      480
TGCCCTCCGTT GAGGTGGATT CAATTGCGTA TTCTGCGCAC CAACTTGGGG GCGATTTTGT      540
TGATTTTCATT AAACGTGTCG AGAAAaATA CCTGCTAGTT ATCGGGGATG TATCGGGGAA      600
AGGTCTGGCA GCGAGTATGT CAATGGTGAT TTTGAAGTCT GTACTGAGTA CCTTCTGCG      660
GGGACTGTGC CTGGAAGAAA CGGCAGTATT TACAACCTTT ATTGAGAAGA TAAACCGGTT      720
TATCAAAGAC AATTTGCCGT GTGGGACTTT TTTTGCGGGT GTATTCTGTA TTCTtGACct      780
GGCAACCCAT ACGCTCTACT ATGCGAACTG TGGCATACCG CTCATGTCTGA TGTACGTCTGC      840
TTCATACAAG AACGTGGTGG AGATACAAGG CGAGGGGCGC GTGCTGGGTT TTGTAAAGA      900
TGTATGCCC TTTTtGCGGG TGAGGAAAGT TCAACTCGGT CAGGGGGACG TGGTGGTATT      960
TTCCACTGAT GGAATGGTAG AAGTACAAA TTTGCAGCGG GAGCGCTTTG GTAACGAGCG      1020
TGTGGATAGG ATTCTACAGG AAAGTCATGG TCTTCCGGTT TCTCAAATTA CCCGTACTAT      1080
TTATGCTCGG CTGTGTGAGT TTATGGCGCG AGATATGCAG GATGATGTAA CTGTCTGGC      1140
AATAAAGTGC CTTGGGCCTC GGTAGGAAAT GAGGAAAAGT TCGGGAGCGC CGTATGGATA      1200
ATATAAATAT CGCCAAAGAC GTTCGGCCTG GGTGCGTTTT ATTAACGGTG ACTGGAGCGG      1260
TCAGCTCCTA TACTTACGGG GAGTTTGAGT CGCGTGTGCA TGGGGCGCTC AAAGAGAATC      1320
ACGTTGTTTT GGATCTCTCC GGCCTGACGG CTATGTCTTC TTCGGGATTG GGGGTGCTTA      1380
TCTCTGCATA CGATGAGGGA CTGAAGTACC AGCGTCGTCT GTGCATTCTT AATCCTTCTG      1440
AGAGCGTAnC AGAGCGATAG AG                                          1462

```

(2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1013 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

```

TGGAACGCGC GGTATTACG CGTCCTGCAT ACGCGGTGGA TTATGCGGTG CTATCCCTG      60
TACAACTTGG TATTGATTTG CAAACAAAAA GGGTGAGCGG GCTCTTTTCT GCAGGTCAGA      120
TTAACGGAAC ATCCGGCTAT GAAGAAGCTG GAGGTCAGGG TATTATCGCC GGGATTAACG      180
CTGCGCTGTA CGCGCGCAGT ACTAAAACCA AAGAGGAGTA TCATCCATTT GTTCTGAAAC      240

```

821

GCGACGAAGC ATATATTGGC GTCATGATAG ATGATCTTGT AACACAAGGA ATAGACGAAC	300
CCTATCGGAT GTTTACCGCG CGTGCGaGTA TCGTTTGAAA CTCCGTCACG ATACTGCGGA	360
TGAACGTCTT ACAGAAAAAG CTTACGCCAT TGGGCTGCAG AAGAAATCTG CTGTAGAAAC	420
GTTGCAAAAA AAGATGCGTA CGAAGCACGA GATCTTGCAT CTGCTTCAGA CCAACAAAGT	480
TAGTCTTACC CATGCAAACG CATATGTTCA GCTGAAGCCG CATATAGGTA AATCGTTTGC	540
AGcTACGCTA CGTGATCCGG TAATACCTCT TGGGCTTawC kCTTCGCTGA ACGAGCAGAT	600
AGCGCAGTTC CCTTTGGAAG TGTTCCAGTC GGTGGGGTG GAGATACGCT ACGAACACTA	660
CATCGCTGCA CAGGATCAAA GAATTGCACA AGTGGAGAAA ATGGAAGGAA TAAAGATACC	720
AGCGCATTTT GATTACGCGC GTATATCAGG TCTCTCTGTA GAATCCCGTA CACGATTGGA	780
ACACGTTCGC CCGGACACTA TCGGGCAGGT TGGGAGAATG CGCGGAATCA GACCCCTCTGA	840
CGTAATGCTG TTGCTCGCCC ACTTAAAGCG GTAGCAGCTA CCGCAGAGAT AGAAGAACCG	900
CCTTATCAGG CAGGTGTTTG TACGTACTTT TAACGCACAG CAAGGAGCGC TTCGGCGTGA	960
AGTTCGGTGA TAAGGCCACA GGAGACCATA TCAAACAAnT GTnCGCTATT TGT	1013

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

GTAGTCACGG CGTGTGCCCC GCGTCAACCA ATGCGGTAAT ATCTGCCAGC CGAATTTTTT	60
CATGTGCAAG GCAGTCCCCT ACGCGGTTTT GCGAATCGAC GAGTACTGAC AGATATACAT	120
CTTTCAGTTG TGCAGGCGCT TTATAACGCA AGAACTGAGA AGCTGCTGTC CGATCAGCAG	180
GCAGGCGCAT ACGTGACGT GCAAGATCTA GCGTAAgcTG TGCGTTAATG GTACCGTTTT	240
TCCAATCCTG CACCGCATCG GTGTGTACGG CATCCTGGGT CTGCGCACCA GACGGCGCGT	300
GAGAAAACAG AACAAAAAGG AGGAGGAGAA TGAAACGCCT CGCACTGCTG CGTACCACAT	360
GGGGCGCACT TCGTGCCTC CACACCAGGG AGAGAGCGCC GAACGGAAAA CGGCACTGAT	420
TTGAAAAAGA GGCAGCACGC GTCAGGCAGG ACACTCCCAT ACCCTACCGT CTCGGCGTTT	480
TGAGAATCAT TCCAAGGAG AGCGTGCGGT CTACTGCTAG ATTGTTTTCC TCTGCCAGGT	540
TTTCTACTGA AACGCCGTAG CGCTTTGCTA AGGACCAGAG GGTATC _s CCC TGCTGCACTA	600

822

CATGCTTGCC GACAAAGGGT GCTGCAGGGG TTGCCCGCGC CGCTGTGCTT TCCGGCGGTG 660
GTGGCACGCT CGGGGGTGCC GCGCGCTCTG CTCCCGCGCG CGTGTCGCGg CCCCCGGGCG 720
TCGGCGGCGT CATTGAGGAC GAGGGAAnTG CGGACAtTCC GGCAtGCATG CTCTTtCTGA 780
TCCATTACTC CAGGTGCACG CGTGCCTGCC CCCCAGGc GCGCGCCGGG TCTGCCCArT 840
CCGGATGGTG GGAATGATGA GCTTTTGTCC AATCTTCAGG TGAGTGGCGC TGTGTGCGCG 900
GTTATGGGst TTTAGCGTAT CGACGCCCAA CCCATAGCGG CGGGCGAGTG CGTAAAGCGT 960
GTCTCCTGAA CGGATGGTGT GCAGGGTGTG ATGGACGAGC ACGGCGCCTG GGCGGTTGAG 1020
TACTGCCTGG ACCGCTGCG CATGTGTGCT TGGCACCCGG AGGGTGTACG CTGCATTCCG 1080
GGGAGTAATT GAATAGCGGA GTGCAGGGTT GAGCGTGTGC AACAATTGC 1129

(2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1713 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

GTGAGCTGCG TGCAGTAGAG ATTGGAAAGC TGAAACAGGC GATTTATTCC CTCGAAAACG 60
ATTTAAGGAA TGAGAAAGTT TCGGCTGAAA GCGGCTCCG CGTCCTCGTC TCATCAATCA 120
TTTTTTCTGG CTCGTTGATC ACTATGTGAA TGTGCAAGAA GACAAGAGGA ACATCGACGA 180
AGTGTTACTC AAAATTAAAT TGCTTGATGA AGCGGTTTAT CATCGCTATG TGAGGATAGC 240
GTGAAAGTGA GGGTGAAGTA ATGTCAGAAC ACATAGAACA CGACGTTCCG GAAATGCTCA 300
ATGAAGAAAA ATGGACACGC GCGACCTTAC CGCGTATTCT GCGGAAAAGT TTAAGGAACT 360
TGACAGAATC ATTGCGGAGG CGAAAAGACa ATCTATCCTT GATGTACTGA AAGGTATCTG 420
TGACGAACAT CTGGCGCACT CGAAGAACAG TATAATCGCG TTATACATTT CTGGGATTAT 480
TTCGCTTTCT AaGCAGTTGT TAGATGATTC GTGTTTAGTG ACGCTGCTGA CTATCTTTGG 540
TGATAATCAC AAGAATCAAA TAGTTGAGCA CCTCTGTACC CGTGTGCTTG AGTACGGTGA 600
ATCAAAGCTT GCGTTGCGTG CGTTAGGAGA ATGTTACAAA ACCTCTGGAA ACGAACAGCT 660
CTATGATGTT TGGGAACGGT TAGTTAGGAT CGATTACGAA GAGGCGGAAA TCACTCGTGT 720
GCTGGCGGAT AAaTACGAGC mGGAAGGGaA TAAaGAGAmn sCTACGGAGT TTTACAAAAA 780
AGCGCTGTAT CGTTTTATCG CGCGGAGGCA GAACGCGGCC ATAAAGGAGG TTTGGACTAA 840

823

```

GCTTGTTGCA CTGATTCCAG ACGATGTCGA GTTTTTTAT CGTGAGCAGA AGAAAATTTT 900
AGAGAAACTG GGAGAAGGGC GCGGGAGCGT GCTCATGCAA GATGTATATG TCTATTACAA 960
AGAAAATGAG GATTGGACAA CGTGCATCAA TATACTCAAG CATATTCTTG AACATGATGA 1020
GAAGGATGTT TGGGCGCGTA AGGAAATCAT AGAGAATTTT CGGTGTAAGT ATCGCGGACA 1080
TAGCCAGCTT GAGGAGTACC TAAAGATATC GAACATTAGC CAATCTTGGC GCAATGTCTT 1140
TGAAGCCATT AATGATTTTG AAAAGCATAT TTCCTTTGAC GAGGGTAGTT TTGTTTTTCA 1200
TCGAACGTGG GGGGTAGGTC GGATTGCGAA GGTGTGTAAC GATGAGTTAC TGATCGATTT 1260
TGCGAAAAGG CGTGCGCATA CCATGCTTTT GAAGATGGCT ATTAGCGCGT TGCAAACCTT 1320
TGGCAAAGAG CATATCTGGG TGCTTAAGTC GGTACTGAAG CGGCAGGATC TTGCTGCGAA 1380
AATAAGGcAG GATCCTGAAT GGGCACTGAA GGTGATCATC ACAAGTTTCG ACAATAACTG 1440
TAACCTCAAA AAGGTTAAGC AGGAATTAGT TCCTTCTTTG CTTtCTGTGG GGGAGTGGAC 1500
GAGTTGGAGT ACGAAAGCAC GGAAGATTTT GAAAGAAAGT ACTGGATTTG CTGCGAATCC 1560
CAGCAATATC GATTTTtATA CGGTGCGGAG CTGTCTGTtT TCCCTAGAAG AAAAActtGC 1620
TGTGGAATTT AAGGCACAAA AAAATTTCTT CGCGCGCATC GACATCCTCA TACCTTTATG 1680
GACAAGGGCA GATACAGATT TCTGGAACGG GCC 1713

```

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

```

CCGTTATGGT ACAGGAGCGG AAGACTTCGA GTAATAAAAC CAAGCGACTT GAGTGCTTCG 60
TTCAAAAACC CCTGGTTCCC CAGGATAGTG ATCCAGGCGT TTATCCTGAT GAGAGAATTG 120
GTCCAAAAGG GGACGATAAT TAGGAACAGG AAGAACGTTT GCCTCCGGCT GCGAGAGAGC 180
GCGTACCTGC AGGAAGTGCC AGGAGCACGC ACAAACAGGT GACGCCTGTA CTGATAAGCA 240
GGGTGCGAGC CAGCAGTGCG CCATAGCCGG AGGTAAGGAC TTGCGCATAC GCCCGGATGG 300
AAAActtCCA CACAACGCCT CCGTACAGGC CCTTTTGCAA AAAGCTGTAC ACAGCGACCA 360
CCGTAAGGGG GCACAGAAAG AAGACTGTAA GCCACGCAGA CAAGGGGAGC GTGCACCAAA 420
AACCTAAACT GCCTACGGTA CGcGTCGCGC CACGCGCAGC CGGsTGCTcA CGaCTCGATG 480

```

824

TCCTCAACCA CGTAGCCGTC GTGTGCAGAC CAGGACACGT AAACAGTGTC CTTCCACGCA	540
ATCTCAGGGC CAGTGTGCGAG ATACTTCTGG TGTGCTGAA ACACTTGGAT AATAGCGCCA	600
CTTTCTAACT GGACGAAAAA CTTAGATTGG AACCTGCAT ATACAGGCTC CTCTACAAAA	660
CCGCGAAAAA CATTGAGCGG CGCACTGGTG GTACCCGGT CTTCAAGGGA AATGTGG	717

(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

GCTATGTCT GTCCAACTC AGTACGTGTC TTTGCAAATG CTTTCCCCAG GGCGTACCTC	60
AACTGTTTTT TCGTATCGTT GAGAACAAACA TCAAGCATTA CCTTCTCGAT ATGCTGATAC	120
AAAGCACTGA TGGTATATTG CATCCCTGCT GCAGCAACGC GTGCACGCAG TGTGTCGCTT	180
TTTTTCTCAT CCAGGAGGAC ATCACGTAGC CAATCATTTT CTTCCCCAAG ATTATATTTA	240
GCAACAAGAT CAACAGCCTT ATGTAACACC GCATCAACGG GATCAGACTG TGCCCGGTAC	300
AAAACATACG GGAAATACGA CGCACACAAC ACCCGTTCTG CAACTGCTAA TGCCCTCTAGT	360
CTTGCTCTGT AaTGTGTATC CCTAAAACCT TCAATGACAA TATTACGCGC TTCATCTGTA	420
TCGAGCAAAC CTGCTCCTTT AATCGAGGCT ATTCTCAGAA TAGGATCTGA CTCTCAGAT	480
AACACGGATA ATATTTCAC CGCATCGGAA CGTCCAATAC CTGCCAGTCC TACAGCAGCA	540
GAAGCTCGAA CGACACTATT TTCCTCCGAG CTCATTACCA CCAGTTTAAA AAAATCAAAA	600
GcATGCTCAG CATGCAACTG CTAAGAGCT GCCATAACGT TTTGTTTCCT GATCAACGTC	660
TTTTTATCGT CATCGAAATG AATATTCTCA TAATACCTCA CTAAAAATTC GGAATCTTCC	720
GTACTCCCCA TGTTTCCAAG TGCACAATG CATTCATCAG CATACTGAGA CACTTCACTG	780
CTCAACACTT CCCTTAATAA AGGAGTCAAC TCTCTCGCCT CAAGACCTGA GATGTATCGT	840
ATCGCTGACT TAACTACCAT CGGATTATGT TCCGTTACCT GTTGCAATAC ATCCACCGCA	900
ACAGACTGCG CACAATCATT TTTCTGAAAC AAGAAAAAAT CAAACAACAA CGCCTTTAAT	960
TCAGAACTTT TTGTGCGTCC GCACAACATA CACAACGTTT CGTTTAATGA GGCGTTATTT	1020
TCCTTCTTTA ACTCTTCTAT CAAGGAGATA ATATCAGAAA CTAATCCATA CTTGATGGTA	1080
TTCATCCTTT TCTTTAGAAG AACCGTTTTT TCATCAGTGA TATCTATATG ACGCTCCTGT	1140

825

TCTTGCACGT GCTGCGTTCC CGTTTCCTTA GCAAACATGG GGACACCCCT CCCTAAGAAA 1200
AGGATTGCnA CATGCACGCT ACAGTAGTGC ACGAAAAGAC TGChCCCTTT CACCCCATTT 1260
CCCCCTCCGTT CCATTCTATA TCT 1283

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2529 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

CAAATCCAAC TGnAAATAGA TACCCCGGcT TAACCCCCAG ACAAGTGAGC GCGTGAAACA 60
GTGTGCACAG CGTCTCTACC GAATCGTTCA CCCCGCGCAA CAGTACCGAC TGCgATTGCA 120
CAGGGAGGcT GCGCcTACGC AGGCCnCGAG CACCGCGCGC TGCgTAGAAC CGAGCTCTGC 180
CGGGTGATTA ATATGCGGAA TTATCCACAC CGGCTTCATC TCCTGCAGAA ACGCAATCAG 240
CTCGGGAGTA AAGGCCTGCG GAGCAAAGGT GACTGCGCGA GTGCACAGAC GAATAATCAA 300
ATCCGGCGCT AACTTGgCAG TGCsCGGAAA AGCGATGTGA CCTGTGCAA AGAACCAGTG 360
AGTGGAACAC CACCTGAAAC CAGGATTTCC TTCACCGAAG GGGTAGCACG AAGATACGTA 420
ATAATCTTCT CGCGCTCTTC GTTGGGGATC CACCCTGCAC GTTGGGCGAT GAAACCGCGG 480
CGAAAACAAT AGCGACAGTG TGAAAAGCAA CGTCCTGTTG CCAACATCAA CACACGATTC 540
GCATACTGAT GCACCAAAAA GGGTGTACG CATACCGGTC CTCACCCAAT GGGTCGGCAC 600
ACTCGCAAGC ATGCACCACA CGTCCTGTG GCGCAAAGCA CACCTGACGT TTCAGCGCCT 660
GgCGTCCGCG CCCTGCGcTT GTGCAATTAA ATGCGCATAC GCTGGAGAAA TATGCTCCGT 720
CAGCGCATCT GCCGCGCAAG AGGCAGGACT CAACGTCCGC CAATGCTCAT CAGCACGCCC 780
TGCACCTCGT CTCTTTCTCT GTTCCCGGGT AACTCAGCC ATAGACACGG ACCACGAGTG 840
CGCATCCTAC GGTAAAAATG CATGCGTGTA CAAGTCACGC CGTGCACCGC ACCCGTGCTG 900
CAGGATCGCA TACCGTAGTG TTGACACACG TACCTATTTG CAGAGACCCT GGTCCCCATG 960
GTCAGACTCG AGCGGCTAAA GAAGACATAC GCAGGTGTTT CTATACTTCG AGATATTTCT 1020
CTAGAGATCC CAGCGCACGG AATGTATGGA ATCATCGGCA AAAGTGGTGC AGGAAAATCA 1080
ACGCTACTGC GCATCATGAG TCTTTTGGAG AAACCTGACG AAGGAGCCGT TTTTATCAC 1140
ACCACGAGGG TAGATTTACT GCGCGGTGCT GCCTTGCGTG CACAGCGCAG GCGCATAGGA 1200

826

TTGATCTTTC AACAAATTTCA TCTGTTTTCT TCCCGCACCG TCTTTGGGAA TGTTCCTAC	1260
CCGCTTGAGA TTGCACGGTA TGCACGTAAG GACGCCTACG CGCGCGTGTT GCATTGCTA	1320
CACTTG GTTG GTCTTGCAGA CAAAGCACAG GCGCGTATCA GCACGCTGTC AGGTGGGCAG	1380
AAGCAGCGCG TACCATTGCG CGCGCCTTGG CTGCAGAACC TGCAATACTC TTCTGCGACG	1440
AAGCAACAAG CGCTCTCGAC CCTCAAACAA CACAGTCAAT TCTGACGTTG CTGAAAAATG	1500
TGCAGTGCTC ACTGCGTCTG ACGGTCGTAT TGATTACACA CCAGATGGAG GTGGTACGCG	1560
ACTTGTGCGA TCGGGCCGCC GTATTGCATG AGGGAGAAAT AGTGGAAGAA GGAAGGGTGA	1620
CACAACTTTT TGCTGCGCCA CGGCGGCTGA TCACACAGCA GTTGTGTGTCG GGCTGTTCTT	1680
TTGCCTCTTT TGCAAAGTCA GAACCCTTCC ATCGAATGTC TTCGGGTGCG TGTGCCGTGC	1740
ATGCTATTGA CAAGGCACAC TGGTAATGGC GAACCAGACA CTGTGGCTTT TAGTAGCTCG	1800
TGCAACCGGA CAGACAAGTC TGATGGTGTG TGCTTCAGCA AGTATTGCGC TAGCAGCGGG	1860
AACCCCGTTG GGGATATTGC TGTGCGTAAT GTCGCTTGA CACGTGTGGG CGCATCTGCG	1920
TGGCATCGTG TGTTAAGTTC GTC AATGAAC GTCTGCGCGC TTTCCCATTT GTGATTTTGC	1980
TGGTGGTGTG GCTTCGCTC TCGCGTATGC TCACAGGACG CACAGTGGGA ACGGCGGCGG	2040
CTATCCTCCC GCTTGCgAta cTGCCTCCC TTTCGTGGCA CGGGTGATTG AAAGTGCTCT	2100
GCTGGAGGTG GAGCCAGGGA TAATCCAAGC GGCGGTGGCA ATGGGTTC AA GCATGCGGCA	2160
ACTTGACTA AAAATCATGC TGCCTGAGGC TGCTCTGCA TGTGTTTCTG GTGTAGCACT	2220
GATGTAATT AATCTAATTG GATACTCAGC AATGGCAGGG GCGATTGGGG GAGGAGGTTT	2280
AGGAGACGTA GCGATCCGCT ACGGGTATCA GCGCTTCCAA CCAGAGGTGA TGACAATGGC	2340
AGTGCTTGCA ATCCTGGCGC AGGTTGCGtA ACGCAATGGA TCGGGCGTAT AATCTGTACC	2400
CGAATACGAG CGCGtCAGgT AGTACCCCGC CAGAGTTAGG CAGGACGTCT GTCCTTGCA	2460
GGGTAATCCT TTGATCTTTT CTACGGGGTC TGACGCTCAG TGGAACGAA ACTCACGTTA	2520
AGGGATTTT	2529

(2) INFORMATION FOR SEQ ID NO: 166:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4060 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

TGACGGCTCT	TACCCGATTG	AGCGAAAAGA	AGGGAGCAGT	ATATGGCAGA	GATATCAGCA	60
ACAGCTTATG	CTGkCCAGGT	TGACGACCTG	ACGCTTGCGT	ATCGGCAGAA	GCCGGTGCTT	120
TGGGACGTGG	ATGTGCGTAT	TCCAGAGGGG	GTTATCGAGG	CCATTATCGG	TCCTAATGGG	180
GCGGGCAAGT	CGACCCATT	GAAGGCGATC	ATGGGTCTTC	TGCCTCTCGC	TTCCGGAGAG	240
GTGCGTGTCT	TTGGGCGTCC	TTTTTCAAAA	GAGCGGCGAC	KTGTTGCGTA	TGTCCCGCAG	300
CGCAnTGCAG	TGGATTGGGA	TTTCCCTACT	ACCGTTTTTG	ATGTGGTGCT	CATGGGTTCG	360
TACGGTTTCG	TCGGTTGGAT	TCTTCGTCCG	GGAAAAAGAG	AAAAGGCGCG	TGCCCGGGAA	420
GCGATCGAGG	AAGTAGGAAT	GGGCGCCTTT	TTAGACCGAC	AAATCAGTGA	GCTTTCAGGC	480
GGTCAGCAGC	AGCGCGTGTT	TCTCGCGCGG	GCCTTGGTGC	AGGACGCGGA	TCTTTACTTC	540
ATGGATGAGC	CATTTCAAGG	TGTGGATGCA	GCTACTGAAC	AAGCAATCGT	TACTCTTTTA	600
AAAACGCTGA	AAGGGCGTGG	GAAAACGTTG	CTTGTTGTGC	ATCATGATTT	GCAGACGGTG	660
GCAGAGTATT	TTGACCGCGT	GCTGCTTTTA	AATGTTTCGG	TCATCGCTGA	AGGGGCCGTC	720
GTGTCTGCCT	TCACCGAAGA	ATACGTTCAA	AGAGCCTATG	GCGGACGGAT	TAGTTCCACC	780
CTTTTTCCGA	GAGGAAATAA	GGAGGATGTG	CACGATGCAC	GCGCTCATGC	GTCTGTCTC	840
TGACTATACG	CTGCAAAATG	TGGTGTTAGG	CACGCTTTTT	TTGGGTTTGG	GTTCTGGGCT	900
GGTCGGCAGT	TTTGCGGTGC	TGCGTCGACA	AAGCCTTTTC	GGTGACGCAG	TTTCTCATGC	960
AACCTTCCGG	GGATTGTTAT	CGCGTTTCTT	TTAACC GGCA	CGAAGTCTAC	TGAGATACTT	1020
TTGCTGGGTG	CTGCCCTCAG	TGGTTTAGTA	GGAAGTGTGG	TGATGCTAAT	GGTGATGCGT	1080
ACTACAAAAA	TTGATACCGA	TGGTGCGCAG	GGCATTGTGT	TGGGTGTTTT	TCTTGGGTTT	1140
GGGTTTCTAT	TACTCACCCA	CGTGCAGAAG	TCGCCCCAGG	CGGCAAAGGC	TGGTCTGAAC	1200
AAATTCATT	TAGGGCAAGC	GGCCACGATT	TTGCAGCGAG	ATGTCCTGCT	CATCATTGCG	1260
ATGGAGGTGG	TGATCGGTTT	GCTTGTA	CTGTTTTGGA	AAGAACTGAA	GCTTTCTACC	1320
TTCGATCGAG	ACTTCTCTGC	GGTGCAAGGT	TTTTCTCCAC	AGCTTATGGA	GTTTCTGCTC	1380
ACGGCACTCA	TCGTAGTTGC	AGTTGTCGTA	GGGGTTCAGG	CAGTGGGGGT	TATCTTGATG	1440
AGCGCACTGC	TGACTGCGCC	TGCAGTGGCA	GCGCGGCAGT	GGACAAACAG	TTTAAGGGTT	1500
TTATGCGCGC	TTGCTGCTTT	ATTGGGGGT	GTCTCAGGTG	TTTCAGGTTT	GGTGTCTCT	1560
GCCCAGGTTT	CCAGGCTTTC	TACTGGCCCC	GTGATAGTGT	TGGTGCTGAC	GGGTATTGCG	1620
CTTGCTCTTA	TTATGCTTGG	TCCTCAGCGG	GGTGTTTTGT	ATCAACTGTG	GCGGAGAAGA	1680
CGGGTTTCGC	TTCTTCAAGA	GGAGGGGTAG	AATATGACCA	TGGAGGTTGT	GCTTATTGCA	1740

GTGGTTCGTGT	CGGTTGCGTG	CGCGCTGTGT	GGGGTTTTCT	TAGTGTTCGG	TAGAATATCG	1800
CTGATGAGTG	ACGCGATCAG	TCATTCCGTT	ATCCTGGGGA	TAGTACTCGG	TTATTTTCTG	1860
AGTCGTACGC	TTTCTTCTTT	CGTGCCTTTT	GTGGGGGCAG	TGATTGCGGG	GATATGTTTCG	1920
GTAATCTGTG	CAGAACTTTT	GCAGAAGACA	GGGATGGTAA	AGAGCGATGC	AGCaGTCgGG	1980
CTTGTTGTTCC	CTGCAATGTT	TGGGTTGGGG	GTGATCCTTG	TGTCGTTGTA	tGCAGGGAAT	2040
GTACATCTTG	ATACAGATGC	GGTACTGCTT	GGGGAAATTG	GACTnGCGCC	CTTGGATAGG	2100
nTTTCGTTTT	CAGCTTGCTC	CTTGCTTAGG	AGTnTGGTAn	AGATGGGGTC	CGTCTGTGT	2160
GGATTACTGC	TGTTGCTTGC	GCTCTTTTTT	AAGGAACTCA	AGATTTCTAC	GTTTGATCCG	2220
GTGCTTGCCA	CGAGTTTgGG	TTTTTCTCCT	ACGCTTATTA	ATTATGGGCT	TATGCTCGsG	2280
GTGAGTATTA	CCTGTGTGGG	AGCCTTCGAT	TCGGTGGGTG	CAGTGTGGT	CATTGCATTG	2340
ATGATTACAC	CGCCTGCAGC	AGCGCTTTTG	TTGACAGATa	mCTtgTwGt	GATGTTGGTC	2400
CTTGCTTCAT	TGCTCGCCTC	TTGTGCGTCC	ATTAGTGGGC	TTTTTCTTGC	GGTGAAGATA	2460
GACGGCAGCA	TTGCAGGAGC	AATGGCTACC	ATGGCGGGCG	TTCTGTTTCG	GTGGTGTAC	2520
CTTTCTCTC	CAAACACGG	GGTGTGCGC	AGGTGTCTGG	TAATGCGTGC	TTTGAAACTT	2580
GATCTAGATG	TGGTGACACT	TGCCGTGCAT	CTTGCAAcac	ActTACACGG	TGGAGCGCAG	2640
CGTGGAGTGC	GCTGAAGTGC	ACCTGACAGA	ACATGTGAGT	TGGTCTGcGC	GCAGGGCGGC	2700
CCGCGTGGTG	CGTACCGCGC	TCAGGCGAGG	GATGGTAGAG	CGTCACGGTG	CCTTGCTGCT	2760
ACTCACTGCG	CAGGGTGTGT	nCGCTCGCGC	AGGCGCGATT	GGATGTATCC	GTGTAGGCTG	2820
AGTCGATGTC	GTTAGTGTCA	GATATTGCAG	CAGAGAATTA	TTTGAAGACA	GTGGTAAAGG	2880
CGTTGGCGCG	GTCTCGTCCG	GAGCGCGTGG	GTACCGGGGA	GTGTCTCGC	CTTTTACACG	2940
TGACGCCGGG	GAATATCAGC	ACAATGGTGA	AGCGCTTGA	AAAGGGTGGC	TATGTGCAAC	3000
GCACGcATCG	TCTTGGCTGT	ACGTTAACCA	GAAAGGGGGC	AgTTTTTGA	TCTGCaGTGT	3060
TAAGGAAGCA	TCGCTTGTG	GAGAGTTTTT	TTTCCCAGGT	ATTGTGTTTA	GAAGCAGGGG	3120
TGGTGACAA	AGAAGCGGAA	ATGCTTGAGC	ATGCGTGTTC	TGACGAGCTC	ATCGACGTTA	3180
TTGATCGCTA	TTTGACAGTAT	CCTACGCGGG	ATCCTCACGG	GCAGCCGATC	CCAAGAAAGG	3240
ATACGCTTTT	GGATTGTAT	GTTGAGGACG	ATGTGCCAGG	TGTATGATCT	TTTTGTATGG	3300
GGTGAGGATG	CGCCTTTTGT	CAGATAAAAG	GGGATGTGCA	AAACGTATTG	TTGAGAGGAG	3360
AGGGCCATGA	AGCTTGTGTT	GATCCGTCAT	GGAGAAAGTG	AATGGAACAG	GCTGAACCTG	3420
TTCACTGGTT	GGACAGATGT	TCCGCTTACC	CCACGTGGGG	AGTCGGAAGC	CCAGGAAGGA	3480

829

GGCCGCGTAC TGCAAGAAGC GGGGTTTGAT TTTGACCTAT GCTACACTTC TTTCTTGAAA 3540
CGTGCCATTC GTACGCTCAA TTTTGTACTC CAGGCACTGG ACCGTGAGTG GTTGCCGGTT 3600
CACAAAAGCT GGAAATTGAA CGAGCGGCAT tATGGGGATC TACAAGgTTT AAATAAGACA 3660
GAGACGGCGC AGAAGTATGG TGAGCAGCAG GTTAGGGTGT GCGCTCGCTC CTTTGATGTG 3720
GCTCCTCCTC CGCTTACTGT AGGGGACGCA CGTTGTCCGC ATACTCAAGC CTCCTACCGG 3780
GGGGTATGCG CGTCTGGTCG GACGCCAtAC TTCCGTTTAC GGAAAGTTTG AAAGATACCG 3840
TTGCGCGTGT GGTGCCGTAT TTTGAAGAGG AAATCAAACC GCAGATGATT TCCGGACAGC 3900
GTGTGCTTAW TGTGGCGCAT GGTAACTCGT TGCGCGCACT GATGAAGCAC ATAGAGTCTT 3960
TGGATGAGAC TCAGATAATG GAAGTAAATT TGCCTACCGG TGTACCGCTT GTCTATGAGT 4020
TCGAGGCGGA TTTTACCCTG TGTGGGAAGC GTTTTTTAAG 4060

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2074 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

CTTTTTACCC AACTCATTGC CAATGCGGTT ATGGAAGCGG GTAACGAGCA TGGTTTGAAA 60
ATCATTGAGA ACTTGCAGGA TGAGGAGAGT GGCGATGAGC TTGACGAGTC CGTTTCCTTG 120
CACGAGGAAG GGCGCGAAAT TACTGACTAT GAAAATTATA CTCCTCCTGA GGAGCGTGAG 180
TATTCTGTGA ACGATGAAGG CGATGTGTTT GATGAGGATG AGTCGCTCTA CGAGGGGCGT 240
TAGGTGTGCC CTCCGCGGTC TCTTTTGGA TGTGTGTCTG GGTAGGCATG TTTGCATCGA 300
AGTCTGATCG GAAAATGCTG TCAGGAGGGG TACATGGAGA TTGCTGCTCG CGACGTTAAG 360
TCTTTGCGTG ATAAAACCGG GGCCGGGATG ATGGATGTAA GCGTGCGCTC CAGGAGTGTG 420
CAGGGGACGC TCTGTGTGCA GAAAAGTATC TTAAGGAGAr GGGGCTTGCT GCCATCGAAA 480
ACAGGCGTGG GCGTGCCACT GCTGagGGAG TCaTCGTTAt TAAAGCACgG CaTGcAGAgG 540
GCgCgGCCTG TgGGGCGAGC GCTGTAGCAA TGGTTGAGCT TGTTTGCGAA ACAGATTTTG 600
TGGCAAAGAA CGCAGAGTTC ATCGCCCTTG CTGAGCGTAT AGCTCAGGCG GTGCTCGAGC 660
ACGCGTACAC TGAGGTAAAC CAGGThTGCG CGATATGGTG GTGGACCTCG CAACGCGCGT 720
ACGGGAAAAT ATGAGCTTgN ACcGCCTTGC GCTCTTACGT GCCGcAGTGC CGGTGCAGGT 780

830

CAGTACCTTT CCTnTACGTG CACCCTGATA AAAAAACAGG GGTAGTGCTC TCCTTTTCCT 840
 CCGATGCGCC GGATGTGTTC CTGCGATCCG ATGTGCGGGC cTTCGCGTAT GACTGCTGTT 900
 TGCACGCGGC GGCATATACC CCTCGyTACG TGC GCGCAGA GGACGTGCCT GCTGAGTATG 960
 TGC GGGAGCA GCGTGAGGTG TTCCAAGCGC ATGTTGCGTC TCTCCAGAAG CtGCGCATGT 1020
 CAAGGAAAGT ATCGTGCAGG GTAAACTAGA GAAGCATTTG GCTGAGATCT GTTTTCTGAA 1080
 GCAGCCCTTT GTTAAGGACG wCAAGCTTTC TGTTGAAAAA AAGATGGCAG AAGTGGGTGC 1140
 CCGCGCAGGG GGTGCGCTTC GGTTTACTCA GGC ACTGATA TACCAGCTAG GGTACAGTG 1200
 AGTGGGAAGC ACGGATAGAT CCTGCCaCCC TGCAGGATGG GGAGCAAGCA GCGGTGGGGG 1260
 AGCTCGTGCT TCTCTCTTGC CGCACTGTGT TGTGAGGGGA AAAGATGGGT ATCGCTGAGT 1320
 GCTATGAGCA GAAGATGAAG AAGTCCCTCT CAGCGCTGCA GGAGGGTTTT AACACGCTGC 1380
 GTACTGAACg TGCGACTGCA CATTTGCTTG ATCAGATTAC TGTCGACTAC TATCAGCAAC 1440
 CAACCGCGCT TAGTCaGGTG GCTACCGTTT CGTACCCGAG GCGCGTTTGA TCATTATCCA 1500
 GCCTTGGGAT AAAACGCTCC TTGCGGATAT CGAGCGTGCA ATTTTAAAGT CAAAATTGTC 1560
 GCTCAATCCC TCCAACGACG GCAAGGTTAT TCGTCTAGTG ATTCTCCAC TTACCCAGGA 1620
 GCGAAGGAAG GAGCTTGTCa GGCAGGCGCG CGCGTTAgCC GAGCAGGCGC GCGTTGCTAT 1680
 TCGCAATATT CGCCGTGAGG GAATCGAGGA AGCAAAGCGC GGGCATAAGG AGGGACTGCT 1740
 AAGCGAGGAT GCACTGAAAG CAGCAGAAGA GGCCTTCCAA AAAGCGACTG ACGCTTCTGT 1800
 CGCAGAgTtG CACGGTACTT GGCCGAGAAG GAAAAGGATA TCCTGGAAGG TTGAGTGCCG 1860
 TGCAGCACGT GGCCATCATC ATGGATGGAA ACGGGAGATG GGCGGAAAGG AGAGGGTTGC 1920
 GGCGCAGTGC AGGGCACCGG CGGGGGCTGC AGACAGCGCG AGAGATTGTC GCGGCGCTGT 1980
 GCCGATTCGG GTGCCTTTTG TTACTCTGTA TGTGTTTTCT ACTGAAAACT GGAAGCGCTC 2040
 TGCnATGAAG TGCATTTCTT GATGAATTTA ATCA 2074

(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2685 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

CGCCGGGnTA TTCCTTGCGT ATGCATCGAT GATCATTTGC ACGTTTTGCC GACCTAAAAT 60

ATCCGCTGCA TTGGTACGGA TTACCTGAGT CAGGTGCGTG GCGATGATTG CAGATGGAGC	120
AACTACAGTG TAmCCGACAC GCTCAGCACG ATCGCGATTT TCTTCAGAAA TCCACACAGC	180
AGGGAGTCCA AATGTAGGAT CAATTGTTTCG CTCCCCTGGA ACCTCCTCTG TAAC'TTGACC	240
AGACTTTATG GCGAGAAACC ATCCCAAGCG CAn'TTTyCCC CGCGCAACTT CTAATCCTTG	300
GATTTTGAAA CAATAACTGC TCGGATCTAA ACGCATATTG TCAATAATTC GAATTTTAGG	360
AGCAACCAAT CCGAGATCCA ACGCGGCATC TTTTCTAATA ACTGTAATTC TACTTAGGAG	420
CTCTGCACCC TTTTCTTTAT CAACAAGAGG AATTAATCCA TACCCAAGTT CTAGCGAAAG	480
TGGATCAAGC GGCACAATAG GACCCATTTC AGAAGTACTA TCTTGAGTCT GTTGCATACC	540
CTTTTTATCT GAACTTTTTT GCATCTCATG TTCTTGAACG TGTACCCGTT CCCTTTTCCT	600
TAGCTGCAGT CCCACAAAGG CAAAACACAC GGCCATAAAA AATAAAATAC TGTGGGGAAA	660
ACCCGGCAAT ACCGCCATAA CGATCAATGC ACCTGAGCCA ATAAATATAA CAAGTGCAC	720
TTTTGAAAAT TGTTCCCTGTA CGTTTTGACC AAATGACCCT TGATCGCTTG ATCGAGTGAC	780
AATAAACCT GTTGCAACAG ACAACAACAA AGAAGGAAGC TGTGCAAGCA ACCCATCTCC	840
TATCGTTAAA TTTGTATAGG TCTGCAATGC TGCCTGAAAA CCCTCCCTAC GAAATATGAC	900
ACCCACTATC AGGCCTGCAA TCACATTTAC AATGGTAATA AAAATACCAA TTTTGACATT	960
GCCCGATACG AACTTACTCG CTCCATCCAT TGcTCCAAAA AAATCTGcTT CACGCTGaAT	1020
TGCGCTcTtA yrCTcTCGCG cTTcTTCwTC GGTGATAACA CCTGnCATTA TATTcAGCAT	1080
CAATAGACAT GcTTTTGGTT GCATTGAAGT CTAAGGTAAA ACGCGcAnAA ACTTCTGcAA	1140
TACGCGTCGC ACCCTTAGTA ATAACAAAAG CTTGCACTGC AATTAAAATG ATGAATACCG	1200
TAAACCAAT TACTAGACCT TCGTCCCGG ATCCTCCAC CACAAAAGAA CTAAACGCAC	1260
GGrTCATATA CCCGCTAAAC CGATCTCCTA ACGTTAAAT CAACCGGGTG GAAGACACGT	1320
TCAGTCCAAG TCCAAAAACG GTTGAGGTCA ACAAGAGCGA GGGrAATACA GrAAAAATCTG	1380
TTGGTTTTTC AACAAATAAC ACCATAAGTA ATATCAAAAG GTTAAAGATA AGATTAAaGG	1440
CCwTCAACGC aTCGAGAATT TGCGTGGGCA GAGGAACAmC AATAGAAAaG ACAmCCACCA	1500
AACTGAAAT CGCAACAAAA GCGTCAGTAG TGAAAagGCA CTCTTACCGT GCGCCATAGT	1560
ATGGGTACC TCTTACGCTG TGCATGTGTT TTAAATTTAT CCAGCTTGGT AAAAATCAGC	1620
ACTAAgCATT AAAATATTCG TAGGGAAC'TT CTCTCCCGAT AGCAACtGCG TGTACAACGC	1680
ACGTGCAAGC GGTTTGTTTT CTTCTATCAA GATACCTGCC TCTTTTGCCA ACCGTTTGAT	1740
TCGGTATGCA GTCCCATCAG ATCCTTTTCGC AACCACAGTC GGCGCAGTCA TGTATGCAGG	1800

832

CTCATATTGC ACCGCAcTGC AAAATGAGTC GGATTAGTGA TCACAACATC AGCGTCAGTG	1860
GTATTCCGAG CAGACTCTCT AACAAGAGAT TGCATCTGCT TTCTAACATA ACTTCTCACG	1920
AGCGGGTCCC CTTCCTGCTC TTTTAACTCC TCTTTCACCTT CCTGCCGAGA CATTTTTAAC	1980
GAATCGATGA ATTGCCTTCT TTGGAAGAAA TAATCGGGAA GCGAGAACAC CACTAACAGC	2040
AAACTTACTT CGAGGAGAAC TTTACCCGCA AGGGATGTAA TGTAAGAAAAT ACTCTGGGTA	2100
AGACTCACAC CCAATAAgAA ACAAACATAA AAAGATCATT ACGTATAGTA AAATACGATA	2160
CAAAAAaTAT CGCTGTaATC TTTATGAGAG ATTTAAGTAA ATTGAAAAGC CCTTCTGTTG	2220
AAAAAATGA GCGTTTGAAA AAACGAATTA CATCTGGAGA TATTTTCTTA AACTGCGGTC	2280
GAATCGACTT TACCGAAAAT AAAACGGTCT TGTTTTGTAC AATGTTTGCC GCAACGCCAG	2340
AGACCAGCGC AACAAAGGAT ATCGGAAGTG CAAGTTTCAT AAAATACCGC ACAAATACAA	2400
AAAACCATCC AGTATTCTGG ATGGACGCGG TAGTAGCACG CGTAAAGAAA AACCTGAGTA	2460
CACCGATGCA CTCTCTCAAT ATAAATGGTG CAAGCAAGAA CAAGGAAGTT GATGTGAAGA	2520
GCATCACAAA CGCTCCATTT AGATCCgGCT TTeGGAACAC GTCTTCTTC TCGTGCTTAC	2580
GGAGTTTTgt TcGGTAGaTC CTCTGaCCTC CCTTCaTCCT CAGCGGCAAA CCACTGGCAA	2640
ATCAATAATA AAAAGAGGAA GCGGAAATGT TCCTTCTTGT TCTAT	2685

(2) INFORMATION FOR SEQ ID NO: 169:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 634 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

AATCTTGAC GCCCTCGCTC AAGCCTTCGT CACTGGTCCC GCCACCAAAC GTTTCGGCGA	60
GAAGCAGGCC ATTATCGCCG GCATGGGGnC CGACGCGCTG GGCTACGTCT TGCTGGCGTT	120
CGCGACGCGA GGCTGGATGG CCTTCCCCAT TATGATTCCC AATAAAAATT GCGCGTGCCG	180
CACACCGTAA TCAGTTTACT GAAGAAGTGC TCCAATCCCT GCGGATTTCG CACCAATGCG	240
GTCTGTGTTT TGCCGCCTGT ACTGCGCGTA TTCCTCTTGC AAAACTTTTG CACGATGCAC	300
AAGAACGCGC ACTGCATCTT TCCCGTGCTC CAGTCACCAA AATAGAACCC CACTCCACAC	360
AAAGCGTCGG GAAACTATC CGCGAGCACC TGCCAATGCG CACCGCTGGA GTACAAACAC	420
GCACCCTTCC TTTACACCGG CTTAAGTGCT GGACAGAACA ACAGTGTA CT GTTGGCGCTG	480

833

CTTGTTGCGC ACGTGTTTCGT CGTTGCAGCC ATGCGCGACA CGGTCGnTnT TTTTCCATCG 540
TCAGTACCGA ACTCGGCGCA CTGAGCGCGC GCTCGTTCAA AACTACGCA CACCACATGT 600
GCCCCTGAGC GACTCTCTCG TACTGGGCCT GCTC 634

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4042 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

CTGAACACGT TGCACGGTGC GACGCTCCTT ACAGGAATGr AAAAAAAGA ACgCCGCGCA 60
CAKTCACCG CCCACATATG ACGCACACCG CCTAGTTTTTTC ATCACGAAGA CcTTCTGAAG 120
AAAAACACGC GCGGTGACAC GCTTCGAGCT GTCCATTTTC CACGTGTGTG TACACCTGGG 180
TAGTTGCAAT ATCTGCATGG CCGAGCAGAC ACTGAACCGA ATGTAAATCG ACACCGCCTG 240
CAAGCAAATG CGTCGCATAT GAATGGCGAA ACGTATGAAC GTGCGTCTCC ACCCCTGAGC 300
GGATTTCAAT ATCCTGCAGG CGCTTCCATA TACCTTTACG ACTCAGACGA CCCCCCTGCC 360
TGTTTAAAAA GACAGCTCCT TTTTTTTCAC TATTCTCCGG ATGCTTCGCG CTCGTAAAAAC 420
GAACACGCGC CTCACGTATA TACTGCaTGA GAAAGTAACA CGCCTGTTCT CCAAAGGGAG 480
CCATACGCTC TTTGTTCCCC TTACCTGTCA CTTTTAGCAG ACGTTCTGCA AAAAAATGT 540
CAGAAAGGGA AAGAGAAACT GCCTCACTGA CCCGCAAACC TGCAGCATAA ATAAGTTCAA 600
AGAGCGCGCG ATCACGCACG CCACCTGGTG TGCACAGTGG AATGGATTGC AGAAAAGTGT 660
TGACCTGTTT GGGAGACAGC ACGCGCGGCA GTGAATACGC ACGACGCGGT GCATCAACGT 720
CTTGCAATtGG GTTATCAGGA CGCACCTGCT CCAAAaTGAG AACTGATAG AACGCGTGCA 780
GGCCGCCATG TCCTTtGCAA TCGTTTtGCC TGAGACACCC GCAGCACTCC GCTTTTCGAT 840
AAAACGTACA CAATCGTGCG CATTGGCGCT TTCAATGTTA CACGGCGGAT CAAGGTTTTT 900
CTGAAAAAGC ATCAACGTAG TCACGTACGT CCGTGCGGTC AAAAGCGCGT GCGCCTCTGC 960
CGAAATTAAG TACGCGTAAA AGGATTGCAC ACGGATATCG ACGTCTTTCA CAGACCCTTG 1020
TTCCTATTTT TCAAAAAGGT CGGTTTCATCC AAATCTTCAT TTACCGAGGG GAGCGGAACG 1080
CCAAACGTGT GGCCCTtCAC TCCGTTCTTT TCCATACGCG TTTCTTGAAC AGCGCTATTA 1140
CGCGTAGCCA GACCAGGTAA GTTTGGCTGT TTAGAGCTTT TAGCTCTGTT CCATTCGTCA 1200

GAAC TAATAT ACACACCGGT ACTCACC GCA CCGTACGATG ATGTTTTTAT CTTT TGAGAA	1260
CTGTGTGTAT CTCCCGCTAT CGAAATACTC GCTTGCGGTA CACCCGTTGC GATAACCGTA	1320
ACCC TCACCC TATCCTGCAT ACTCGCGTCG ATGGACGTGC CATGGATGAT AATCGCATCC	1380
GGATCAATGG TCTTTGCAAC CACAGACATC ACGCCATCGA CTTCTCCCAT GCTCAAGTTC	1440
TCTGAGCCAC GTACCGCAAC CAGCAGTCTG GTAGCACCTT CTATCCGCGT CTCTTCCAAA	1500
AGCGGATTAT TAATTGCAGC GGTTGCCGCA TCTACTGCGC GGTTTTCCTT TTCTCCCTCT	1560
CCCACACCGA TAAGCGCGTA CCCCTGCCCT TCCATGGTGT TTTTACATC CATGAAATCT	1620
AAATTCACTT CTCCAGGAAG GGTAATTAAA TCAGAAATAC TTTGCACCGA CTTGCGCAGc	1680
aGATnCATCT GCAACCAGAT ACGTCTCTTT AATCGGGCAG CGTTATCTA CCACACTGAG	1740
TAAATTCTGA TTAGGGATCA CAATCACGGT GTCCGAGTGC GTGCGCAATT TTTCGATCCC	1800
TCGCTCAGCG AGCATCATCT TTGCTCTGCC TTCAAAGCGA AACGGCTTCG TGACTACGGC	1860
AACTGTCAAA GCACCAAGTT CCCGTGCAAT CTTTGCAATA ACTGGGGCAG CACCTGTTCC	1920
CGTACCTCCT CCCATCCcTG CGGTGATGAA CACCATGTTC GCGCCCTGCA ACGCACTTGC	1980
AATGGCTTCA GCATCTTCCA TTGCAGCCTT CTCGCCAATC TCAGGATCAC CGCCTGCACC	2040
CAACCCCTT GTCACCTTGG TGCCAATGGC AAGCTTTTTA GGCGCGGTAG AATAGCTCAA	2100
CGCCTGcACA TCTGTATTTG CTGCAATAAA CTCGACGCAC TGCAAACCGC AGCTCATCAT	2160
CCTATTTACC GCGTTTGACC CACCACCACC GGCACCGATG ACCTTTATGA CCGTTGGACT	2220
TAGGGTAAAC TCTTCGCCTG AAGGTGCAAG CTCTATATTC ATCATTCCCC TCCCATCCCC	2280
CTACACCGCG TGCCGCATGC TGTGCGCGGT TTAAAACAAG TTCCTCCAAA TATCCTTCAC	2340
TTTAGTAAAC ACTCCCGCAC GCTCCATCTC AGCACGGCCC TGATAAGCGC GCTGTCCCTG	2400
CTTATGGGTA TATTCTAAAA TCAGTCCTAA CACCACTGCA AACTCAGGAC TGCGATATTC	2460
CCCTGCCAAT CCTCCCAAAG TACCTGGTAT TCCAAGGTGC ACGCGCGGTG TATCAAAAAT	2520
TGcTGACGCA AGCTCTACCG CACCGGTAAG cTGCGGCCA CCGCCGAGA GAATAATATT	2580
TTCAATGATA CCACGACCGC TTTGcGTCTC CACCGTCGAA AGACGATCGC GCACTATCGT	2640
AAAAACCTCA CACATGCGCG CTTCAATTAT TTCGGCGATT TCTCGTTTAG AAATTTCTAC	2700
AGGAATCCGA TTTCCCTGGC TGGAGATGAG AACACTCCCT TCTCCCTCAA GCAGGGGGAT	2760
CCAGCAACAT CCATCTTTAA TTTTAATGCG CTCTGCAGTT TCAAGCGGGA GGTTTTTTAC	2820
CTTTGCAAGA TCAGAAGTTA CCTGACTGCC CCCAACAGGA ATCGAAGTGA TAAGCACCGG	2880
GGAACCCCTG TACATTGCAA TAACATCCGT AGTTCCCCCA CCAATATTAA TGAGCACACA	2940

835

CCCTACATTT CGCTCGTCAT CGTTTAACAC AGAACGAACA GCAGCGAGCC CGTTATGCAT	3000
TAAAAAATCG ATGTGCAAGT TCGCcCGTTC ACGCAATCGA TTACACTGCG CATAACGTT	3060
GCAGAACCGG TGATCATATG CACyCTcTTC CAGGCGAACC CCAATGATAT TCGCGGATC	3120
GGTGATGCCG TGCTGATCAT CCACCGAATA AACTTTGGGA ATAACATGAA GAATTTTACG	3180
ATCGGGAGGA AGAGAAACTG CACAGGCAAC TTCAaGCACC cGATCAATAT CGCTTTGATC	3240
AACTTCGCGA TGCCCcTTCC CcTTATCTGC AACCGCCACA ACACcTTTTA AATTTCTACC	3300
CTCGATGTGG GTACcTCCAa GCCCCACAAG CAGTGCGCAA tTCGATACCG GACATCATCT	3360
CCGCAGCTTC AACCGCGTGG TGGATACCCA CAACTGTATT CTCAATATTG ACTACTACAC	3420
CCCGCCTCAA ACCCTTTGAA TGACCGACGC CTACACCTAC AACCTGTAAC GCACCACCTT	3480
CCAACCGCTC GGCCACTACC GCCCTGATCG ATTCGGTACC GATATCTAAG CCGACAATAA	3540
CCTCACCCAT AACTTTCCCTC TTCTAGCGAT ACACCGCCGT CCCACCTCTC ACGTCAAGCT	3600
CCTTAATGCG CCTCTGCGTT TGCCACTCCC GCAGCGCATC AACGAGCAAT ATGACATACC	3660
GCAACTTTTC TTCGCTAAGG TTTTGTCCA TCGTACTCT GATAGGTGCA CGCACCAGGT	3720
AAAGCGCTAA ATCATATCCC CCGTGTCTTT TTTGTTCAAT GCTTATCTCA GAAATTTAC	3780
CGAGCAAAAG AGGGTTCCGC TTGCTCAAAT TATCTAACTG CACAAAAAGA GGAACAAGCT	3840
GATCGTGAC GCGTAGCCCC ACGCGCGGAT TACGAAATTC AAGACCACTT ACTACCGGCA	3900
ATACTGTATC AAGAGGTGCC GTCCCAACAC TAAAACTGT TCCTGTCTTG TCAATCTGCA	3960
CCGGCATCGC ACGGCCTTGA ACGTGACAA AACCAAGTGC AATAGCAACA CGCTCTACCA	4020
CATGAACATG CATCGTATCT GG	4042

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

TTGCCTTTCA AATAAATAAG TATTTTTTTA AAAGGnGGGA GGGGGTTTAT ACTTCACAAT	60
ACTATTATAG GACATGGTGm TTTATCCCTT GCGTAAAGAA CCTGGAAGTG TTAATGCAAC	120
TTGCAAAAAA AGAGGCATTG GTTACTTGGA GTCACAGGGA GTCAAAGGAA GGTATTAAC	180
CCCTTTTTTT GTTCTGTTTT CGTTTGTTTT CAAACAAGTA ACTGGCCATG ATGATACAAA	240

836

CACATACACA ATGACTTGTT AAATTACCTT TTCAAACAAA AAAAGTTATT TCACCCCTGA 300
 GACCAACCAC CCATGAAACA AGGGAGAAAG ACAGAACCAA GTTAGAGAAG CCCCAAAAGC 360
 AACATGCTGC ATTGCTCCAA AGACTGCCAG GTTCCCTTgc AAATAAAGTA CTTGCAACac 420
 CCCCCTTGAG CTATGTGGcT CTGTGTGTGT TTacTAGCAA AGCCAGTCTT TGraATCTTG 480
 AAAC 484

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

TCCTTTACAC GGTATTGCTC CACCCTGAGG GCATCGAACG CGCTGTCAAA CTTCTCCCGT 60
 GAGCTCCCCG TTGCCAGAAG GCGATTACTg CATCGGCAGG GTCCTGGTGT TGGTTACCGG 120
 CGTCGAGGGC GAAGGAGAAG CGCCGCACAT ACCCTTGCAA TCCCTCGCCT GTAAACTGAG 180
 CGCGCACAGC CCCACGGGGA AAACGCGCAC CCCACCGTA CCCGTCTCTT GGCCACACG 240
 ACAACCCCTC ACCAAACCAC CTTCACCCCA CAGATAAACG TGCCAAAGTA ACGCTCAGAC 300
 CACATATCTC GGCAcACCCA TGTAAGGAGC GTCAGCAAGC ACCCCCTGTT CCCACTGGGC 360
 GCTGAGCTCC ACTATCAGTG GCAACTTCGT CAGCGTAGAG ACGAGCGTAC CGTCCTGCAG 420
 CGTGAGGGCA AGCCCCACCC GTCGAGAAT CGAGGACTCC GCCATCTGTC CCAGCAAAAA 480
 TTCAAGATAC TTATCCTTTA CACGGTATTG CTCCACCcTG AGGGCATCGA ACGCGCTGTC 540
 AAAC TTCTCC CGTGAGCTCC CCGTTGCCAG AAGGCGATTA CtGCATCGGC AGGGTCTTGG 600
 TGT TGGTTAC CGGCGTCGAG GGCGAAGGAG AAGCGGAAGC CGGCGCCTGG TTCGAGGGTG 660
 AGTCGGCCTC CTACTCCCCA CAGGAGTGCT GTTTTGT TTTT CGTTCGTGGA GTCTTcGGTA 720
 CCCTTACGGT AGTGCTGCTC CAGTGTGGCA TTCCCTGCCA GCTCCAACGT AAGCAGCCGC 780
 TGACGGTCGA CGCCATAGGA AAGCGTTGCA TCGGCCCCGA AGCCATACTT GCTGTGCGTG 840
 GTGTCAGTAC TATCCCAGGC ACCATTGGA AGGAAGGAGA GGAAACCGAT GTCCACATCT 900
 ACTCCGCTGT TTCCACATT GTGGGCCTGG TAGCCGAGTT TTGCCCCGGA GCCGGAGAAA 960
 CCAGGGGCAT AGCGAGTGTC CTTTCTGAA TAGGCACGGG TGACAAAGGG TTTCCACAGC 1020
 TGGGCAAAGT TAACCACACA GGAAGGACTG GTACCCACTG TCAGGTAGGC CCCATAACAG 1080

TGCAGGGTTG	CCTGGAAGGA	AGCGGTAGGT	TTGGTAAAGG	ACAGGGCCGT	TGAGCTTTTA	1140
GAAGACGCAA	GCTCTACTGC	CAGGTCCTTC	AGCTGCAGCT	GTGCCCACAC	CCCTGAGCGT	1200
GCCTCCCCTC	GGcGGGTGTG	GGTGTGCTTT	GACACCAACG	GcAGGGAAAT	AGTCAGACTA	1260
TTGGTAGTGC	GAAACCCATG	GGTGTGCTTG	CCCGGGCCAG	TGCGTGGATT	CTTCTGGAAC	1320
GCAATGCCCC	ACTGGAGCTG	GGCTGTGCCA	CTGACCTGCG	GAGTGAGTAC	GCCTGCATAA	1380
CCAGAAGCAG	CACATACCAT	GCCCCGAAGT	ACCCCcGCTT	GCATCACCTG	CCTGmCCACT	1440
CACTCCCCCT	CCTCTcACTT	CTAmCTCACC	CCCCCCCCAC	CCGTCTAGAA	GACACGGAGA	1500
GCTCTATCTC	ATGAGCACCT	ACACACTCGC	CTTCTCTTGG	GGGACAGACA	GAACTTCCGA	1560
AGAGAGAACA	ATAGGTTCCG	GCGATGTTTC	GAATAGGGTA	AGGCGTTCTG	ACGCCTcCTC	1620
TAATGACTGC	GCCAGACGCG	CTACCGTGGC	TTTGCTTAAC	GCAACGTtGC	TgCGCCGATT	1680
CGATCATCGC	CTCGTACTCT	TTGATCCCCC	GTCGATATnC	CnCGGGGGGG	GGGGGGGnGn	1740
nnnnGCACAC	ACGCTGGGcN	GACTIONAGCT	TTTGACGGAG	CTTGCGGCAC	TCTACCTGAT	1800
ACCCCTGCACG	TGCCACGCGC	ATCCGCGCTT	CTGCCACGGT	ACGCAACAGC	GTGCTGAGTT	1860
CATCGGGCAC	CGTCGGTCTT	GTCTTCTGAG	ATAAAGGAGG	CTGAGCAAAT	CCTTCCTCGG	1920
TAAAGAAACA	ACTTGCGTAT	GCAGCACCGA	TGCGCGCGCA	CAGCCATTGA	TATCCTCATC	1980
CAGTTCACTG	ACCTGCGCTG	TGAACGCCGC	AACGCGCTTC	AGCGGCTTGG	CACCACAGTC	2040
AAGGGcGCGC	AGgCGgCGTC	GAgTGCTTCT	TGCTCATCCA	TAAGCTCcTG	GCTATGTTGA	2100
AGGTTGCTCG	CGTAAACGCC	GCGGTCGGAT	ATGAGCCGTG	CGTACGCGGC	ACTGAGTGCG	2160
GAGGAAAGCT	CGCCTGCGTG	ATACATGCGC	TCGACGTCCG	GATGCGCAAT	GACATCCGGG	2220
GTACAGAGCG	TAATAATCTT	TTGAATTTTT	GCTTCGAGCA	CGCGAATCCT	GCGCTGAACA	2280
ACCGCGCTCT	TCGCCTGGAG	GCCAACTCTT	TCAAGAATTG	AACCAAATGT	GCATGTTTCC	2340
AAGAGCTGGT	CACGCTTGGC	GCGTAAATCC	TGCAGAGTAG	ACTCAAGCTC	CGCCGTACGC	2400
GCATAGATCG	GTTGAGCGC	AGGTAGGCCT	ACGTGCGCGT	AGGTGGCATA	GTACTIONGGCT	2460
ACAAAACCTC	TGAGTACATC	CCGCTCCTGA	CGAGCATGGC	GGTGCAATAC	TTTGCTCACC	2520
CGCTTTCCAA	GAGCGGCAAG	TTCTTCTTGT	CTTTGAAGTA	TCGACTTAAT	ATCAAGGATA	2580
GACTCAGCAA	CCTGATCGCG	CTGACGTTGA	AGCGCGTGGC	ATCGGCTGAT	GTCAGTGTCC	2640
TGTACGCCAA	GTCCGCTGAT	GTCACACGCA	GCACCGCCGC	GCACAATATG	TTCACCGAGA	2700
CTGCAACAAT	GGCTCTGCAG	ATCCTGCTGC	GCACGCTGAC	ACGCGGCATT	CAGCGCGGAA	2760
AGACTCTTAT	CCGCGAACAT	GACCGCATTG	TAAACACTTC	CCCTGCGTAT	GTACAGGGCA	2820

838

CCTCACTCCC TCTTTACCCA TGCAAGGACA GACGTCCTGC CTAACCTCTGG CGGGGTACTA 2880
 CCTGCGCGCT CGTATTCGGG TACAGATTAT ACGCCCGATC CATTGCGTTA GGCAAcCTGC 2940
 GCCAGGATTG CAAGCACTGC CATTGTCATC ACCTCTGGTT GGAAGCGCTG ATACCCGTAG 3000
 CGGATCGCTA CGTCTcCTAA ACCTcCTcCC CCAATCGCCC TGCCATTGCT GAGTATCCAA 3060
 TTAGATTAAT TACCATCAGT GCTACACCAG AAAnCACATG CAGGAGCAGC CTCAGGCAGC 3120
 ATGATTTTTA GTAC 3134

(2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 635 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

ATtnTTTAAT nATAGGATCC CGTCACGTCA TACACAACTT TCTCCGCATA AAGGCACTCA 60
 TCTAAGTTAA GCTGAAGCCC CTCATACAGG ACATCAATAG AACGTGCTAG GTGATAAATA 120
 TTGTCTTGAA ACACAAAATT CTGCACCACA GACCTCCCCA CACATACGTG ACCGACGCGG 180
 GCACACAGGA AAGCGCACCT TCTGCGAACA GGTTCCTCAC CTCGTCTGCC GTAAGAGCAC 240
 ACGCACGAAT GTACCCCTC AGACGACGCT GCGCCGTCGG CAGCATCGGA TAAAAGGACA 300
 AAAGACTTGA TGCGGCACAC AGATTTACGC TACGCTGGCG TCTCGCCGCG CGTTCTGCGC 360
 ACGCTACTCC TCCTTGTCGG GTGAGTCTAG TGCAGCCTGA TAAGGTGAGC CGTCCATAGG 420
 AGTTATTATG AGGACCTACG AGnTAATGGC CGTTTTcAGT GCACACGAGG ATCTCTTTCT 480
 TCAGGGTTCC ACCGCCGTTC GTGCCCTCCT ACAGGAAAAC GACGCATCAT nCGCCCGCGA 540
 AGACCATATT GGAGAnCGGG AACTTGCGTA TCCTCTGAAG AAGCAAAAGA GGGGCCGTTA 600
 nCTGCTCTTC ATTGTTCAGT GTTGAGCCnG GGAAA 635

(2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1644 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

CGGTACCTTC GGTTCCTGGG CAGGGCTTAC TGCAGCCGAG CAGCTCGTCT TATTCAGCCG	60
GTAACCTGGCA CCGCCACGTC TCATTGCTTG GCGTGCTAAG TGCACCTGCCA AGGAGGTAGG	120
CGCCATACAC GAAGAGTCGG CGTATTAAAG GGGTCTGTCA GAACTATGCG GTGCCGGTGC	180
AGCTGGGGGT ACAGCACTAT TTTAGCGCGC ACTGGGGGAT AGACGCGACG GCTACCGTTT	240
CGTTTGGCAT TGACACCAAG CTGGCTAAGT TCCGCATCCC GTATACGTTG CGCTTTGGCC	300
CCGTCTTCCG CACCTAGGGG ACGGCGCTGG GArAAAgAG TCCTGCCGGA AGGccCTGCG	360
GCGGGTAGTA GCTACCAGGA GAGGGTGACG CCGCACACGA TGCGGCCGAT TCCCTGGGTG	420
AGGCACTCGG ACACCAGCAG GTACGGGACA TCAGAGAGCA TACCCTGTTC CCAATCAAGG	480
GAGAATACCG TCTTCTCTAT GAGACTGGCT GAAATACCAG CACGCAGCTG TGCACAGTAC	540
TCCTTGGTTA GATAGGTAGC TCCTACTGCT CCACCTGCAG CAGGGGCATT CAGGTGTGCA	600
CGGTGGTAG AGGCATGGAC CGTAACGCTT GGCTTCACCC AGCCGTAATC CTGCACCGGG	660
ATGCGATAGC TACACCACGC CTTCCCCACC ACCGGTGGAC GGATATACTC CTTTTCCTGA	720
ATGCCACGCA CAGCCGTCCC CCCGTTATTT TTGTATAGCG CATAGGTGAG GGGGATGTAC	780
ACGCGTGTTC CAACGCCGGC GTCCAGGCCG GTGAGCAGGT GGGTGTAGGG GTCACCGCTC	840
TTAGTTTCGA GCTTAAGGAA TCCGGCAAAG TCGCCACAGC TTGCGATGGT GTTATCTAAC	900
ACCCTGGTGC CAAAAACGTT TGCCGGTGCT GTGGCAAAGT ATATGCCAGA AGACAGCCAC	960
TTCCACTGCG CCGTAAACAG CGCATCGAAG GCGACATTGT AGGTGTCAAG ATACAGACAC	1020
ACGGCGCTGA CTCCCATTAG AAAGGCACGC CATGCAGACG CACGCAGGTT CTGTATAGCC	1080
TGACGTATCT GCTGCCCCGC GTCCAACGCA TCCGTCTTCT TCTTCACTTC TTCGGTTACA	1140
AACGCTGTAC CCTCAGTGAA AAACTTTGTA GCCTCAGCCG TAAGCTTTGG AATAAGATCG	1200
GCGAGATCGT CCTTCAGTAA TTTTGTGTA TCCGGAAGGT TGAAGAGGCT CATCGGATTT	1260
CCCTTATGCG GTGCAAGCAA CGCATCAGCC ACGTCTTCTA TTGCCTTGGT AAGACCGTTG	1320
ATGAATGCCT GTGCTGCAGC CTTGCTCTGA GCCACAGCCG CTTGCACTTT CTGGTTAATT	1380
TCAGCAACGA TTTGCGTCTG TACCTGCTCA AACCCCTTCA CCACCTGcTC CGCATCGTAC	1440
TGCAGCAAAA CCTGCCCCAT CAGGGAAAAT GCAGGAAGCG CGGGAAGCGG TGACGGTGTA	1500
GGAGGGTCGG TAATGAACAC CTTCAGGTTC GTCAAAAGCG TGGCAGCTAC CGGAGGGGTG	1560
ACTTTTACGT TTGACACTGC CGTTATGTAC GCGTTTCCCC TCGACTGAAG GGCGGTTTCs	1620
GTGGyksCgT TACGGCATCA AGCA	1644

(2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2535 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

CACGTACCGT CTCTGCAACC GTAGAAGCCT TCAGAGAAgG ACAACCCGAT CAAgTGTAAC	60
TGATCTAGAT ACGCAGCTTC TGCAAgGCag TTTGCACCAA CGCTTCTGCA CGCGCATTTCA	120
cTGAcTGCAT CCCATCCGCG TAACGCGCCG CAAtGCGCGC TTCACCACAC CCGGCAGAGA	180
ACCGGTATTC ACCCCAATAC GCAAAGCAGT GCCGGTTGCT CGAGCCTTTT CTACCACCGC	240
ACGCACGCGC TCACGCACAC CGATATTCCC CGGGTTAATA CGCACTTTTCG CTACCGGTCC	300
GTCCATACAC CGCAGCGCAA GCCGGTAATC AAAGTGAATG TCTGCAACAA GCGGCATACG	360
CGTGCGCGcG CAAAGCsCcA CAAAAAGCTC AGCCGATTCC CTGTCAGGAA CGGCAAAACG	420
CACAACGTCA CACCCTAATT GTTCAAGTTC CAAAAGACGG TCCACAATGG ATTGGAGATC	480
TGCACCAATG AGCGGTTCTT TCCACATTGT TTGGATAGGA ATCGGTGCGT CACCCCCAAG	540
AGGCAACGCA CGCACATGTT CCTTTCCTCC AATTACCAAT GATCGTGCAC GGTAGTGGGA	600
CGCACGCGGT CTTAATTTTA ATGGAACATC CAAAAGTCCA CTCCCATACG GACTATTGCA	660
GGGAGACACA CCGGCAGATG AATCCACCTT TTCTCTGgC tGCCGCGCag CACGCTCGTC	720
CCTCTGATTc ACCGGGCCAC CACTTGCGCA CGCACACTTT GCGCAACTTC CACTCCACAG	780
AGTGCTTCGA TAACTGCGAA AGAAACTCT TCTGCCGCAC CTGCCGCACA CGCGGTCAAA	840
AGATTTCCAT CACGTACCAC CCGCGCGCGC TCAGGTTTAC GAAGCGCACG CGATTCTCTC	900
TCTTCCGTCC TTTTCCCAAC CCCATCGTCA TGTGCGGAGA ACACCGCCGG CTCCATACCC	960
GGATAGCAGG TATAGCGACG TGACCCAGG AGATTCCACG CAGAGAGCAC TCGCGCCGGG	1020
GCAGCACACA GCGCAGCGAC GAGTCCTCCG CGCAGGTGCA CGCGCATGAC AAAATCACGC	1080
ACCGCCGCAC AGGCGGCAAG CGTATGACAG TTTTCCAACC CCCCGGAAG AAGAACCGCA	1140
TCTGCGGCGC ACGCGGCATC CGCGATGCCC GGAGAAGCAC AAAGCGCCTC AAGACTGCAG	1200
TCGCAGCTCA CACGCAAGCC ACGCGTAGAA ACAACCTGCT CTGCCCCAAC ACCCAGGAGC	1260
GTTAACGCTA TCCCCGCACG TCTGAGATAA TCCAACGGGG TGATAGTCTC CACTTCCTCA	1320
AATCCGTGTG CAACAAAAG GTATACCCGT ACGCTCACCG CAACACCCCC GTACCTGTTT	1380
TTACAGCAAC AGTGCAACCC CGCGCACACA GACTACGGAT AATCGTCCTC CGTTCAAAAG	1440

841

CGACGTACTA GCCGTGCGCC CCGCGAGCGC AgCACTACCT TAGGATAGAA GAACTAAAAA	1500
CCACGCGGAG CCTGTGCCGG ATCTATTGGT TTATTTTTTT TATATACCAT AAAGTACAAT	1560
CGTGATCGCG CCGCTGCTGC GTCAAACCCC AAATTACCGA GCACGTCGCC GGCAGAAACA	1620
TAATCTCCTG ACTTTGGCAA AATACGCTCA AGTCCTCCAT ACACGTACAC GTGCTTTCCC	1680
GGCGACTCTA CAAAGAGCAC CTGACCATAA CCCCAGTGGG TCCCCCTGGA GATTACCTTA	1740
CCAGACATGA GTGCACGCAC GGCAGCATTT CTTTCCGAAT CAATAACAAC CCCGTAGgTC	1800
TTGCCCCGCA CGTACGCAAG CGAAGTCGGG CTCACCGGCC AGCGCGCATT CTTATCAACT	1860
TTCTTACTGA TATACTGACG CGGATCACGC AGAGAAATTT CTCTCTCTC GGGGGCCGGC	1920
ACAGCAGCGG GGGGAGAAAC AGGAGTCTGT ACGGGATCGG CACGGGCACG CGCCCACTGA	1980
TCCCCATCGG GCAAAGAAGA CACAGATAAG ATGCGGTCCG CGCCCGCCAC GGTAGGAGGC	2040
GACTTTTCAC GCGGAGGAAT CACGAGCACA TCACCTGGGT GAATAGTGTG CGCAGCAGAG	2100
ATTCCGTTGG CTGCAAGAAG CGCGGCAAGT GAACAGTTTA GCATACGGGC AATCGAAAAG	2160
AGGGTGTAC CCCGGCGCAC CGTGTATCCT CGTGGAActa CTATGCGCTG CCCAGGCACA	2220
AGCTGGTGTA CGTTTGCCAG ATTATTGCCC TGCGCAACGC AGAAAGGGGC ACGCCATAGC	2280
GACGCGAAAG TGAAAAGAGG GTCTCGCCCT TAGCAATCAC GTGCACGTCT GCGCCGCGCC	2340
GTAGGCTGCT GCCAACAAAA AACACCCCGC AAGCGACAGA AAAAAACCGC CCATACCCGC	2400
CCCCTTCTCG GCAGATAAAA AAAAAGCATG AGCGTCACCT ATGCGCGCCC GTTCCCCCTG	2460
TCGTAAATAA CAAACGTTCA CCCGCAGCCG AGACACTCCA CAGCCGGCAG GAGCACGCAC	2520
TAACCCTACT TGTCG	2535

(2) INFORMATION FOR SEQ ID NO: 176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1226 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

TGGTCTTGC GCCGATTTCG TGACGTACTT GAGTCCAAAG ATGCGCAAGG AACTGGAAAA	60
TGGAACGTAT TAAGGATTAA TGCTCATGGC AAGGAAGAGG CGTGCTCCGC GCGGGCGGGC	120
ACAAGGGTGG CTAACGACAT ACTCAGATAT GGTACAGCTT ATGCTCTGTT TTTTGTGCAT	180
GCTGTTTAAT CCAACTGAAG TTGATATCAC GGTGTTGCAG AGTATTGCTG CATCGATTGT	240

842

AGGTGATCCT ACCGGTGGAG GGGTTTCTGC CTCTCAGGG AGGCTCGCTG ACTTGGGAAA	300
CACCGTTAAC ACGCTGCCtT CACTGGAAAA GGGACAGAAG CTGGCGACTG CGCTGAAGAA	360
GGCGGTTTCG CTTTTCGCTC CTGAGATTAA AAGCAATAAG ATTGCGGTGA CCAGTGATGA	420
GCGCGGTTTA GTTATTTTCG TCACTTCGGA TTCGTTTTTT TATCCGGGGT CTTCCGATCT	480
GAATGTGGAG GAATCTCGGG AGGCGTTGTT GCGTGTTCG CAGTTTTTGT CTGATCATGC	540
GCTCGCCCGT CGACGGTTTC GCATTGAGGG ACACACCGAC TCAGTTGAGG TGCCCGAAGA	600
TGGGAGTACA GACAATTGGG AACTTTCTAC CCGTCGGGCG GTGCGCGTGT TGCATTATCT	660
TACTGATTTT GGTGCaCAGG AAAATCGCTT TTCCCTTGCa GGGTACGCAG ACACACGCGC	720
AAAATTTTCA AACGAAAGCc TGAAGGGAGG GCGTACAACC GGCGGGTTGA TATTGTCATC	780
CTGGACGAGG GTCACTTTGT ATGGTACACT TCCGCTTCCC CTTTCCCAGA GGTGAGTTTC	840
CGGTATCTGC ACAGCCTGAG TTTGAGCTGG TGGCgCGTCT GCACGCCGCT GTAGTACGTG	900
AGGAGGATGT ATGGCAGAAA AGGACTCCAT AGGAGATATC GCTGATGATT TTGAGGAACA	960
GCTTGTCGCT CCTGCTGCGG ACAGGGTGGG CTTTCTGCCA GGATTGCTCA GATGGGTTC	1020
CATTGCAGTA GGGGCGGTCA TCTTCATTGT GACGGTGGTG ACAGCCACCG CGCTGGTGCT	1080
CGCAAAGCAG GGGAGTAGCC ACACGGCGTA TCCGGTTcAC AGGAGTTTCG GgAGTCTCGC	1140
GAGCTTTTGC AATAcTACGA GTmCATGGGC CTATCCGTAC CAATACTGCA GATGCGCTAC	1200
CGGGGACGTT GTAGTGAGCG TTGCGT	1226

(2) INFORMATION FOR SEQ ID NO: 177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1079 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

ATCAAATATT CCGGGGATAT CGTCACATTT CCTGAAAATT CTACCTTTGC AAAAGAAGTT	60
GCCGGAACAA CAAAAAGATA AAATACAAAC TCCACACACA ACACGAGCAG CAATATAACA	120
ATTACCACCT TCAGTACTGC AACTCTCACC CGCATAGACA TATACCCTAC CAGAGGGTAC	180
TTGCACGCTT CAGTATTTCT ACACAAAAAC TGTTCCTTCA CGTCCCTCC tTATCTTCTC	240
ATCCCCTGAA ACATTGATGA TCAATCCACA TAAAGAAAGC GTTACCACAA TAGATGAACC	300
TCCTGAAGAA AAAAAGGGAA GAGGAATACC AGTGGCTGGA ACTAGACGTA CCACCACTGC	360

843

AACATTCAAA ATTGACTGTA AAACAATTGC CGCCGACGCG CCGAAAGCCA AAAAAGTATT	420
AAAGCGATTA GCACATCTGA GTGCGATAGA AATGCCAGTG AGGGTAAACG CAAACAACAA	480
CATTAAATAT AAACACACAC CAATGAATCC CATCTCTTCT CCAATAACGA CAAAAATAAA	540
ATCCGAATAT ACTTCGGGCA CGCTCGCAAT TTTCCTCACC CCATTTCCAA TACCACGCCC	600
CCACAACCCT CCATCCATCA GTGCCTCGAG CGCCGCGTTT ACTTGGTATC CTGCGCCAAG	660
CGGGTCTCTA TCTGGATACA AAAATGAAAG CACTCGACGC AAACGATTGG TGGACGTGAC	720
GATCATAAGC ACTGCTATCG GCGCAAGAAC CATTATGCCT CTAAAAACC ACCACAGAGG	780
CGCACCTGcA ATGAAGAACA TAACCACTGT GATAAAAAGC AAAACATAG CGGTAGAAAA	840
ATCGTTTTGA AAAAAACTA CTGACACAAA AATCACGCTC ACAACAAAGG GAGGAAAAAT	900
TGATCGTATA GGTGTATCGA AATGCTCCCG GTGCTTATCA AAAAAAGTTG CAAGAAAAAC	960
AATGAGTACC AGCTTCACAA ATTGAGATGG CTGAAAATTA ATATCAACA CCTTAATCCA	1020
ACGCGTCGCT CCATTGCGCG TTGAACCAAT ACCAGGGAAA AACGTGCACA CACAGAGCG	1079

(2) INFORMATION FOR SEQ ID NO: 178:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 556 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

GnTTTGAAGC CGTAGGCATC TGTGCGCTTG CAGAATGTAT ACATGCAGGG AGTGCGCGTA	60
CGTGCCACGT GAGTnCTTGG GGAAGCAGC TTATGTTTAG ATCGCGGGGG GGGGGGGGGG	120
nGnACTTGTA GTGCTTGAAC GGGATGTGGA CCGAGTACTG GAGTACCTGG GAAAGACGGC	180
GCTTGTCCAT TTGCGTCTTT CCGCCGCGGC GCGTGCCAGT TCTTCCCACT GTGCGCAGAG	240
CAAAGAGTAT GTCGGCCGTC TTGAAGAAGC GTGTAAGTAC CTGGGTGTCT CTGGCGAGTG	300
CGCGTTTTCT CCAGGGGATT CTTTGCCTAC CGAAGAAGAC TACACGTTGG CACAGCAGAT	360
ACTTGCAGAA GTTGACGCTT TGCACGCACG CGAACGAGAG GGTGATGCTC CCTCAGTTCC	420
CCGTGGGAAG AGTTCTGTAG CCCATGATTC TGCCAACGAA GAGCAGTTTC AGGGTGAGAA	480
ATGTGCGCTC GGCTCGATGC GAnGCCCGGC ACTGTGTGCG CTGCTTAGGC GTTTTGCCT	540
GCAGGAAnGT GTGCAC	556

(2) INFORMATION FOR SEQ ID NO: 179:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 450 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

TnTGACTAAA GTACATGCTT GCAGCGATAC TCAATGAAAT TGGATTCAAC ACCGGGCTAT	60
ACGCTTCTCC TCACGTTATG GATCCGAGAG AGAGAATAAC ACGCGCGGGT GTGTTTTTTT	120
CACCTGCCGA GTATGCAAGC GCGTGCACAC ACGTATACCA CACGGTGAAA AAAACAGAGA	180
ATCTGCGCGA CTACGGCCAG GCGACGTGGT TTGAGCTTAT AACGCTACTG GCGTTCATGC	240
TATTTGCACA ACAACGCATG GAATGGTCCG TTTTGAAGT AGGACTTGGA GGAAGACTAG	300
ATGCAACAAA CATCATTTGT CCTAGTATCT GTCTCCTTCT CCCCATAGAA CAAGAACACA	360
CGCGCATATT AGGAACACGT ATAAAAAGTA TTGCAAAAGA AAAGGGCGGC ATTATCAAAC	420
CCTATACGCC TATTTTTGTT TTGATCAGCC	450

(2) INFORMATION FOR SEQ ID NO: 180:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 605 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

TGGGATCTTG CAACTGACGC TCCCCCTGAG CGTGTGCGTA TGCTTTTTAn ACGCACGGTT	60
CCTACTGGnA TTGAACACGG CACTGTTACA ATTCTTTTCA nAGGGCATTC TATTGAGTGC	120
ACTACGTTCC GTGTGAGTC GGATTATTCC GATAGAGACA TCCGGATTCT GTTTGCTTTG	180
CCGCGCGCAT TGAGGACGAT TTGGCAAAGC GCGACTTCAC TGTCAATGCT TTCGCTGCCG	240
CGCTCCCCTC GGGGGAAATC ATCGACGTAT GTGGCGGTTA CGCGATTGTC GTAACGGTCT	300
TATCTGTAGC GTTGGGGATG CACATGCTAG ATTTTCTGAA GATGCGTGCG TCCTTTGCGT	360
GGCTGTGCGT TTTGCAGCGC ATTATCTTTT TCCATCGAAG CGCGCACGnT GAAGCAATTA	420
TCGCGCTACG GCTTCATACT GCACGTAATT CTCGTGAnCG GGTGCGTGAT GAACTTTCTA	480
AGATGCTTTG TACTCCCCGT CCGATATTGC GCTCCGCTAA TGGAAGAGAn TGGGATGCTG	540
CAAACACTTT TTCTGCGCT GGCAGTGT GTGGGAGAAA CGAAnGGGAA GGAGAAGGAG	600

ACGCA

605

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

ATGnCGTTTA AACGAAAAGG AGAGTTCGGT TTTTGCACGT ATTGAATAAA TGTTTTAAAC	60
CAAGTGGATG CATTGTCGTG TGTAAAAAAT AATTTTTTGGT AGCAGTCGAG CGGAAGCATG	120
GAAAATGAGC ACAGTACCGG GGGTGTGCGC GTACCGTGCG ACAAGTTGCG CATAGAATGT	180
TTGAGCGGGG GTGTCAATCG TCAGTTCGCG GTACGTAATG CAACAAGGCA TTTGCTGCTG	240
TCCTCAAGTA CTGCAGGTTT AGTAGCGGGC ATATCAGAGG CTTCGAAGAG ACGGTAATCT	300
AGGAGACAGT ATTCCATTCC GGCCTTTACG AGTGAGGGAA TGAGCGCGGC GCTCCATGCA	360
GATGCTTCCA GAAAGCAGCC CCGTGGGCGT TTTATAACGT GTTCTCGCAA GGTAAGAAGT	420
AGTAGCTCAA TTTGACTAAT TACATCCGCC TGAGGGAGGA GGGGAAGATA CGGCTGGTAA	480
AAACCGCCGC TGAGTAATTC AAGCCGTTTG GAACCAAGCA GATTGTTGAT AAGATAAGGA	540
TAGGGAGAAT TCTTTTTTTG TATAAATTGA AAAAAAGAAC CGGTCATGTG CACCGTCAGT	600
GGGAGTTGTT CGTGCCTGCA CAGACCTGAA AAAAATGCCT GGTACTGAGA AGGATCGTGC	660
TCTGCGTGCA GGGACTGAAC ACATGCTTCC GTTAACTTCG CAGCAAATGC GATACGTATT	720
TTGGTATTGT CTCCTTTTTT CATAATCGGG TTCTCATCCC CGCCGCGGGT ATCGGAAAAA	780
GCCACAGCTC GTCAGTACCG TACAGGCTCA GTGCAATAAA mCCCATACTT GCTAAGAGAA	840
GTGCAGCTGT TTTCTCCACT GcAGTGCCGT TTCCCTGCGT GATGCGCTGA TGTATCGCGC	900
GTAAGATGGT GGAGAAACAT AAAAAGCCGA CACAGCTCAC TCCCCACATA ACGAGCGCCT	960
CAAAAAGGTT AAGGGCAGTG TACGTAATGT AAAATACGAG TGCGTATAAA AGACCCCACT	1020
CGCTCTGAGC ACGGTGTGAT GTACACGTGC GCGACAGTTT TCCGCTGCAT GTACTCAGAC	1080
AAAAGGCACT TGCGCCACG CCAACGGTG TAAGAAAACG CAACGCAAGC GGGTCATATA	1140
CGTAATGTAT ACAGACCCAG TTACCGGTTA TCAATATTCC GCnTAGGAAA AGGAAGCGAC	1200
ATGTATGGAA GAGCGTGCAA CGTGGAGAGA GCGCAGCGAT GCACAGGCGA TCTAATACCG	1260
ATGCC	1265

(2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

GCACCCGAT GACCGTTCnT GATCGAGCGG GTACGTCCAC CGTGCGCCCC ACACCGAATG	60
TnGAGCGTCC GCGCTCCCC CTGCATGCGG TACACAAAA ATCCGCTCnA CGCCGTCACT	120
GCCAGACCA GCGCCACGCA GCACCCGTCC AGCAGCGTCA GCATTCCGCC GCGCGCGGCA	180
GCCGACCCGA TTCGGGGGAG AGGTGGAGGC ACGATCATTC TCGCCGCAGG CCACGCGTCC	240
CCCCGTTAGC GCTCAAAATA CGCACGCGCC TGCCGCGcCA GACGCCGCCG CCCGAGCATC	300
CCCCGCACCC CGCGGGCAAA AAATACGTCC AACACTGCAC GGGCGTGCTG CACCGCCGCA	360
TACCCACGCG CCACCAGCTC tGCGGaCGAG AAAAATCACT CTGGTCccGC CGCGTTTCTA	420
CCCGCACACA CGCGCTCGGG TAATTGCGCG CCTGCGTGGC AACC GCATGC GACGCACACG	480
AAAGACTGCG CACAACCACG TCAAACCCCG TCCGAAAGTC ACTGAGCCCC AGCTGCTCAA	540
ACCGGTCAAA CGTCACCGCC AGCACC GCGT cAAAACCTG CGCGCGCGCA ATCCACACCG	600
GCGTGTGTGT CAATATACAG CCGTCCGCCA AATACACCCC CTCCTGCCGC ACCGGCGCAA	660
AAACACCCGG GTACGCACAC GAGGCGCGCA ATGCACGGGC AAGCACCCCA CTGGAGAGCA	720
CAACCTCCGC GCCCGTACAC AGATTGACCG CATTGCACAA AAACGGAATT TTACAATCGT	780
GAAAGGATTT CCCCCCGTC ACCCGCGTCA gsAGcGTGGC AAAC TTTTCT CCCGAATCAA	840
GCCCCAGCCC CCGCACGAGC GTGTTCAAAC TCACCCCCAG CTGCACCAGC TTGCCCAAGC	900
GTTGAAACGC AGCCCGCGCC CCCCACACCA TCCCCGCTC AACGCACGCA GAGGGATCCC	960
GTGCATTAC ATAGTCTGAA ATAACAAAT CACGCTGAAA AAACGCCTCC ATCTCCCGCA	1020
CCGACATCCC CAGCGCATAG AGCGCCCCCA CCACCGCACC CATAGAACAT CCTACGACAC	1080
ATTGCGGCGG CGGAACCTGT AGCGCTTCAA GCGCCTTGAG CACCCCAATG TGGGsAATTC	1140
CCCGCGCACC ACCACCTGAA AGAACGAGCG AsCACTTCAC GTGCGGTCAT TATGAGCGTT	1200
TTCTCCCTG CTGTCCATTC TCCCCCAGT GTGATACCGT TCCAGTACGC AgTATGGAAT	1260
CGTTTGTACG CAGCGCACTT GCGGCGCGCA CACTCCCCA	1299

(2) INFORMATION FOR SEQ ID NO: 183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1115 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

```

TTAACCGGGC GTTTCCTTGC AGGTTACGCA GGATTGCTTG CAGCAAGCGG GGCAGAGGGT      60
GCCTTTGATT GGCAGAGAGC GGACGCGATT GCAGCGTTAG ATCAGGCAGG AGCGCAACAT      120
GCGGTTTCTC CTATCGCTCA TCCTGCAGGg TGGATGGAAC TTAATCCGGC TGTGCTGTCT      180
GATGTGTATA GTGTGGCTGC AGGATATCCG AGTGCGGAGG GACTCCCTCA TGCGGGGGAT      240
AACCGGGCGG CGCTTGCAAT CGCATCGTTG AGAAATAGCC CGGTTATGAT TGGCAATCGA      300
CACACGTTTG ACGAGTTTTT TGcAGAAGTG ACAACAGCAA TCGGTCTTAA GGGAGAACAr      360
GCGGAgCGTT CGATGCAAAT GCACGCTGCA ATTCTCAAGG AGCTCACAGA TATGCGTGAT      420
GCGACGTCGG GAGTGAATAT TGATGAAGAG TTGGCGGACA TTATTAAGTT TCAGCACGGC      480
TATAATGCGT CTGCGCGTTT TATTGCGGCG GTGAATGAAA TGCTCGACAC CGTCATCAAT      540
CGTATGGGTG TTTAATTTTC AGATAGTGCA CGGTATGAGG AAGGGAGGAT GGGCGTGAAG      600
CGTATCAGCT CACACATGCA GGGCACAGAC AGTGCCTTTT TCTTAAGGGA GCAGGAAAGT      660
AGACTACGGA AGGTAAACAA TCAGCTTGCA ACGCAGCGTA GGATCCAGCA GtTCGCGATG      720
ATCCGCTCGC TGCAGGTCAT TCTGTGAGGT ACAAGTCGTC CCTGGCGCGT TTAGATCGCT      780
TTGAGAGAAA CACGAAACT TTACGTGACC AGTATCAAAT CGCCGAGGGG TTTATGACTT      840
CTGCGCTGAA CGTAtACAGC GTCTTCGGGA AATGgCTGTC GCAGGAGCGA ACGGAACCTA      900
TACTCCTGAC GATTTAAAAA AAATGGCGAG TGAAGCAGAT GAGCTTTTAC AGGAGCTGGT      960
GCACAATGCA AATGCAGTGA GCGCAGATGG GGTGCGGGTA TTTAGCGGTA CCAAAGTTTT      1020
CACAGAGCCC TTTGAAACGG TCATGGGGAA TGTTGAGGGA TTAGGGTCTG AAGTGATCAC      1080
TCAGGTACGC nTnTTTCCCA AACCGGGGGG TTTTTT      1115

```

(2) INFORMATION FOR SEQ ID NO: 184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

CAGCCTTGGG CGACTTCCTC TGTGAATGTT CAGGCCTATA CTAGGCAAAG ATTTGAGAGG	60
TTATCTCGGC AGACCTCCGC AGCTCTCCCT CCACCGTAAC AATCTCCTCT CAGGACCATG	120
ACCCATCTTT TACCCTCTAA GCTCAGATCT CTCACACTTC ACAGATTCCC AGGCCCTGGC	180
TTGGTTCCTC CTCCCTGCAC GACAGCCTGG AAATGGGCTC TTATAAATCA GTGCAGTTGT	240
GGGCATCACC TTGGCCTTCC CCCATCTTAG GGATCATAGT GCTAAATTGC ATGTTGTCCA	300
AAATCTGAAA GCCATgTTTT ATGTATTTCC CCACTTTTCT CATGTTTAAG GTGATGCAGT	360
TAATCTaCCT CTGTTAcTCC GCCTgACTGA AATTGGAAGT CCCgTCTgTG CTTCTCTCCC	420
AGATTcATAC CAkGCTCAGT TAnCTGGTCA ATTTTGTCTG TTGA	464

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

CGCAGGTTTT GCCGTGTAAT CTAATGCTTG AgCtctGCGG ctAACTTCTG TCCaGAAaTCA	60
GCAaTTTCCC CAAAAACAC GCTACaTGcm TcAAaGGCAT AATCACGTAG AGCAAACAGC	120
GCATATACGA TAAAAAACCC AAATACAAAC TGCATATCAA GCGTAGAAAA ACGGTGCACC	180
CAAAATACCG ATATGTAACC TGCTGTACAT GAAAACCCCA CCGTGCATAA CACAAAACGC	240
GATAGCGCAA ACACCACTTC TTAAAGGAA ACAATTCCAG TAGACGCAA TGCCCACTGA	300
GAAATAAAAA CTATAAATAC ACCTCCTAAG GGAAAAACA CAAACACCCA GGGAAAAACC	360
GcAAACAAGA ACAAGATAAT. aACCCACGTG aTaAAACCCA AAGCCACTGc CCCCgGAGa	420
AACAGGAGTT GTTGCCGATA TGcAATACTT TTCATCATGA ATGCTTTTTT cACCAAAGTT	480
GCGAACGTAA aCAGGGAATG ATTAGAAAAA AAAGCGCCGC GTTATAACAC AnTACCCGAA	540
ACAGAAGAAA ACAAATAATT TTGGTAAAAAT TTAAAACTTC	580

(2) INFORMATION FOR SEQ ID NO: 186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

AAACCGCGCT GCGCAGCCTG GGTAAACGT TGCCTTGAA ATAGAAAATC AGCAGGTTGT	60
CGGGsCGAGT ATGGGGGAAG AGAGTATTCG GCAGGGTACG CGCGCGCTGG TGTGGGGGCT	120
GTGCGCGGTG CTCTTATTTA TGCTGGTGTG GTATCAAGAA GCGGGCGTAA ACGCTTGTGT	180
cGCGCagCTT TTGAATCTGT ATATCATGTT CCGTGTGCTT TCAGCGTTTA ATTTGacCTT	240
ACGCTTTCGA GTATCGCGGG GATGATTCTC ACTATTGGTA TGGCAGTGGA TCGAATGTC	300
GTTGTCTTTG AGCGTATACG GGAAGAACTT GCGCTGGGCA AAAGcCGCGG GGCTGCTGTG	360
TGTArCGGCT TtGagCGTGC GTTTTGGGCA ATTATGGATT CAAACGTGAC GACGTTTATA	420
GCAGCGCTTT tCCTTTCGgT GCTCGgTACC GGTCTATtA AGGGTTtCGC ATACAGTTTG	480
GCTATCGGGG TGGTGTCTC CGTATTACG GCATTGTTCG TTTCCCGTCT GATGTTTGAC	540
TACGGGACGG AGGTTTtACA CAAAAGACC GTGCGCATTG GATGGAGGAT TGCTCGCGTA	600
TGAGACAGGT GGTGCGTTTC AGTTTGCTGT TCCTGCCATG CGCGATACTC AGTGTAGTTC	660
TCATTGGTGC GGGAGTGCTC CGTTGGGCAT TGTGGGGGAT GAGCTTTGGT ATCGACTTTC	720
AGTCTGGTTT GATTGAACGG CTGAGGATAG CACCTCCTGC TTTCTCTCTC GTGTACACCG	780
GAACGCATCG ATGCAGTTTT TTCAGGATGA ACAGAAGGTT GTGTTTACTG TCTCTTCGCC	840
TGGGGTGCTC GGTGagCGTT ATGAATTTTT GTATACGGAG TATCCAACCC TTCGTGCCTT	900
CTCCGagGGA GCAAAGAAGG TGGAGCACCT CAGTGTTACG CTCCATGcCC CTGagACTGT	960
GtAcATGCGT GAwACATtCT CCGGGGCGGA GGGCTCCACG TTGTCGAGTG CTTCGTGTTT	1020
TGTGCATTAC TTCTCGGAGG ACGTTCGTGC GCCAGGGGTG GAGGAGTTGC GCCGTGTGCT	1080
GAAGGATGTA CCGTCTGCGG TGGTACAGCA GGTAGGGGTG CGCGCTGAGC ATACCTTTCA	1140
AGTTCGCGTT GCAGCTGAAA CTGCCTTCCC GTCCTCCCTT TkGCCAGAGC AGGGAGGAAC	1200
TGCTCTGGCm CAGTCCGATG CTCCCATCT TGTTACCCCT CAAGGTGCGG TGGAAAGCGT	1260
GGTGTAaCGC GGCGCTCGTG CGCGCGTATG GAGCAGATCA tGTGGTCCGT TTAGCGATGG	1320
ATTTtGTCGG ATCTCGTTTT TCTCATCTGT TGGTGCCTC AGGCGTTGTT GTTGGTT	1377

(2) INFORMATION FOR SEQ ID NO: 187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

CTGCTGACCA TGGCGGCGGG GTGTCTGCTG GTGTGTGCTA AGTGTTGAG AGTCCCTTGT	60
ATTGTTAGAT TCCACAACCTG CACATTGCGA TGTGCCTGTT CGATACAGTG AGCAATGTGT	120
GCGAAnATGT CTGTATTCCG TCGGAGTAC TCGGTGGTGC GCTGCAGGGT GCGCATGTGC	180
CTGACGAGTA AGGAGAAAAA AAGGGACACG GCGTGTGCT GTTTGTGAGC TTGGAAAAAA	240
TGCAGCGTAG AATCAAGTGA GGTAAGATCn AnTCCTGATA CTTGAGGTTG AGTACCTACC	300
GAAACCCAAG TATCAGGAAT GATGCGTCCG ATACACCTAG CGTGCTGGCA CACATACAGC	360
CAAAAGTACA TCACGGACGT TTGCACCTCT TCTAAAGAAA ACGACAAAAA CTGGATATAA	420
ATAGTGGCAA GAGTACACCC TGTGTGTTTT TTGCATCGGT CGGTCTGTCA TGAAATACGC	480
GTG	483

(2) INFORMATION FOR SEQ ID NO: 188:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 846 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

TTTTCAGCAT TACATTGGGC GCTTTCGAGA ACTGTGGCAC CAAGGAGGTA ACGGACGCCT	60
ACTCTATCTA TGATACCACC GGCCAAGTGA TGTGGGATAA AAGCTATCTA TTTGGGATGC	120
AGGTGCCATT TCGTTATTAT GCAGAATGTG CACTTCGTTT TCATAAGACA CCTTTGTATG	180
TAGATGTGCA TGTGCCAATC ATTTCTGATC CCTTTTTTTC TACTGATTTT TTACAACGGA	240
tGAaGATCTC AACTGGTTTC ATCTTGACTT TAAGTCCTCG ATCGCTCAGA GAGCTTACGC	300
AAAGCACCAT AAGCAGCTAT GACTGGAAAA TCTCTGCTTC GCTGCGCCCT GTCTGGCTTG	360
TACTTCATCC TTGGTTGCGC GATTTTTTCG TCGATCCGAT TTCGTTACAC GTACATTTTA	420
ATTCGAAGTC TGATAGTAAA AAAACAACCT CTTCTCCAGA GCGTAACTTC TTCTACCCTC	480
ATTCGATGGA ATCTCGAGCA GGATTGTCGT TCTCTGGTAC GCTGTTCTCT CATGTGTGGG	540
AAAGACAAAA ATCTCAACAA AAAGAATCGT ACGCGCCAAA AGArATACGT AATCCACTTG	600
CATACACTCC TGCAGACGGG TTATCTAGGG AGGGWTCTCC TCCTGAACAG TCCCCTGnCA	660
GTATCAAAGG AGAACAGCGA GACTGATTCT ACCTTCGATT TTTTATGCC AGAATTTCTG	720

851

GAAGAAAATG AACGTCGTAC TGGTACTGAT CATGCGTATG TTTTACGCG ATACGCTTTA 780
GATTACAAAG GTAAAGGTGA CATCGTGTAC GATGCACAGT TCAATCACGG TTCGTGGGGA 840
TGACGC 846

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 689 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

CTGnCACAGG nACAAACGGC GACCCCGGCA GTTTAACGGT GAACCCTAGG TTAGTAGCGG 60
AAAGACCGAC GTACATGTTG GGTTCGTGAG AGCTAAAGAA CTTAGCAACG TTCCCCACCC 120
ATTGCAGACC CACGTCGGTA CCCAGCGACA GGTGCGTTAG gCCCTGCGCG TCGCGGAACC 180
CCGCCTTCAG GTTAGCCCCCT ATGGAAAGTC CCCCAAACCG ACGGGAGAAG TTCACAATCC 240
CCAAGCCCCC CAGTTTMTTA ATTGGGTTGG AGGCAGGCGT GCACACGGGC CCCGTGGAGG 300
GAGAAAAGTT AAACCCGGAT TCGGGGAAAA ACATACGCAT CGACGCGCCG TATCCCCAGT 360
TGCCCGACTG GCCAACGTAG GAAAGCGTTT CGGCATGCGA ATTGTTAAAT CCGACGGTGT 420
GGGCAAAGGT TAGCTCACTG TCGTCATGT TCGCACTCCC TGCTGGGTTT GCCTCAAAGA 480
AGCTGGCATC GTTTGCCAAT GCGGTGAACG AACCGTCCAG AACACTCAGA CGCCcTCCGG 540
AAnGGGAGGA AAcTGCGCGC CTCTTAACT CACTCATCTT TGAGCGAGTC TTCGCCGAG 600
CTTCTGAAGA GGCAATCGCC ACGCTGGCTC CCGCGAGCAC GAAACCACAG ACGAGCGCTG 660
CGCTCTTATA AAAACAGAT TTGTAATGT 689

(2) INFORMATION FOR SEQ ID NO: 190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 942 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

TACTCCCCTC TCTGAACATG GGGAGCTGGG TGTTTGCGCA GACGCGGGGA CAGGTGGTGT 60
GTCCGAAGGA GCGGCGCTGC CGTGCGCAG GAGGGGAACG CGTTCCTAAC TCCCTGCCGA 120

852

```

AACAGGTTGC CGGGTGC GCG GTGCCTTCTG CAAAGGACTC ATCAAAGGCT ACCTCAAGCG      180
GCTACGGCTC GGGGTCCGTG TTGCGCGTAG ATGCGAAACG CATCGATTAT CTTCTGAATT      240
TGGTAAGTGA GACGGTGATT ATCAAGGCCT CGCTCAATCA GAGTGCCTg AATT'TGGGGA      300
GGTGTACACC CTATTCCAAA ACGCTAATGG CGCGTACAAG GAGCGTTTGC GTAAGTTTTT      360
TGATAGGGTT CCCGCTTACT TAGAAAAGGT AAAGAACGGT CAGGACGCAG ATGCGGTGCG      420
CAAGGGGATG ATAGCAGAGG CTGTCGGTGT CTTtGACATT TTTTCTTCGT TTGAGAATGG      480
ACTGAAACAG TCCGTCAC TA AGTTTCGGTC TTCTGCTCAG AATT'TGGGGC GTATT'TCTGG      540
TGAGCTTCAA GAAGGTGTGA TGAAAATCCG CATGGTGCCT ATTAGCCAGA TTTTCAGTCG      600
TTATCCGCGT GTGGTGC GCG ATCTCTCGCG GGACTTGCGT AAAGAGGTGC GGTGGTCAT      660
TGAAGGAGAG GAGACGGAGC TTGATAAGTC TGTGGTTGAA GATT'TGCTCG ATCCCATTAT      720
GCACTGCGTc GTAATTCTCT CGACCACGGC ATAGAAGCGC CTGAAGTTCG CGCGCGCTCT      780
GGAAAACCGG CGCAAGGTAC GCTTcTCCTG CGCGCAACAA CGAAGGAAAT ATGATCGTaT      840
TGAGGTTGCC GATGACGGGC GTGGcATCGA CGTGGAgGCA tGAAGACGAA AagCAGTTGA      900
GCGArGTGTG TTGCACCCAG GcAAGAACCT CACTGAGGTT GA      942

```

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

```

CAAGTACAGC TACGCCGCGC ACAAGCTCAA ACAAGGACAG AGCCACTCAA TCCACAGTGC      60
ACACACAGCC GGACGCAACC GGCAACCTAT CTCACGCACG AACCTAACCG GGGTAACCTCT      120
GCTGGCAGAG GTCAACAGGA CGGGGATTCT ACCTCCGATT TGCACAACGT TCAAGCACTC      180
ACGTACGCAA GATATACGCA CCGCTTTTTC CTCAAGTGCA CCCGGCGTAT TCCGATACCC      240
CTTACCAAGC ACGGGGTGCA ACGGCAGGGA TGCCAnGGCG GCTGGTCCGC TTGAAAGCAC      300
CAAAGGAGT ATGCTTCATG ATTCATCATC ACAACATGAG CGTATGTTCT CTCAAAGAA      360
CGCTCGGACA CAnAAATTGT CCGTCCAGAA GAACnTGGAA GTTGTCTTCA GGA      413

```

(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

TACATACCTC GCTCTGCTAA TCCTGTTACC AGCCCCCTG GGCGCAGGAG TTGTCCAAGA	60
AGTATTGCTC TAAAACGGTC AATCTGTACT TCGTACATGG CAATATCCGT GACTTCCTCC	120
CCCATCGCGA TATTCAGGGC AGCTTCTCCT TCGTTGCGAT TAATGACTAC ATATCTGAGG	180
TTATCTTCGG TAACCGGGAT ATCATCGTCT TCTATGACAA ATCTGCAGGG CTCACATTTT	240
GTCTACAAGA AATGCTGAGC GCTTACTTAG AGCGTATGCA TGCCAGTAT CCTACTGAGG	300
CACTTGCTGA CTTTCTTTTCG CGTGATCCGG TGAAAGCTTT TCGGTACCTT GAGCGCTACT	360
TTATTATGAA CATGAAACAG AATAAGCGTA GGTCCATC ATCGACTATC TGAATCTCTC	420
GTTCCTCAG AAGATATGCA AACTAAGCGA AACAGATCGC TATGCTCGTC ACCCTCAATC	480
GCGGGCAAAT GATCCGGTGT TCA	503

(2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1038 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

CAATTGCGTC GGTCGCCGT TCTTCTCAGT GCCTTGTTTCG TGCTGCTTCC GTTTGCGCTG	60
CCGCGCTGCT TGCGCACAAG AACCTAGCGC GCGCGGCGGG TTGCAATCCT TTTTTCGCT	120
CTGGGCCTCA TGCTGTGTGG TACGCTCTTA GACGGGCGTT CGTGGCGTAA CGAGCTTCCC	180
TTTACCTGT GCCCCGCAGC GCTCATTTGA GGGTCGCTGT ATTTATCAC CCGCCGACCT	240
ATCTTTTCA ATCTGCTGTA CTTTGGCAT TTTGGCTCTT TCGTTGCGGT ACTCTATCCG	300
GATCTCACTC GGGCGCACAC CATCTTGTA GCGTACTTGT TCATGCTCAC CCATTGCCTT	360
GAGCCTGCGA TGGTCGTGTT CAGCCTGCTC CACTTGCGCG AsGCATTAGC AAGCGTGGCC	420
TGCAATGCGC ATGCTTGGCT TTCTTCTGCT TGCAGCAAAC GCACTCTTTT GGAATCGGAG	480
ACTCGGCGCC AATTACCTTT TCATTAGCAA ATACCCGCTT GAGATCCTTC GGGTAATCCG	540
TCCTTTTTTT GTGTATCAGC TGCTGTTTGT CAGTGCACTG TGCCTGTTAA TGCTGGTACT	600

854

CTACCTACCC TTCCGGCCAA GCCAACACGG AAGAAACCAG CTCTTCGTCA TTTAGCTGCT	660
CGCTGTGGTT CCATCGGACC CTTCTGCCAA GGCAGAGGGC ACGCGTGCCg TTGGGaCATC	720
GTGGTGGAgT TGCAGCGCGC TtGcGTCaMa mGGCCTtAmT CCGCGGTCAA cGCGAACGTA	780
TAATGGTGCG CtGTGACTTC TGTAmCAAAA mCGCTTATCA TCcAAGCAGA CCGCTCCATT	840
TTACTTGATG TGCACGCTCC TGAGGCGGTA GAGCACGCAA GCGCTCGTT TCCTTTGCAG	900
AACTGGAAAA ATCTCCAGAG CATCTACACA GCTACCGACT CACTCCTCTT TCTCTGTGGA	960
ACGCCGCGAG CGCAGGGATT CAGCCCCCAG AATGGATTGC ACAAACACTG ACGCGTTTCT	1020
CACGGTTCA nTCCCCCG	1038

(2) INFORMATION FOR SEQ ID NO: 194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

TTGTCGATAC G nGATATATC nTATCTGCTG GGCAAAATGA CCAAAATGTG GCAGTCCAGT	60
TGCAAAAGGG GGACCGTCAA AGAAAACATA AGACTTCCCC TGCGCACGCT GCGCCACAGA	120
CTGCTCAAAC ACCCGGCGTT CCCGCCAAAA GCGGAGAATA CGCCGCTCCT GCGCGACAAA	180
ATCAACCTTT GGGTCCACAG GCGTATACAT ACAACCTCCG TTGCTCAGAA TCGCATAAGG	240
AGCGTAAGGC ATTATATCAT TTTCGTCTT CCTTTTCCCC ATACGTCTTA TGACCGGCGC	300
CACACCTTTC CCCACCTGCA CCAGATACCC CACGTGTGGC GTAATCGCAG TGGCTCTGCC	360
ATTACTGCAT GAGTATTACT ATGCAATAAT GCCCCACATT ACACCTTCTG CAATCGAATA	420
CGAAAAAGGC ATCATCAGAA C	441

(2) INFORMATION FOR SEQ ID NO: 195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

CAAACAGCGT TTTGACGCG ACATGATGCA ACAAATATTC ACTGACTGCC TGCCTATGG	60
---	----

855

ATAAACCGTC TTCAGTTGCC GTTCCCCGTC CTA~~CT~~TTCGTC CATGATAACA AGGCTGTCGC 120
GGGTTGCTGC ACGCAGGATG TGTGCTGTTT CACTCATTTT TACCAAGAAG GTAGATTCCC 180
CGCGCGCAAG GTTATCGGCC GCTCCTACCC GACAAAAAAT ACGATCGACG GGGGTGAGCT 240
CTGCCTTTTC TGCAGGGACA AAGGAGCCAA CCTGCGCAAT CAGGCAAATG AGCGCATCTG 300
ACGCAAAAAA GTACTTTTTTC TGCCATATTC GGTCGGTGA TGAGCGCAA A~~n~~CGGGCAAC 360
AACGCATGTT CAATTGAAGA AAGTGTGAGA TCATTGGGTA CAAACTCCCG GAGGAGATGA 420
AATCCACCA CGGATTCTGC CCCCGTATAC GATGCACGTC TTGATAAGAC GGTGATCAGC 480
AGTGACGCA~~n~~ GGCGAAAGTG GGACTCA~~n~~TT GCAC 514

(2) INFORMATION FOR SEQ ID NO: 196:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 407 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

TTTGTGACAA nTGGTACCGG CAACTGGnAA GGCTTTCGAG TAGAATCCAA ATTTACAAAA 60
CATTCCCATT AAAAGCACAG AAGGAAGAAA AATAAGGCAG GCGTTTCAAG CTACTGTTGG 120
GCATGAGTTA ATTTCCGGCAG ACTATACACA AATAGAGCTG GTCGTGTTGG CCCATCTATC 180
TCAAGATAGA AATCTTCTCA ATGCATTTTCG ACAGCACATT GATATTCATG CATTGACTGC 240
TGCATATATT TTCAATGTGT CTATAGACGA TGTACAACCT GCAATGAGAA GAATCGCAAA 300
AACTATTAAC TTTGGAATCG TGTATGGAAT GAGCGCTTTA GATTGAGTGA CGAACTTAAA 360
ATTCTCAGAA GGAAGCGCAG AGCTTCCATT ACCGTTATTT TGAAACG 407

(2) INFORMATION FOR SEQ ID NO: 197:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 410 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

GGGTGGnGTT GGTCGGTCCC CCAGGAnGGT AAGACGTTGC TTGCACGCGC ATGGCCAGGT 60
GAGGCGTCAT GCCCTTTTTT CGCATCAGTG GCTCAGACTT CATCGAAATG TTTGTGGGGA 120

856

TTGGCGCCTC GCGTGTGCGC GATTTTATTC AAACAAGCGC GGGAGAAGGC GCCAGGGATT 180
 ATTTTATCG ATGAGCTTGA CGCAATTGGA AAAAGCCGCC TGAACGCTAT CCATTCCAAC 240
 GATGAGCGGG AACAAACGCT TAACCAGCTT CTGGTAGAAA TGGATGGGTT TGATAACACC 300
 ACCGGTCTCA TTTTGCTTGC TGCTACCAAT CGCCCCGATG TGTTAGATCC TCGCTCCTA 360
 CGCCCCGGTC GTTTGACCG ACAGTTTGC TAGATCGGCC CGATCTTAAG 410

(2) INFORMATION FOR SEQ ID NO: 198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

nGACGCAACA CTGACAACTG ATGGnTTCGC TCATCTCTCT CGGTTCCCTG AGTCTTTTA 60
 CATACGGTCT CTTTGCCACG GCGCGTATAG CAATGGGCGT GCATGCCAAC GACACGGCAC 120
 TTGTATCGCA CTATGTGGCG GATTTGTATT TCGAATCAGC TGCAATGATC GTAACGCTCG 180
 TCACGGTGGG TAAATACCTG TCCGCCTTGT CTAAAGGGCG CACTTCTCGC GCACTCACAC 240
 AACTGCTAGA CATAAAACCT AAAACGCTCG CGTTATCGTC AGTATCTGTT CCGCGCGGAG 300
 ATCCCTTCTT CCCCACAAT GCAACGCTGC ATCAGCCCAT GAGACCCATG AATTGAGATA 360
 GAAATCTGCA CAGGACGTAA TTGTTCCGAG AnACGTAATT GTAAAAGCCA GGTGAGTAAG 420
 TTCCGGTAn 429

(2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

CGCTATCGTA nGGAGGATCG CTGGGCTAAT TCGGTAAAGG CGGTCATTCT CTCCTTCATG 60
 GATGGTGGGT ATCACCTGAC GGGGTGAAC TGCACTATCC TTTCTCAGAT TCCTCCTGAT 120
 GCGGGGCTGG GTACTCCCAA TGCGCTGAAG TTGCCATGGC CCTTGCTGCTT GGAAGTTGTT 180
 TGCCGCTACG CTGCCAAAGG AAAGTGTGTG TTCGATCGTG GAACACGCAA ATGAGCGCTA 240

857

TCTCAAGACC CACGCACATC GCGCGGATAT TCTGTGCGTG TTGTTTGCAA AGCAGGGTAA	300
CTGCGTGCGC ACTGATnACC GCAAGAAGCA nCGGAACTG TGTCAATTCC CTCGGAGGGA	360
AACGTATGTG CTAC	374

(2) INFORMATION FOR SEQ ID NO: 200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

TGCAGCAGGC GTCTGGATGT GCAGGAGCTT GCGCAGTTAC GGTGTGATCT GTCTCGAGTA	60
CAGGAGCAGG TATATGCGCA GAATGAAAAA AACCGAGCCC TCCTCCGTGC GCAGTCAGCG	120
ATTTGCGCCA CAGnCTCGAT GAATTTCTGTG CGGCGCGTGG GCTGGTGAGC TATGAGGACG	180
GGGAGGACTC AGGGACGGTA ATTGATCTGA GTTTATAAGC GCTTTTGCCA GACCATCTCA	240
GGGAGGAGG TGCGGCAAGC TGGATTTTTTC CAGTCGGTTG TGTGACAATG CGCTGTGGAA	300
CCCCTGTGTA TTTTGCGTCC CCTTTTGGA AAAGGTGAGT TAAAGCAGAT GTGGAGCGTG	360
CGCAACGCCG CGGnTATGTG CT	382

(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

GGGGCCAAAT AATTCCGnTC CCAAATGGCC AAGnGGTTAA GCCAAAAAA AAAAAGGCCC	60
CGGATTTTGG GTTCTTAAGG AGGAAGGGAG GCCCCAAAAA GGCCAAAACC CACCCCCCCC	120
ATTATTCGGA CTTCAAGGAG GACCATTAGG TCGGGCTTTC AGGCCATTAG AGGCCGCAGT	180
AAGCAGCTGG CAGGCGTACC GAGCCTCCCG TTTCGGTACC GAGTGCAAAC GGTGCCTGGA	240
CCGCCTGCGA CGGCGGGCAG nCAAACCGCC GGAAC'TTCCC CCGCTGGTGC GGCTCCGATC	300
CCGAGGATTA CGCGTCGGCC CATAACAGA ATACTCGGTG GAAGAGCCCA TAGCAAAC'TC	360
ATCCATGTTC GTTCTCCCGA GCGGGATAGC ACCTGCGGGC GCGCAGnCGG CAAACAACGG	420

858

TGGGCATCGT ACGGGAGCCC TATAGTCTGC AAAGAGTTTA CTGCCACACG TGGCAGTGCT 480
 TTCCTTTTCA CTGAAATATT GTCCTTGACA GCCAAAGGGT AGACCTAACA AAGGCTTACC 540
 T 541

(2) INFORMATION FOR SEQ ID NO: 202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 722 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

CAGTAACAAC GCCAACCGGT CTCATCAGCA ACACGGTCCC AGATGnACCA CCTTCnGAGA 60
 CGCTTCGGCT ACGGTCACCA ACTAGCACTT TGAAAAACAA GAACAACAAA AGAAAGAAAA 120
 TGACGTtCAA ACTGACCAAC CGAACGGCAT TTAACCCACG AgCAGCCTCC TAAAGAGAAC 180
 TCTCAATGAG TACATTGTAA CCTcCACCTc ATGTGTGTTA TGCCTCGTCT ACTCCCGGCA 240
 GGCCATCTTT TCAGGAAATA CCAAATGTTT CTGAAAGAAG ACTGGCACAT TCCCAGCACG 300
 ATATTGCTTG CGATAGTCAC GCATAGATAC AACGCCACCG GaTGcAGTGT CACGATAGCA 360
 ATCAGGTTGA TGACCGTCAT aAATACCATA AAAAGATCCG CAACACCCCA AACAAAATGA 420
 AAACTCGCAT GCGCACCGAC AAATACCGCA CTGACACAGG TAACTCTGAA AACACTCAA 480
 ACCATTTTAT GGTcCTTAAT GAAACGTACG TTTGACTCCG CGTAgtAATA GTTACCCATC 540
 AGTGAaCTGA ATGCAAACAG AAAGATCGCA AGCGTCACCA AGTGCACCCC CACGGGGCCA 600
 ACTTGCTTGG ACAGCGCTTG CTGCACGAAC TGCATTCCGC TCACATCCAC TGATCCTGn 660
 AACATCAGAG AGCAGCAACA CAAAAGCGTC AACTACAAA TTAGCATCGT GTCTATAAAC 720
 AC 722

(2) INFORMATION FOR SEQ ID NO: 203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

ATCnCTCCGA GAGTTTGGTC GAAGGAGGCA TGGCTGTGTT CAGCATTTCTA GAAAAGAAAC 60

859

```

AATTTTCTCC GCAGTGT TTT ACTTGAAGGT GCATGCACCT GATATTGCAA AAAATCGTGC      120
TGCAGGACAG TTTGTGCTTG TTCAACTTGa TGACGAATAC GCTGAGCGCA TACCGCTAAC      180
GATTGCGGAC GCGCATGsGA TgAAGGGTGG ATTGCGCTAG TGATCCAGAC TGTTGGCGCC      240
ACTACTATGA GGCTGTGCGA AAAGGAAGTG GGCGATTCCA TCTCTGTAGT TCTCGGTCCG      300
TTGGGAAATC CAACTCTCAT TGAAAATGTA GGAAGTGTG CCTGCGTTGC AGgGGTGTG      360
GGGCAGCTCC GctGkATCCT ATTGCCCAGG CGCATAAAAG GGCTGGAAAT CACGTCATTG      420
TAATCCTTGG GCGCGCAAT CGGGATTTAA TTATTTTGA AGAGGAGATG CGCGCGCTTG      480
CAGAcGAGCT GGTcATTGTC ACAGACGACG GCTCATATGG ACGCAAGGGC TTAGTGA CTG      540
AGCCCCTGCG TGAnTGTGCG AGCGCGCGTC CTGTCCACAG GAGGTGGTTG CTATCGGTCC      600
GCCGATTATG ATGAAGTTTT GTGCGGAAAC GAnGCGnCCC TTTGGGAT      648

```

(2) INFORMATION FOR SEQ ID NO: 204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

```

TGCACTGTAC TACACAGTGT ACGAATGCGT GAAGGTGATG TCTTCTGAGG TCGGTGCGTC      60
TTTGTACGTG CACATCCCCT TCTGTGCGCA ACGCTGTGCT TACTGCGATT TTTACTCCCT      120
GGTGCGTTCA ACCTATTTTA GGCCTCATCA GCCTTGTCG CATTTTATCG ATCGGCTGCT      180
ACAGGATGTG GCATTGCAGC GGGAGTGCTT TGGGGTCCAG GGTGGCAGA CAGTGTATAT      240
GGGTGGAGGT ACCCCTTCGC TATTGGCACC GCAGGACATT CGTCATTTTT GCGTACGTTA      300
CGCGCCGCGC AGGnATTCCG ATTCAGGAGT TCACTCTTGA GGTGAnTCCT GAGGATGTGA      360
CCGAAG      366

```

(2) INFORMATION FOR SEQ ID NO: 205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

860

CATAGATGAC TTTGACGGTG CCTCCGAGGA TCAGGGTCTC GCCTGGCGTG CTGCGGGGAG 60
 CAAGTTCATC ACAAAGGGCT TCCCTATCCT CAAGTATTTC GAGGGCATGC CACAGGCGGT 120
 GCGCATGGCG GGCTCGTGGC AAGGGAAGGA CAAGGAAGCC CGGTTTCATCG GAGTAGAGTG 180
 CAAGTTCAAT CGACAGGGGA ATAAGTGGCT GGACCTAATT CCGACTAAGG GTGGTAGCGA 240
 TTACGAGATC CCCCTGCGTG GGGTGGTCAG TGGGTTCGAC GTGTGGGTGT GGGGTGCAGG 300
 TTATCAGTAC TCGCTCGAGG CTTTGGTTAG GGAAGTGCACG GGACGAGTCC ACACCTCCT 360
 AATAGGCaAC CTCgAcTTCC aAGGGTGGAA rAAcCTTAGt GTTTCGGTTC CCACACACAT 420
 CCCACAGACG TCGCGCTATT TGGGGAGCGC GCAACAnCTG AATTTTGTCTG GTTTCAGGAT 480
 CCGTACTAAC CCATCAGAnC GGGTGGATGA TTTCTACGTG TnCTTTGACC AGTTCAAGGC 540
 GCTTGCTAAC ATGCATATCG ACTTTT 566

(2) INFORMATION FOR SEQ ID NO: 206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

CAAAAGGCAG TTGACAGATG CAGAGGCGGA TTTTATCCAG AATTGTGTGA AAAATGATGA 60
 CCTTATCATG GCGCTGAATA TTTTCTCTAA CCGGGTGCAG TTGTCTCCTT GGACGTACGA 120
 CGACCTCATG TTCGTTGCTG GTGGGGGAAG TGAGTnAGTA CCGAGAAGTA GCTCTCTTTT 180
 CATAAAAATC TTTTCGGGAA GAGTGCCCTTA TCAAGCCAAA GACGAATGCT TGTTGTTTAC 240
 CGCAGCGTTG AGGGTACTCA CTCCCGCGAA TATCTTTTTT AGGGGTGCG TGGTCTTTCT 300
 GGTATGCTC ACCCTCACCA TATCaAGCAT GGTCTTTTTG GTTATTGAGT ATCTGaGCGT 360
 GCGCCGATTC CaGTGCGcAC AGGGGGACGC GCGCCCTCGT CtGCTGGACC TCAAGGTAnG 420
 CGCGCTCTCG GACAGAnGAG GnCCCAGGTn TCGCCTGGTA CACCGCCTGA GTGTCCAGTG 480
 TCCGTCTTTT GAAACTCATG GGCAGGACCT TGCTTCTAAG GAGAGCGTGA GCGACCTCGn 540
 AAGGTTTACA TTTGTACAAC CATTCTGACG AGGAGCTTTT TTCCATACAT GACTCGGTGT 600
 TCCAGGAACA TACAGGGSgG GAGGGCCGGA TGTCTTCCTC TTCCGGTGAG GAAGGGTGCG 660
 GGCAGACGCT GCTTCCCGTT CATGAAAAAA AGAGCACCTA TGGTCTTTTC AATCCCTTrx 720
 CCGGrGTCGG TTGGCGGGCC TATCTGGAGG AAAGGCTTGA GGCAGAATTA GGACGCGCCA 780

861

CCGCTTCCGA ACAAGACCKa AsGCTAATGA TAGTACAGGT GGAGCACCCC GCGCACCAGA 840
 CAGCCGTTGC GGACGCAGCG AAAAAGCTCG TGGAGTTCTT CAAATTTTCGG GATATGCTCT 900
 TTGAATTTCGA GGGTAGTTGC TGCTTCGCGG GTATCGTACA AGACGCAAGC CTCGAAGAGg 960
 AnTGGTaCTC GCGAGGGaTA TACACAAGKa GCTGTGCGGC GCCATTGAGA GCGCACGCgT 1020
 CCTTATCGGC ATCGCGAaCG cKTACGTCCA GACTAACTAC CGcGGcCCAC TTaATTGAGG 1080
 ArGCGCACGC GTcGGTGAAG AGGGCGCGAG AAGACCCCGC ACACCCCATc ATCGcTTTCG 1140
 AGGCCCCCCA CCAGTGTGGG CGCCCGTATC GGTCTTCAGC TTATAGGGAT GTCCCGGACC 1200
 GGTCTACCTG CTAATAATGG CTTCTTCTC GCCGCGCCGC GCACTCTGCA GAAGCGCAGC 1260
 ACCCAACCTC CTGAAACTCT GGGAAGAAAC AGTTGCACCG GTGACCACAT CCACCATCTC 1320
 GGGATTACCC TTTTCAAGCA AAGCATCGGC GAGCTCTCTG AAGGCCTTTT CAGGACCTAT 1380
 GCCCGAGGAT GCATACATGA CCCGATGGTA GTCAGCGTCC TGGGACTTAA ACCGCCCTTC 1440
 TTTATGCTGA TAATCGTAAA CCACCTGCAC CATCTTGCCA CCATCAAAAG TAACCTCGAG 1500
 AAAGTCCTTC CAACCATTCT CATCAAAATC CTGATACGTC GCCCGGTACG TGCCATTCGG 1560
 GATAGAACTA AATGAACACG CCCCAAGCAA CACCGCAAGA C 1601

(2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

GTTGTnTCCT GTGCGACGCG nAAATACCTT CCCACACCTG CTGGTTAAAG GACTTGTCAT 60
 CGATGTCCCC TGAATCGGTT ACCATTCCAA CGACGAATCA CCACCTTCTG CGCCCCCTGC 120
 GTTTCCCATC TCGGGCCTGT CGCTCTTAGA GCAGCCGATG AGCAGCATGG CGCAAAAAAn 180
 GCCCGCAAAn GCGCGTACCC ATTCTCTCTC ACAAGAATCC TCCCCCCTTT ATCGACAAAC 240
 ATGCGnAAAA TAAnGGGTCA CAGTGTAACC CAAGGGACAA nGAGGTnCAA AGAGTGGTGA 300
 GTTTTTGCGT GTGTGCAAGT GGCAAGGTGA AGGGGTACTA GACAGGCCCG GGGGGGGGT 359

(2) INFORMATION FOR SEQ ID NO: 208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

TCTTGCAGAA AGTGAGGCGG ACTTCCGTGC AGGAACCGAA ACACTGCAGG ACCTTTGTCT	60
GTGAGTCTTT CCGGGCATAC GCACACAAA GAGGAGGTGC AGGCTGAGGT GGAGGCAGGA	120
GAGGTTCACT GCCCAGCGCT TTGCCATCAG CCGGTACTCG TGCAGGAATG CCTGACGTTG	180
TTGGAACCTG CAATTGTGGG TATCTCGCGA GGTGCAGACA GCACGAGAGA TGGGGCGGGG	240
GCGTTTTTTA TTGACGGGAC ACTGGGGGAT GGGGGACACA CACAGGCGTT TTTGCACGCG	300
TACCTTGcGC TCCGTGCGCT CCGTGTGAA ATAGATCCGT CAATGCTCGC ACGGGCGCGA	360
GCGCGCTTGA CGCCGTTTGG CAAGCGGCTT cGCTATGTCC TGGGGTGGTC TGATGTCTTT	420
TTGCCTCCG CATATGCATC AGCTCCTGCC TCTCCTGCAA CGGGAAGGAC TGCAGCTGGC	480
GCCGAGTGT GCCGGGTGCG TATCCGGCGC CGCAGA	516

(2) INFORMATION FOR SEQ ID NO: 209:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 541 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

CCACAnAnAG GACCAAAAAG GACCAATGGC CCGGGGCCGG CCCCACCGG CCACCTTCCA	60
GGAACCGGCG GTGGCGGGTT GGCCCCCGC GGTTTTTTTAA AAAAAAACC GGCCGGCCCT	120
TTTTTTAAAA AACCTTACCA AAACCGGCGG TTTTCCAACC CAGGCCAACC CGGGGGGGGA	180
AACTTGCCCC TTTACGGGGG AGAGGGTGT AACACCCGG CTTATTGGGC GCGATGGAGG	240
TACGCACACG TGCAGCGTTT TACTCCCGAC GGCTGGCTCC GTACAGGGGA CGCTTTGGGA	300
CAAAGACAGA AACCGGTAAT CTCCTCCCTT GGCAGCAGCT CGTGCCATAT GCAACTCGGT	360
GCGCGCGGAG AAGCGGTGTA CGCAGAnGAT CTTGTTTGTG TGCTTATGCA AnATCCGTGG	420
CGTGGTGGCA GCACACGTGC GCGTTAGAC ACGCAAnGG CAAGCGCACT GCGCCGTATG	480
GGTAAACAA GGAGCCGAAC GAATACGGGC ACCCTTCAGA TAGTGTGCTT TTTGCGCACC	540
C	541

(2) INFORMATION FOR SEQ ID NO: 210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

```

GGTGACCGTC ACCTACCGCA CCGTACATGG CGCATGCTCT TTTTGCCGCA ACTACATCAT      60
GGCTAGAGTG ACTACCCGGA CCGGTCATAA CCCCgATGTG ATAATCCTCC ACCGCTTTCG      120
TGCCCCCGGT ATTTTGTGGA GCACGCGCGC CCCCACAGCG ACACAACAGT GCACCGACAC      180
ATACCACCCA TACCTTCAAT AGAAACTGAC TTTTCATAGT CTCCCCTTAA CGATCTGCAC      240
ACACCATCTC TCCAAAACGC TTAGGCGTAT GGTCCACCCC CCCCCACGGT GGGAGGAnAA      300
nAATTTTCCC AAAATTTTGT GGTGGGTT                                     329

```

(2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

```

TCGTTTGTAT CGTTGAGCGT GTTATCGCTT CAAGGGACAA AGGTGCCATA CTCATTTTTC      60
TGCCAGGGGA GCGTTCtATT AAAAATTGTA TTACCCGTCT TTCCCATGAA CGTTGGTTCC      120
GCAAGCTCTT TCTTTTGCCC CTCTATGGAA GATTGAGTAA AGAAGAACAA GAGCAAGTTT      180
TTAACCGCGC GCCATTTGGA AAAAGAAAAG TCGTCATCGC AACGAATATT GCAGAAACAT      240
CCATCACCAT TGACGATGTA ACTACCGTCA TTGACTCTGG TTTTGGGGGG TTTnGGGAAAA      300
AGGGTTTTTn AAAAAAAATT TTTCCCGGTT nAAATTTAAA AAACCCCCC GGGGCCTTTT      360
TTTTCCCCC TTAAATnAA ACCTTGGGCC CAAAAAGGTT TTTTTTGGGG GGAAAAACCG      420
GGAAAAAAA AnCTTTCCCC CnTTTAAATT TTTTTTCCT TCCCAAGGGG GGCCTTTTTT      480
CCCGG                                     485

```

(2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

TTGCATCGCG CGTCTGCAAG CGCGTGnACC AGCTTAnCCA TTGAAAAAGT ACACAAACCA	60
AAAACAGGAG GGATTACGCC GAGCACCATA GAGCACGTat TGGCGGAGAG GCATACACCG	120
TGGTGCTCGA CCGCTCGTGG ACGTATGAAA AGGGCTGGAC CATTGCGCTG TTCCCCGATG	180
ATAAGGCGGA TGAGGCTGGA GCGTATGTAA AAYCCCTTTC GGTtTCAAAA AACAAAGAGG	240
GAAACTGGAT GGTtGCCATT CCCAACGCGG CGCTCAAAAC CGGGTCGTAC ACGCTGCGCG	300
CAATAACGCC GCGGAATATT TACGCAGAGG TGCGGGGGAT ACTGCATGTA GTGCTCTGGC	360
GCAGGCCCAT CTTtTTCTAT TATGACCTGA GCGTGGGATA CGCGCCGGTG TATCGGCCGC	420
AGaCCACGCC GCGACAATCA ACGGTGTTTC TGACTTTTTC AAAATCTGTT CTCCTATCGG	480
GTTTGTCGGC ACGTTTGAGA TGTGCTTTTT TAAGCGCAAC AGCAGCACCA TCAGCGCTGG	540
CTTTAACGCG CAAATGCACT CCGATTCAAA ACAAGTGGAC GTGAAGCTCG ATGGAAACTT	600
TGCGTATCTA TACGAACTTT ACCCGCGCAT CGAGGTAGGC GGCATGCTTG GGTtGGGGTA	660
CTCGCTGCCA TTCGGACAGC GCAAGGAAGA CGACAGCATG TACTCCTACG TGACAGGAAC	720
GATGAAGTAT TTTTACTAA TAGCATTACC TGCGCGTTCA ACAGCAGCAC ATGTTGACCG	780
TAAAGCCGAG TtTCACAGGA GTGAGCCT	808

(2) INFORMATION FOR SEQ ID NO: 213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

CTGCGCCCGC AGGnAAAAAA GTGTGTGCAG CAATCCAGTC TCTTCATTA GGCGGAnGCA	60
ATACTCGGAC GGGGAGTACA AGCTCTTAGA AAGTtCTCAC GCACCCGCTC AGAGAATACG	120
TGCGTATGAG CGCGnAnATA AATTGCTTCA CGCGTGCGCG CTTCGATGGA AAAAGAnAAC	180
TGCGCTGCAA AACGCACAGC ACGCAAAGGA CGCAACGCAT CTTcAGAAAA TCTTGCCTGT	240
GCATCCCCCA ACGCTTAAGA TAAGAACCGT TACGCAAATC GGAGTAnCCG CCACATTACG	300
TCGATGATTT CC	312

(2) INFORMATION FOR SEQ ID NO: 214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

```

CTGCTCTATG TAGCGTTTTG CCTTTCGCCC TGTTCATCATT TCCACGATTT TGCCGTGGTG      60
GAGGACGAnG GAACCGAGGA TCTGCACGTC ATAGGGACGC TCGCCTAAAA CACGACGAGC      120
TGCCTCGCGC GCAAnCATAT ATTGCCTGAG GnAAAAAAGC GTCAAGCGCT TTCTTCCTGC      180
AGCGGCACGC GCTCTTTAAA CTCAGCTGTT TTTTGTGTTG AACTCAGACT CCTGGAGAGG      240
AAGTTACCCA GGACTTCCTG GGTGCTTGT ACGGTCATTT CAAAAGAGGC AGGTAGATTT      300
TTTTCAGAnC GCGCTCGTGT CTGGGTAGCC AAAGnAGTAG CCTGTAGTGT CAGTGTCTGTA      360
CGTAGTCATG GTAGTTACTG TTAGCGGTC TGTAACCAAn AAAACAAGGG TAGACCGTCA      420
CGGTCACCCC CT                                     432

```

(2) INFORMATION FOR SEQ ID NO: 215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

```

AGTGGGAATA AGAGAGGGAG GAGACATACA GTTCAGCACA TGCTCACTCG ATCTTACTCC      60
TAATGATAGA GCTAGAAACG TGCCATGGGA CTCCAAATCC CCTTAAATTG GCAAGTACCA      120
ATGCCATCTT AACTACTTAA ACTGATCAGT TTCAGTTCAT AATTGATCAA AAAGATAGGA      180
TTAAGTGTCa AAAGGATCAC ATGAATAAAA CCAGTGTCCT CTAATAATAA CTGATAGAAT      240
TAAAAAGGAG AGAATGACTC AACATGGGAA GTGGGATACA CAGCAGACTC AGAATGACAA      300
ATGTCCTAAA CAGCACTCTG GCCACACAAT CAGCTCTTAA GGCATTGCGA TCTGGCTAAA      360
AAGCCAATGA AAGTTTCTCA GGCATGGAAA GCCAAGAACT GTGGCAAAAA ATGGCCTAAA      420
TGAAACATCT GTGTGAGTGA GATCCCAGCA GAAAGAACGG GCCATCAAGG AAAGAGGTAC      480
CTTTCCCTGA AGGGAGGAGA GAACTTCAC ATTGACTATG GCCTTGCTTA AATAAGGAGT      540

```


866

TGGCGAACTC AAGAGGCTTC CATAAGCTTG GCAACTCATG ACAAGAGCCT TGGGTGATTA 600
CTGATGCCAT AAACAAGAGT GTCAATTGT T 631

(2) INFORMATION FOR SEQ ID NO: 216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

ACATAGTACA ACACATTAAG GACAGAGATC CTACATGGGG AGTAAGTGCA CAGTGACTCC 60
CTTGTGTGATT TAACAACTGA CACTCTTATT TATGACGTCA GTAATCACCT GAGGCTCTTG 120
TCATGAGCCA AGGCTATGGA ATTCTCTTGA GTTCACAAAC TCTGACCTTA TTTAGACAAG 180
GTCATAGTCA AAGTGGAAGT TCTCTCCTCC CTTGAGAGAA AGGTACTGCC TTCTTTGATG 240
GCCCATTCTT TCCACTGGGA TCTCACTCAC AGAGATCTTT CATTTAGGTC ATTTTTTGCC 300
ACAGTGTCTT GGCTTTCCGT GCCTGAGAAA TTTTCATGGT TTTTTTTTTT GCCAGATCCG 360
AATGCCTTAA GGGCTGATTC TGAGGCCAAA GTGCTATTTA GGGCATCTGC CATTCTATGA 420
GTCTGGCTGT ATATCCTGGC TTCCCATGTT GGATTGTTCT CTCCTTTTTA ATTCTATCAG 480
TTATTATTAG CAGACACTGG TCTTATTTAC ATGA 514

(2) INFORMATION FOR SEQ ID NO: 217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

ATCCCTGTTA AATATAAGAG TGGGAATAAG AGAGGGAGGA GACGTACAGT TCAGCACATC 60
TTCAATTGGA CTTAGCCATA ATGGTAGAGT TAGAAATGGG CCAGGGGATT CCAATTCAAT 120
CCCATCAAGG TGGCATGTAC CAATGCCATC TCACTAGTCA AAGTGATCAG TTTCAGTTCA 180
TAATTGATCA TAATGATAGG ATTAAGTGTC AAAGGGATCA CATAAACAAG ACTAGTGTCT 240
GCTAATACTA ACTGACAGAA TTAAAAAGGA GAAAATGATC CAACATGGGA GTTGAGATAC 300
ATAGCAGACT CATAGAATGG CAGATGTGCT AAACAGCACT CTGGGCCTCA GAATCATCCC 360

867

TTAAGGCATG CGGATCAGGC TAAAAAGCCC ATGAGAGTAT TTTAGGCnGG AAAGCCAAGA 420
CACTCTGGCA AAAAACAAAA AAACAAAAAA AAAACAAAAC AAAACACAC ACACACACAC 480
ACA 483

(2) INFORMATION FOR SEQ ID NO: 218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

ATTTTCATTT AGGGTGGTGT TTTTTTTTTT TTTTTTTGCC ACAGTGTCTT GGCTTTCCAT 60
GCCTGCAAAA CTCTCATGGG CTTTTTAGCC AGATCTGAAT GCCTTCAGGG CTGATTCTGA 120
GGCCAGAATG CTGTTTGGGG CATTGGCCAT TCTATGAGTT TGCTGTGTAT GCTGCTTCCC 180
ATGTAGGATC ATTCTCTCTT TTTTAATTTT ATCAACTGTT ATTTGCAGAC ACTGGTCTTA 240
TTTATGTAAT CCCTTTGACA CTTAATCCTA TCTTTTTGAT CAATTATGAA CTTAAACTGA 300
TCACTTTAAC AAGTAAGATG GCATTGGTAC ATGCCACCTT AATGGGATTG AATTGGGATC 360
CCCTGGCACA TTTCTAGCTC TACCATTAGG GGTGAGTCCG AGTGAGCATT TTCTGAACTG 420
TACATCTCTT CCTTCTCTTA TTCCCACTCT TATATTAACA GGGATCACTT TTCAGTTAAA 480
TTTAAATGAC TAAGAATAAT TGTGTGTAA TTAAGAGTT CAACCAA 527

(2) INFORMATION FOR SEQ ID NO: 219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

CTGAGAAGGG AGAAGCAGCT TCTACACAGC TGCCTCCAGT TCAACCAATA AACTGTAGGA 60
CCTGCTCCTG ATTGGAGGAG AGCAGCGTAC TCGGCGTGTG GGTAACAGAG TTGGGATTGG 120
TGGAAGAGGA CTATAAGGA GGAGAGAGAC AATATGCACC AGGAACATCT AAGGGGAACA 180
TCTGGGGGAA CACCTGTGCA GCCCCGAGA GAGCCGGCCG GCGGTGTGCC GCTTCCCCCG 240
CGGAAGTGGG GAAAGTGGCT AGGGGGAACC GCCCTTCCAC GGAGGTGGAA GGTTGGTAG 300

868

CCAACCCGGG AAGAACCAGC AGCAAACCCG GGGAGGGCCG AGCAGACGAA AGAACAACGC	360
AGGTCTCTGTG TTGTTCTCTC ACGAAGACGG GGAGCGACAC AGTATTCTGT GATAGAGGAC	420
TTTGTAGCAC CATCAGTTAT TGAATTCAAG TCACTTCCAG	460

(2) INFORMATION FOR SEQ ID NO: 220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

CCGTCTTCGT GGAGGAACGA CACAGGACCC TGCGCTGTTC TTTCTTCTGC TCGGCCCTCC	60
CCGGGTTCGC TGCTGGTTCT TCCTGGGTTG GCTGCTGGTC CTTCCACCT CCGTGAAGG	120
GCGGTTCCCC CTGGCCACTT TCCCCACTTC CGCAAGGGAG CGGCACACCG CCGGCCGGCT	180
CTCTCGGGGG CTGCACAGGT GTTCCTTCAG ATAGATGTTC CCCTTAGATG TTCCTCGTGC	240
ATGCCGTCTC TCTCCTCCTT TATAGTCCTC CTCCGCCAAT CCTAACTCGG CTGCCCACAC	300
GCCGAGTATG CTGCTCTCCT CCAATCA	327

(2) INFORMATION FOR SEQ ID NO: 221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

nGGAAATTTT TCCAAAAAAA GGCCCTTGGG TTAACCCCTTA ACCCGGAAAT TCCnTTTTTC	60
CCCGGCCAAC CCGGCCGGG AAACCGGTTA AATTTTGGGG GCCGGCCAnG TTTCCAAAAA	120
AACCAAGGTT TTAACCTTCC GGAAnAAAACn TTAACCCCAA CATTCCGnGG GGCTGGGGAA	180
CCAACGGCTT CnAnAGGGGG AnCCACTGTG GATTTCATGGG TTCGGCAGGC AACGTTGTCT	240
TGnATAGGAT TGCGCACAAAT TGGGCTGCCA AnGCATCGAG CATACTGCTT GCGTTTTTGC	300
TCGTGCAATT TTACAGCGGC AGTCTGCTGG AACGGCGCGC CATTTCTGTT CCGTTAGTTG	360
TGAGAAATGA AGGGCGCACT AACTCCTGCG CTTCGCTTTC CTCAAAGGT GACGGTGCTG	420
GATGCGCGCT TTCACGTGAT ACGCTCGGCG CACTGCCGGG ATCTGACATT GTCC	474

(2) INFORMATION FOR SEQ ID NO: 222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

GCGTCAGTCG CGTCAGATCC CCACGCGTCC GTGCCCCGTTG CACGCGTGGA CACTGCCAAA	60
GCGCAGTGGG CTGCTGGATA CCGCTGCTGC GGGGCTATAT CCGCGTAACA GTGTAAGCCA	120
ACGGTGTAGG AAAGTGGCGC ATTTTGCGTG TATGCTACGG TGTCCGAGAA ATTACCAAAA	180
CGGTGGAGGT GTATTATGAT TATCCTCAGC CTAAACTGCG GCAGTTCATC TGTAATAATAC	240
CAGGTGTATA ACTGGACAGA GCGTGCGGTG ATTGCCGTTC GTGGCCCCGn TTTGGGGGGT	300
TTAAAGGnAA AGnCCGnTT GGGTTTAA ACCTTTCCA AGGGGGCCA AGGGGAATT	360
TCCTTGGGnT TTTTAATTTC CCAACCGGC CCAATTGGn AAGGGGTTG GGCcNAACC	420
GGGGGGCCCC CGGGnAAAGG nnAGGGnAAA AAACCCCCAA ACCGGGTTT TTCCCGGGG	480
GGGGGGGAAA AAAAAAAGG GTTTTCCCC CCCCTTTGGG GnCCCCCCCC CCCTTTTAAA	540
ACCCCCCCCC CAAATTTTAA AACCCCCCG GAAAAAGAn	580

(2) INFORMATION FOR SEQ ID NO: 223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

AnTAnGCTTG GTCCTAAGGG TCGCAATGTC TTGCTTGAAA AAGGTTACGG GGCTCCCACA	60
GTCACGAAGG ATGGGGTTTC CGTTGCGAAA GAGGTTGAGC TCGAAGATCC GTTCGAGAAT	120
ATGGGTGCAC AGCTTTTAAA AGAGGTGGCT ACGAAGACGA ACGACGTAGC TGGGGATGGC	180
ACAACTACTG CGACGGTATT GCGTATTTCG ATGGTGCGTG AGGGTCTGAA GGCGGTGCT	240
GCCGGTATGA CGCCCCCTGA GTTGAAGCGT GGTATGGATA AGGCAGTTGC GATTGCAGTC	300
GATGACATTA AGCAAAATTC CAAGGTATA AAGAGCAATG AAGAAGTCGC TCATGTAGCG	360
TCAGTATCTG CGAATAACGA CAAAGAGATT GGAAGGATTC TGGCAAGCGC AATCGAGAAG	420

870

GTGGGGAATG ACGGGGTCAT TGACGTTGAC GAAGCCCAGA CAATGGAAAC GGTGACGGAA	480
TTCGTTGAAG GGATGCAGTT TGATCGTGGG TACATCTCGT CCTACTTCGT CACTGACCGA	540
GATAGGATGG AAACGGTGTA TTGAAATCC TTACATCCTT ATCCTACGAT AAGTCCATCT	600
CGACTATGAA GGATTTGCTT CCGCTACTCG AGAAAATTGC GCAAACAGGT CGACCGCTGC	660
TTCATCATAG CTGAnGATGT CGnAAGGCGA AA	692

(2) INFORMATION FOR SEQ ID NO: 224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1000 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

AGCGGAGACT TACCAACGAG CCGATATGAG CCGCGTATGA CTTGCCATTT ATCGTATGCT	60
TTTGCGTATT CGCTTTTCTT GCAGCGACGG TTTGCTGGTT GAACACAAGA ACTTGCTGGA	120
TTGCAACCGC GGTGCGACTGC GCAACCCGGG CCTGTACCTG CTGGGTGATA ACGTTCCTGCA	180
CCACGCCAGT AATCTGCCCC ATAATGGGCC TCGCGGCGGC CGCCCCGCA CTAAGGAAGA	240
AGAGCTTGGT TACATTGGC AATTGCGCTG CGATTGCGGT AAGTGAAGGC AAGTCAGGTT	300
GCCGAACAGG ACTTTGCCGG ACGTTCACCG GAACGTCACG TcAATATTCA CTACTTGTGT	360
TCCATPGGTG CGTTTAATCT GATCGTGTGC CTGCTTCACC GCTCCTTCAG CGATCTGAGT	420
AATAACTGAT CTTGCCACCT GCACCGAGTT ATCTATGGTG CTACCAACCG TATCAGCCGC	480
CTGTTTAGCC TGTTCTGCG CAcGTGcGTA AAAATTGCCA GTGCAACCTC CTGTGCACGC	540
TCGCGTGTC TTTGCGTCCT CATCGCCGCG GTAGCCTCAC TCTGGTGTTG GTTACCGGCG	600
TCGAGGGCGA AGGAGAAGCG GAAGCCGGCG CCTGGTTCGA GGGTGAGTCG GCCCCCTACA	660
TTCCACAGCA GTTTATCCTT GTTCTGATTG TTTGCGTCCT TCTGTGCACC GATGAGGTAT	720
CCGTCTTCTA GCGTAACATT GCTGGCAAGC TCTACCGTGC ACAGAGGGTG TCCTGCACGC	780
GCATACATTA GCTTCAAGTC TGCCCCAAAG CCATACTTAC TGTGCGTGGG GTCAGTACTA	840
TCCCAGGCAC CGTTAGAGGC AAAGGAGAGA AACCCACAT CAAGGCTGAC CCCACTGCCC	900
CCAATGTCCT GTGCCCCGATA ACCAACCTTG nCGGCTAAAA CCCC AAAACC CGGGGCATAC	960
TGTAACGCAT CCTCCTGGTA ATGCGGTGGT CAAnCCAAGG	1000

(2) INFORMATION FOR SEQ ID NO: 225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 842 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

TCAAAAATCT GAATATCCTA CCATATGACC CAACCATCCC ACCCCTGGGA ATTTACCTAA	60
GGGAAATTAA ATCAATAAAT AAAAGAGTTA TCTGAACCCC CAGGTTTATT GCAGCTCAAT	120
TCACATAGCT AAGACATGGA ATCAACCTAA ATGCCCATCA ACCAATGACT GGATAAAGAA	180
ACTATGGGGT AAGTACACTA TGGAATACTA CATGGGCAGT AAAAAAAAAA ATTGAAATCT	240
GGTCATTGGA CAACAAAATG GATGAATCTG GAAAACAGCA TAATTAGTGA ATTAAACCAG	300
TCCCAAAGGG ACAAATACCA TATGTTCTCC TTGATCTGTG AGAACTAATG GAGTACCTAA	360
AAGGAAATCT GTAGAAGTGA AATTGACACT TTGAGAAGGG ATGACTTGAG CTGCCCTTGT	420
CTTGACTTTC AAGGAACAGT TTTTCTTTTT TCATTTTTTT TCTTCAGCT ATTTGCTGAA	480
CTCTTTAGTT AACATAGAGT TAATCATATA AAGTCATGTA GGATGGATCT CAGTAAAAAA	540
TAAGAGTGGG AATAAGAAAG GGAGGAGGAA GTTTTGTAAC TGTAAAGCTA TATAGTTATA	600
CATACATTCC TATGTACTTA CTCTAAGGC ACAGTTTAAA AACTTGTCAT GAGATCCCAA	660
ATCTCATTAA GCTGGGTGGA AAAATGCCAT CTTAAGTGTT AAAGTGATCA TATTAGTGTT	720
AAAGTGAACA TATAGATACG TTTAAGTGTT AAAGTAAACA TATAAATAGG TTTAAGTGTC	780
TGGAATAAT AATAGATATA ATTAAAAAGG AGAGAATTTT CCAACTTGGG AAATAGTCCA	840
CA	842

(2) INFORMATION FOR SEQ ID NO: 226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

TACAAATTGA GTGTCAGTGT GATTTTCAGG TTAATTCATT CAGAATTCCA CAGGCAGTCA	60
GCTGGAGGGG TGGATGAATC CGGGAACAGC CGGTTTCCTT GCGACTAAAT AAAGCCTTAT	120
ATCATAATGG ATTCTTGCAT TTCTTTGGCT TTTTCTCCG TTTTCTTATT TATCATGGTT	180

872

TATAATGAAT TTTCTGATGT GAGCTTTTGT TTTGTGGCAG GCATATTGAG TTCAGGGCAT 240
AAGAGGAAAT TTCTTTTTC ATCAGGGCAC AGCTGTTGGC TTGCTCCAAT TCTGGTTTGC 300
TGTCAATGTT TTCGGTGCCT CAGCCGATTG TGGTTTCTTG ATCAAAAATT TCCTAAATGT 360
TTTCTGGGTC TGAGTTGGTT TTGCCTTCTT CCTTCCCAA TTTTGTATTC GGATGCAATA 420
CAAACAAGTG TTTGGACAGA GTATGCATTA CGAAATAGAA ACACAACATT AAGGCGTTTG 480
AAGCTTAGAC ATCTACAGGT AGCACGAGCA AGGTGAGTTT TTGTGTTTTG GAAAATCAAA 540
TGGAACACTT TAGCTGAGGT 560

(2) INFORMATION FOR SEQ ID NO: 227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

TGnAACTTC AGTTTGGGAG GCAATTAATA TCTGTCACCT CAGCCAAAGT GTTCCATTTG 60
ATTTTCAAAA ACAAAAAAAC TCACCTTGGC TCGTGTACC TGTAGATGTA TAAGCTTCAA 120
ACGCATATTT GCTGTGTTTT TTATTTTATA ATGTCTACTC TGTCTCACT CTTATTTGTA 180
TCACATCAGA ATACAAAATT TGGGAAGGAA GAAGGCAAAA CCAACTCAGA TCCAGAAAAT 240
TTTTAGGAAA ACACCACTCA AGAATCCACA AATCGCCTGA GGCACCCAAA CCAATGAAAG 300
CAAGCCAAA TTGGAGCAAG CCAACAGCTG TGCCCTGAAT GnAAAAAAA CTCCTCTTG 360
TGCCCTGnAC TCAATATGCC AGCCACAAA CAAAAGTTCA CAGCCG 406

(2) INFORMATION FOR SEQ ID NO: 228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

GAACTTGCAA AAAGCGTGGT AACnGTATT GCACGGGTTA AGGATGATAT GTGTnAACTG 60
CTTGATAGAG GCTTCGTGCG CATTCTTGGC CAAGCAGCAG GCAGAGTCGC CACTCCGGGG 120
AAAAAGCTTT TGCTTCTCAG GCTCCCTGCA GAAATGGAGA TCGCGCGnCT ATACACCGTA 180

873

TACGCGCGCT CGGnGGCGTT nTGAGAACGT CGGGGATCCT CTAKAGTCGA CCTGCAGGCA	240
TGCAAKCTTG kCACTGGCCG tCGTTTACAC ACGTCGTGAC TGGGAAAACC CTGGCGTTAC	300
CCAACTTAAT CGCCTTGACAG CACATCCCCC TTTCGCCAGC TGGCGTAATA GCGAAGAGGC	360
CCGCACCGAT CGCskTCCC AACAGTTGCG CAcCTGAATG GCGAATGGCG CCTGATGCGG	420
TATTTTCTCC TTACGCATCT GTGCGGTATT TCACACCGCA TATGGTGcAC TCTCAGTACA	480
ATCTGCTCTG ATGCCGCATA GTTAAGCCAG CCCCAGACACC CGCCAACACC CGCTGACGCG	540
CCCTGACGGG CTTGTCTGCT CCCGGCATCC GCTTACAGAC AAGCTGTGAC CGTCTCCGGG	600
AGCTGCATGT GTCAGAGGTT TTCACCGTCA TCACCGAAAC GCGCGAGACG AAAGGGCCTC	660
GTGATACGCC TATTTTTATA GGTAAATGTC ATGATAATAA TGGTTTCTTA GACGTCAGGT	720
GGCACTTTTC GGGGAAATGT GCGCGGAACC CCTATTTGTT TATTTTTCTA AATACATTCA	780
AATATGTATC CGCTCATGAG ACAATAACCC TGATAAATGC TTCAATAATA TTGAAAAAGG	840
AAGAGTATGA GTATTCAACA TTTCCGTGTC GCCCTTATTC CCTTTTTTGC GGCATTTTGC	900
CTTCCTGTTT TTGCTCACCC AGAAACGCTG GTGAAAGTAA AAGATGCTGA AGATCAGTTG	960
GGTGCACGAG TGGGTTACAT CGAACTGGAT CTCAACAGCG GTAAGATCCT TGAGAGTTTT	1020
CGCCCCGAAG AACGTTTTCC AATGATGAGC ACTTTTAAAG TTCTGCTATG TGGCGCGGTA	1080
TTATCCCGTA TTGACGCCGG GCAAGAGCAA CTCGGTCGCC GCATACACTA TTCTCAGAAT	1140
GACTTGTTTG AGTACTCACC AGTCACAGAA AAGCATCTTA CGGATGGCAT GACAGTAAGA	1200
GAATTATGCA GTGCTGCCAT AACCATGAGT GATAACACTG CGGCCAACTT ACTTCTGACA	1260
ACGATCGGAG GACCGAAGGA GCTAACCCTT TTTTGCACA ACATGGGGGA TCATGTAAC	1320
CGCCTTGATC GTTGGGAACC GGAGCTGAAT GAAGCCATAC CAAACGACGA GCGTGACACC	1380
ACGATGCCTG TAGCAATGGC AACAACGTTG CGCAAACATAT TAACT	1425

(2) INFORMATION FOR SEQ ID NO: 229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

GGGGCTTTTT AACCATATCT GAATGCCTTA AGGGCTGATT CTGAGGCCAG AGTGCTATCT	60
AGGATATCTG CCATTCTGTA AGTCTGCTGT GTATCCTGCT TCCCATGTTG GATCATCTCT	120

874

TCCTTTTAA TTCTATCAGT TAGTATTAGC AGACACTAGT CTTGTTTATG TGATCTCTTT 180
GACACTTAAT CCTATCATTA TGATCAATTA TGAAGTCAA CTGATCACTT TAACTAGTGA 240
GATGGCATTG GTGCATGCTC AATTGGACTT ACCCCTAATG ATAGAGTTAG AAATGTGCCA 300
GGGAATTCCA ATTCAATCCC ATCAAGGATT TTATTTAATT TAATTTAATT TTATTTACTT 360
AT 362

(2) INFORMATION FOR SEQ ID NO: 230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

CGGATCCCCG GTCAATTGTG GAGACATAT TATCAATTTA CCAAGAGAAA GCCGAGGTGG 60
AAAGAGTTCA GAATTGAATT TGCCCACGGC nAATATnGTT AAAAAGTCTA GATTAAAGGC 120
CAACCAACCA AAGTTAAATA TAGGCATTAG GATCTGGCTG AAGAGCCCAT GAAATTATTT 180
TAGGCATGGA AAGTCAAGAC ACTCTCAAAA AAAAAAAAAA AACTAnATG AAAGATCTCT 240
GTGATTGAGA TCCCAGTGA AAnAATGGGC CATCAAAGAA nGGTACTTTT CTCTTAAGGG 300
nGGAGAGAAC TTCCACTTTG ACTATGACAT TGTCTAAATA AGATTGnAGT CAACAAACTC 360
AAAAGGTTTC CATAGCCTTG GCAACTCATG ACnAGAGCCT AGGGAGATTT CTGACGCCAT 420
AAACAAGAGT GTCAnTTTGT TAAGTCAACA ACAGGAGTCG CTGTGGCACT TACTCCTCAT 480
GTAGGATCTC TATTCnTAAT GTGTTGTACA AGGnGAATTA ATGCTATAAC TAGTACTCAA 540
ACAGTATTTT TCAC 554

(2) INFORMATION FOR SEQ ID NO: 231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

ACCCAACCTC AGCACTAACC TTGACGAGTC ATTTCTTTGA TTTGGTCATT GGTAAAATAC 60
TGACCAACCG TTTGAGCTTG AGTAAGCATT TGGCGCATAA TCTCGGAAAC CTGTCTGTTG 120

875

CTTGAAAGA TTGGTGT TTTT CCATAATAGA CGCAACGCGA GCAGTAGACT CCTTCTGTTG	180
ATAAGCAAGC ATCTCATTTT GTGCATATAC CTGGTCTTTC GTATTCTGGC GTGAAGTCGC	240
C GACTGAATG CCAGCAATCT CTTT TTGAGT CTCATTTTGC ATCTCGGCAA TCTCTTTCTG	300
ATTGTCCAGT TGCATTTTAG TAAGCTCTTT nTGATTCTCA AATCCGGCGT CGTCAAAAAC	360
AGGAAGCCTG GGTAACCCAG GTAGTGCAAC AGGCGACGCA GACAGTAACG GCTGGAGTTC	420
GAAGCGCGCT GGAATCTCGG GGGACTACGT ACATAAACGC GCTAGAGGCA GTTCAGCCTA	480
ATCCTGCTAA ACCTACCGGT AAGGnTGTC AAAATCTTCA CACCCCGCAG GAAGTCCGCC	540
G	541

(2) INFORMATION FOR SEQ ID NO: 232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 628 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

AAATAAAAAG AATCATCAGG AATTCCTACA AAGATCTATA TGCCAACAAA TTGGGAAACC	60
TATAAGAAAT GGATAGATT CTGAACACAT ATAATCTACC CAAGCTGAAT CATGAAGACA	120
TAGAAAGTCT AAACAGATCA ATAACCAAGA CAGAGTAATA TCAGTAAGAA AAACCCTCCC	180
GCTTCCCATG TTGGATCGTT CTCTCCCTTT TTAATTCTAC AGTTAGTATT AGCAGACACT	240
AGTCTTGTTT ATGTGATCCC TTTGACTCTT AGACCTATCA TTACGATCCA ACATGGGAAG	300
CAAGATACAC AGCAGACTCA TAGAATGGCA GATGTCTTAA ACAGCACTCT GGCCTCAGAA	360
TCAGCCCTTA AGGCATTCAG ATCTGGCTCA AGAGCCTATG AGAGTATTTT AGGCATGGAA	420
AGCCAAGACA CTCTGGCAAA AAAAAAGGG GGGGGGGCAA ATGAAAGATC TCTGTGAGTG	480
AGATCCCAGT GGAAAGAAAA AGAACGGGCC ATCAAAGAAG GAGGTACCTT TCTCCGAAGG	540
AGGAGAGAAC TTCCACTTTG ACTATGGCCT TGTCGAAATA AGATTAGAAT CGGCAAACTC	600
AAAAGGCTTC CATAGTCTTG GCAACTCA	628

(2) INFORMATION FOR SEQ ID NO: 233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 614 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

TAATGGAAGT AGAGAATGGG AGGGAAGTGG TAGGAAGGGA GAGGTGTGTG AGGCTGGGAA	60
ACCACTACAA ACTTAATAAA AAATCAAATG CTGAGGTAGG ATGTCAACTA CGTAAAAGAA	120
AATAGACCAT AGAATAATAA ATGAAAATAT ACCAAAAGCA CTTAAACATT TTCCTACTGT	180
TGGGTAAATA GGTGAATTAC AGTTTTTAGC TTCAGGCAAT AAAAGAAAAT CTTGTGGTA	240
AGATTTCAAG TTTTAAAGA AGTTTATCTT CACAATTGAT CACACTGATA GGTCAAAGAG	300
TCAAAGGGAT CACACAAACA AGACTAGTGT CTGCTAATAC TAACTGATAG AATCAAAAAG	360
GGAGAGAACA ATCCAACATG GGAAGTGGGA TACACAGCAG ACTCATAGAA TGGCAGATGT	420
CCTAAACAGC ACTCTGGCCT CAGAATCAGC CCTTAAGGCA CTCGGATCTG GCTGAAGAGC	480
CCATGAGAGT ATTTTAGGCA TGGAAAGCCA AGACACTCTG GCAAAAAAAA GGCCTAAAT	540
GAAAGTTCTT CTCTGTGAGA TCCCAGTGAG TGAGATCCCA GTGGAAAGAA CAGGTCTTCC	600
AAAAAGGAGG TACC	614

(2) INFORMATION FOR SEQ ID NO: 234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

GCCnGCCAAC CCAAGGnTTT TTTACCCGGT TTTTGGCCA CCAAATTTCC CTCCCCGGC	60
CACCTCCAAG GGCCAAGGAA ACCATTCCCC CGGCACCCCA ACCGGACCAC TGCACTGGCA	120
AGTnAAGnCG GCATGGGCAG CAGTCGGTGC AGGACCTGCA GGATCGCTCA TTCCTGGCGC	180
TCCTCTCAGT GCGGGAGTCG GCTCTCGCGG CGnTGGGGAG CGTTGCCTGC GCCAGTAGAG	240
CCGCTGCTCC GCCAGGCGGG ATGACGCATT GGGTGCCTT GCAAGACTGT GGCAGCGTG	300
C	301

(2) INFORMATION FOR SEQ ID NO: 235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

AACGTGGCAG	ACGTGGTAAC	TACGTCATCG	ATAAnCAAGG	CATCACGCGG	CACACGAGCG	60
TGCGCCCCGA	GCTCTATACT	CCCTGCAAGA	TTCTCAACAC	GCGCAGCGCG	ATCTAAAGTT	120
TTGCTGCGCG	AAACGACCCT	CTTACTCGCA	CCAACGCACG	ATTAACGGTA	AAACCAGCCA	180
ATTCTAGTCG	ACGCGACACG	TCCGCAAnCG	GGTCCCATCC	TCTTCTCAGC	CATCATGCAn	240

(2) INFORMATION FOR SEQ ID NO: 236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

AAAAAAAAGG	GnGGGGGGAA	CCCAAAATTC	CCCCCAAAA	nGGGTTTAAC	CCAAAAAAGG	60
GAAAAAAAC	CCAACCCAAA	TTTAAATTTA	AAAACCCTTC	CCCCCTTTAA	AAATTTTTTG	120
GnAACCCAAT	TTGGGAAnTT	CCAAAGGGAA	AAAAATTGGG	AAAAACCCTT	TTAAAAACC	180
CCCAACCAAA	AACCCAACCC	AAAATTTAAT	TTAAGGTTTC	CAAAAAAACC	TTTTTTTGGG	240
AGGGCCAATT	TTTAAAAAAA	CCCCCTTAAA	AAAAAGGAAA	AAAAGGAATT	CCCCTTAAAA	300
AAAATTTTTG	GGCCAATGGG	AnGAAAGAAA	CCTGGCCTAG	GnATTTAACC	CCTnCCCAAA	360
AnGGGATTCC	TCCCCAAATG	GAAGAACCTG	GGGCCAnGCC	TGGAATTTTC	CTCCATCCnG	420
ACCACCCTnC	CCnGAnCTAG	GGGGGAAGAA	ATGGAAAACC	AnCATGGTTT	AAAAAAAAAA	480
TCCCTTGTC	AATCCCAGAA	ATACCGGTAA	CCCCAGTTAG	AnGCCTCCTC	CATTTAATTA	540
AAATGGAAGG	GTGGAAATTT	AAAAAAA				567

(2) INFORMATION FOR SEQ ID NO: 237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

CTCCATCCAG	TCTATTAnTT	GTTGCCGGGA	AGCTAnAGTA	AGTAGTTCGC	CAGTTAATAG	60
------------	------------	------------	------------	------------	------------	----

878

TTTGC GCAAC GTTGT TGCCA TTGCTACAGG CATCGTGGTG TCACGCTCGT CGTTTGGTAT 120
GGCTTCATTT CAGCTCCGGT TCCCAACGAT CAAGGCGATT ACATGnTCCC CCAGTTGnGT 180
TGAAATAGTA ATCAGCAGGT TTTCGGGGCG AGTAT 215

(2) INFORMATION FOR SEQ ID NO: 238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

ACTGACTTTG CTAATAATCA GACCTACATT TAACTCAGAT TAATAATGCT TGCTTAAGTG 60
TCGCTCCCCC TCTTCGTGGA GGAACGACAC TAAATCCTGC CTAGGCTTCA TATCCGAGTC 120
ACGGCACCAT TATGTCGCTC CCCCTCTTCG TGGAGGAACG ACACAGGACC CTGCGCTGTT 180
CTTTCGTCTG CTCGGCCCTC CCCGGGTTTG CTGCTGGTTC TTCCCGGGTT GGCTGCTATC 240
CCTTCCACCT CCGTGAAAG GGCAGTTCCC CTTGGCCGCA TCCCCATTTC CGCAGGGAGC 300
GGCAAACCGC GGCCGGCTCT TCTCGGGGCT GCACAnATGT TTCCCTTAAA AGTTCGCCAA 360
AAAnGTTTCT GG 372

(2) INFORMATION FOR SEQ ID NO: 239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

GCATGCCTGC AGGTCGACTC TAGAGGATCC CGGGCATATA AACAACGCTG CCCCCGTTCC 60
TGAAGCAGGA AGCGTACGAT AGTGAGCCAG CGGAAAGAGA AGTGCTGCAA GGCGGACCGC 120
AAGCTCTGCA GGCACCCGAT CGCAGCAGC 150

(2) INFORMATION FOR SEQ ID NO: 240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

GCATGCCTGC AGGTCGACTC TAGAGGATCC CGGGGAGACG CTGAGCGCTC TCCTCGCCCA 60
CGAAAGACAC CGTGnGnGCC CGGTCCCTAG AACGGACGGT CCGCAAGGTA CTTGTACTCT 120
TGCCACTGTC TCCGCGCCTT CTCTTCTGCG 150

(2) INFORMATION FOR SEQ ID NO: 241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

GAGGGAGGGG AGGAGGGAGA GAGAGAGAGA AAGAGAGAGA GGTCCCTCTGT CCACTGCTTC 60
GTTCCCCAGA TGGCCACAAC GGGCCAGAGC TGAGTCGATC CGAAGTCAGG CGCCAGGAGC 120
TTCTTCCGGG TTTCACACTT GGGTGCAGGG TCCCAAGGAT CTGGGACATC TTCTGCTGCC 180
CTCCCAGGCC ATAGCAGAGA GCTATnAGAA GCAGCCAGGT ACTAGAACTG GTGCTCATAT 240
GGTATGCTGG CACTGCAGAC CnAGCTTTA ACCCACTCTG CnACAGTGCC AGCCCTGAAT 300
GTTTTTGAAT A 311

(2) INFORMATION FOR SEQ ID NO: 242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

TCTTGCATGC CTGCAGGTCG ACTCTAGAGG ATCCCCTCTG GGGTAGAAGG TTTTGGCTAT 60
GACCCGATTT TCCTGTTGCC ACACCTGGGC AGGACGTTCTG CTCAGCTCAG CATTGAGGAG 120
AAGAACCGCG TCTCTCACCG GGCATTGCG 150

(2) INFORMATION FOR SEQ ID NO: 243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 596 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

GAAAATATCG GAGAGAGAGA CTAGCAAACA GCCTAGGGAA AAGCCGACG AAAAAGGAGC	60
CGGAAGAAGC TATTGAAAGC CTAGGCATAG ACTTGATAC GGACTACGGG GGGAAGTTGG	120
GAGAAATCTC TAAGGTCGAA AGCGAAAGTG AAAGCTAGAA CAAACAGATT CGGACGCGGA	180
CTGTGGGGAG AGGCCAGGAG AAATGAGGGA GGAATATCGT TGGAGATAGC TTGGGGAAAC	240
ATACCGGGTA GAGAAAACCTG TTAGGGAAAT TGAAGCCGCG GGGGGCAGGC CAAGGCGGAA	300
ACGAAAGCCA CTTTGGGGTT CTCAGGTTAG CCCGGAATA GGGGGCAAAA AGTTGAAACC	360
AGAAGCTGAG ACGTAAGCCA GATTGGGATC CGTCTGATTA GCCCAGGGAG CAAAGGACGG	420
GAAGCCAAAT CGTGGGGCGG AGACGTACGC TGGGTTGAAT TCGCCAGGCT AGCCCGGGGA	480
ACTTGATTG AATGCTAGTG GTGGAGACGC AAGCTACGCT GTGTTACTCG CGGAAGCCGC	540
CGCGTGCAGA GAGAGCACGG GCGGTGAGTA GATAGGGAAC GGGGCTGGCG TAnGCC	596

(2) INFORMATION FOR SEQ ID NO: 244:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

ATGChTnGCA TGCCTGCCGG TCGACTCTAG AGGATCCCCG TCACTTGCCC CCAGCTCCAA	60
ACATTGCATC GTGACCCGTG CACCTTCTTT TGCAATGCTA GAGAGAATGA TTACTGGAAT	120
ATCAATGCGT AGACGTTTCC GCTGTTCAAG	150

(2) INFORMATION FOR SEQ ID NO: 245:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 489 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

TGTTCTGGGC AGGGTTTTCT GAGTAAGAGC CCCAAAACAC AGGCAGAGAT ATTCAAAGTT	60
---	----

881

TCACATTGG GTTAACTGGA TCATATTTT GCACGTTTCAT GGCTGAAACA AGGTCTTAAC	120
AAAAC TCAAA ATTGACAAAT GAAATCATGT CACATTAAAA TGCTTCTGTA CAAAAGACAA	180
GGTTTTATTT GTTTGTATGT TTTTATATAC CTGACTCTGA AAACCTTATG CnGGGGCTGG	240
TGCTGTGGTG TAGCAGGTAA AGCCGCTGCC TGCnGTGCCG GCATCCCATA TGGGGGCCGA	300
TTTGAATCCG GCTGTTCCAC TTCTGATCCA GCTCTCTGTT ATGGCCGGGA AAGCAGTAGA	360
AGAGGGCCCA AGCCCTGGGT CCCTGCATCC ACTTGCAAG ACCCGGAAGA AGCTCCTGGC	420
TCCTGCCTTG GACAGGCGCA CTCCTGCTAA GCGGCCAACT AnGGAGTGAA CCAACAGATG	480
GAAGACCTC	489

(2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

CTAAAGTnC CCCGGGGGCT AAGCCCTTGG CCGAAATnC AACCCAGCG TACGTCTCCC	60
GCCCCACGG TTTGGCTTTC CCGTCCTTG CTCCCCGGGC TAATCAGACG GATCCCAACC	120
TGGCTTGCCT CTCAGCTTCT AGTTTCAACT TTTGCCCCC TATTCCCGG GC	172

(2) INFORMATION FOR SEQ ID NO: 247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 617 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

ATCAGAAGTG GAGCAGCCGG GTCTGGAACC GGCACCCATA TGGGATGCCG GCACTTCAGG	60
CCAGGGCGTT ACGCnTGGCA CCACAGCGCC TGCCCTGAAA CCTTTTCTTT TACACAAAAT	120
GCAGATGGCT AATACTTCCA CTAACAATGT CCAGTATCAG GTTCAGCTAT GGTTTCTCTA	180
GCTGGGTGTG ATACTTCCTT ATTTTACTT GAAAAGCACA GTGACAAAGA GAGAGGGAAA	240
GACACACATG GCTGGGCCAA GAGGAAGCCA GGAACCAAGA ACTCCACCCA GGTCTCTAAC	300
GTGGATGGCA GGGCCCCAAG TATTTGGGCC ATCCTGCACT GCTTTCCCAG GAACATTAAC	360

882

AGAGAGCTGG ATTGGAAGCA GAGCAGTCAG GATTCTGAACC TGCACTCTGA TATGGAAGGC 420
 TGGCATCGCA GGTGGCAACT TAGCCTGATG GACAACAATG CTGGCCTTGT GATGTTTATT 480
 TTTATGATTT TCTACAGCAG AACAGCAGT TCCCAAATGC AGATATTTCC AAGCCTGCAT 540
 AGACTCATAC TTCTTTTCAG GTAGCAGTGA CTGAGAATAG AATCTGCAAT CCCAGTGTTA 600
 TCAACATTAC ATTCTAG 617

(2) INFORMATION FOR SEQ ID NO: 248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

CCCCGGGCCC AATTTTAAACC GGGCCCCnTT CCTTTCCCCC AAAAAAATTT GGCCAAACCC 60
 CGGGAAGGnT TAAAACCCCTT TTAAATTTTG GTTGGGCCTT TTTTGGGGGn CCAnTTAAAA 120
 AACCTTTCCC CAAACCGGGG GAACCTTCCA AACCTTTTTC CTCCCCCTT 170

(2) INFORMATION FOR SEQ ID NO: 249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 585 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

GAGCATTTTG AGAGGCAGCA AGTGATGGCT CATGTAACAG GTTCTGGCC ACCTGTGTGG 60
 AGGAGCTGGA TTGAGTTTAT GGCTGCTGGT TTTGATCAGG GCCAGCCCTC ACCATTCTGA 120
 CCATCAGCAA AATGAACCTG TAGCTGAATG CTTCTCTCTC TCTCTCTCTC TCTCTCTCTC 180
 CCCCCAACCC CATCTCTCTC TCCCCGGTCT CTTCTCTGT CTCTACCTTT CAGATGAATT 240
 TTTTTTAAAA AAATTAGTAT TTTGATGCAA AATTGTTTGA CATCTCTGAC CTTTTCATAA 300
 TACACCTTCT CCATTATCTT TTTGAGGACT GCTTTAAGCA TAGATTTGTA TGTAGATATA 360
 GATGTCTTTC GTCTTTTTTA AAAAAGATTT ATTTATTTGT TTTGAAAGTC AAAGTAACAG 420
 AAAGAGAGAG AGAGAGAGAG CTCTTCCGTT AGCTTGGTCA CTCCCCAGAT GGCCTAACAG 480
 CCAGCACTGG GCCAGGCGCC GGGTCTCCA CACAGATGGC AGGGACCCAA ACACTGTGTGT 540

CAACTTCTGA TGCTTTCCCA GGCCATTAGC AAGGAGGTGT ATTAG

585

(2) INFORMATION FOR SEQ ID NO: 250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

AACCAGGACA GAATCCGGCG CCCCGACTGG GACTAGAACC CGGTGTGCCG GCGCCGCAGT	60
GGAGGATTAG CCTAGTGAGC CGCAGCGCCG GCCAGGAATA AAGTTAATTA AGTAGGTGAA	120
AGACTTGTAC ACTGAAAATA CAAAACAAAT TAGAGAGTAC AAAAATAAGT GGAAAGACAT	180
TCCAGGTTCA TGGATTAGAA GGTTTAACAT TATTAATAATG TAGTTTAAGG GGACAGCATT	240
GTGGCACAGC AAGTTAAGTC ACCGCTTCCA ATGCCAGCAT CTCATATCAG AGTGCTGGTT	300
TGAGTCCCAG CTGCTCCTCT TATGAACCAA CTTCTTGCCA ATGCACTGGA AAAGCAGCAT	360
ATGATGGGCC CTACCACCCA TGTGGGAAAC CCAGTTGAAG CTCCTGGCTT TTGGTCTGGG	420
CCTGGCCCAG CCCTGGCAGT TGAGACCATC TGGGGAGTGA ACCCATGGAA GATCTGTGTG	480
TGTGTGTGTG TGTGTGTGCG TGACTGTGCA TGAAGATCT GTGTGTGTGT GTGTGTGACT	540
CTGCCTTCAA AATAAATTAA GAACCG	566

(2) INFORMATION FOR SEQ ID NO: 251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

AGGAGGTAA GACCTAGTGA ATGCGTGGAG CTTATGAACT GGAAGTGTGA AAAAAAAAAA	60
AAAGTGAAG ATGTGTGGGA GAACTCAGGG TGTGCCTGAG AAGTGAGTAC TCTCCGTGGG	120
AGACACCACA AACTTGGTAC CTTGGCTAC CCAGTGAGAG CCATTGCAGG GGAATCTGAG	180
CTTACACTGA GGAAGTGAACA GATCCTTTGT GTGGTCCTTG GGACAGAGCA GAGGAATATT	240
ATACACACTG GGGCTAGCGC CCAGGCACTG ATTGCCATCA AGGAGAAAAG CTCAGCTGAG	300
CAAAATTACT TCCCTTCTGA ACACAAAAG AGAGAGAGAA GTTTACTATG CCTAACCTGG	360

884

GTGTGTCACC TTTGGGCACA CCCTTAACCC TGAAGAACTG AGCCGAGCTC TCTGGnCCAA 420

ACCCGTCAAA AGCCTCTAGn G 441

(2) INFORMATION FOR SEQ ID NO: 252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

ATGCCCAAGT CCTTGGGTCC CCGCACCTGC GTGGGAGACT GGAAAGAAGC TCCTGGCTCC 60

TGCCTTCGGA TCAGCGCACT CCTTCTGTTG CGGCCATTGC GGGAGTGAAC CAACGGATGA 120

AAGACCTCTC TCTCTTTCTC TGCCCTCTGC CTCTGGnCC TGCCCCTGCC CCTTCCCCTT 180

nCCnTACCCC TACCTCTATC TCTACTTCTC TGTAAGACTC TTCATTTCAA ATACATAAAT 240

AAGTCTTAAA AAAAAAAAAAG CCAAAGTTTT CTACAGTTTC ATTGGTTCCT GGGAAAAGAT 300

GCCACCACAG TGATTTCCTT CCCAGCTGTG AGCATTCCTC CTTACCCTTA TCGGACCCAT 360

CAGGATGCCT GGTCCAAGTC GCCCACCGTG CATAGGCATA CAGTGGATCT TGGGTGCCTG 420

CTTCTGTGCA CATCCAATCT ATCTTCCTGA CCTCTGGCCC AGAATTATGG TCCTTGATCC 480

TCCATG 486

(2) INFORMATION FOR SEQ ID NO: 253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

nGGAACCCnT GATAAGCAAG TGGCCAGGTG AAGGTGGAAA AATCAAAAAA ATATGGCATG 60

ATATTATAGA AGCCAAGTAA AGAACATGGT TATATAGAAG GAAGTGACCA GCTATCTCAG 120

AAACTGCTAG CTAAGTCATG TACAATGAGA ACTGAGGGAT AATACTTATA AAATGAGAAG 180

GTAAGAAGAA TATGAAAATT GTCTACCAAC CTCTACCCAA AGCTATACCA CTTTCAGGC 240

ACCCTTGAGA GATCTTCCAC CATGTCTATA CACACAGATT TACTTGTAAT GTTAGTAGTA 300

GTTAAGTCAT TTGCATTTTG GAGCTTTATA TGCCCATGGT TTATAAACAG AAACAGAAGT 360

885

TATTAAAATT TTAGAAAGCA TAGGAATACT GAGGATCAGT CTCCCAGTAC TACTATTTTA 420
AGATTTTATT TATTTATTTG GAAAGAGTTA CACAGAGAGA GGAGAGGCAG AGAGAGAG 478

(2) INFORMATION FOR SEQ ID NO: 254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

AATGCTGGAG AGGATGTGGT GAAAAAGGTA CCCTAATCCA CTATTGGTGG GAATGTTAAC 60
TGGTAAAACC ACTATGGAAA TCAGTTTGA GATACCTCAG AAATCTGAAT ATAGACCTAC 120
CACATGATCC AGCCATTGCA CTCCTGGGAA TTTACCCAAA GGAAATAAAT CAGCAAAGTA 180
AGGAGCTATC TGCACCCCCG TGTGTATTGC AGCTCAATTC ACGATAGCTA AGACATGGAA 240
TCAACCTAAA TGCTCATCAA CTAAGACTGG ATAACGAAAT TATGGGATAT GTACTCTATG 300
GAACACTACA CAGTGGTAAA AAAATGAAAT CCAGTCATTT GCAACAAAAT GGATGAATTT 360
GTAAAACATC ATACTTAGTA CGATAAGCCA GTCCCAAAGG GACAAGTACC ACCTGTTCTT 420
CCTGATCTGT GATAAGTAAT AGAGCACCTA AAAGAAAATC TGTA 464

(2) INFORMATION FOR SEQ ID NO: 255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

CCTTTTACT TGTGAACTC TTTATTTAGT GGAGCGTTAA GCCTGTGATG CTAAAATAAA 60
TTAAAAATAT GTTATTGCCA AAATTAAAGG GAGAAGGGAG ACTGGGAnGG TGAGAAGAGT 120
GGAAC TAAGT ATCAAATTCT TAGGACTGTA TATATGAACT ACTTGAAAAC TGTTCTCTTT 180
ATATTAATAA AAATTTAACA TAAAGCACT GAAAAAACTA GTATATTTAA ATCCTCTACA 240
AAATCAATTG CTATGTATTT CTACCTTCAA ACCCATAAAT ACTTGCTTTG TGTGTGTGTG 300
CAGTGTGTGT GCATGTACAT ACCTAGACAC AAAAAAAGT TATGTGGGGC TGGCGCnTGG 360
CACGCTGGGT TAATCCTCTA CCTGCGGCAC CGGCATCCTC TATGGGCTCC GAnTCTAGTC 420

CCGGnTGCTC CTCTTCCATC CAGCTCTCTG CGTGGGCCCA GAAAGG

466

(2) INFORMATION FOR SEQ ID NO: 256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

CAAAGTCACT ACTTATCAAT AGTCATTTTG AATATAAATG GCCTCAACTC TCCAATTAAA	60
AGACGCAGAC TGGCTGAATG GATTAAAAA CAAACCCATC TACTTGCTGC TAACAAGAAC	120
ACATCTTTCA ACAAAGGTGC ATGCAGACTG AAAGTGAAAG GTTGGAGAAA GATATTCCAT	180
GCCAACAGAA ACCAAAAAAG AACTGnCATA GCCATCTTAA TATCAGACAA AATAGACATT	240
AACACAAAAA CTGTTAAGAG AGACAAAGAG GGGCACTATA TAATGATTAA GCGATCAATT	300
CAATAGGAAG ATGTAATAT TATAACATA TATGCAACCA ATTACAGGT ACCGGCAGTG	360
CAAAATAAAT GTTAATGGAC CTGAAAGGAA ACAAACCTCC AATACAATAG TAAAGAGGGA	420
CTTCAATAGT CCACTTTCAG CAnGGACAGA T	451

(2) INFORMATION FOR SEQ ID NO: 257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 638 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

CAGAACCATG GGAAACCACT ATGAAAGAAG GTGAAGGCAG AATATTTCCC AGTAAAAGTA	60
CAAAGGAAAC TCAAAGTAAA CTATAGGAAT ATCTGTGGGA AAATGGTAGG GCCAAGTTGT	120
TACTTATCAA TAATCACCTT GAATGTAAAT GGCCTCAATT CTCCAATTAA TAGATACAGA	180
CTTGCTGAAT GGATTAAAAA ACAAAGCTCA TCTATTTTCT GCCTTCAAGA AACGAATCTC	240
ACCAACAAAG GTACATGCAA ACTGAAAGCG AAAAGATGGA AAAAGATATT CCATGCCAAC	300
AGAAACCAAA AAAGAGCTAG TGTAGCTATC CTAACAGCAA AACAAAATAG ACTTTAACAC	360
AAAACTGTT TGAAGAGATA AAGAAAGGCT TATGCAATGA TTAACGGATC AGnTTACCGG	420
GAGATGTGAC TATnTAAnGT ATAnGCACAC nTTACAGTAT ACTGAAAAC TCTCCTGATG	480

887

AnCATGGTTC ATAGAGAnAT CAnAAGAGAA ATAAGAAATA AAAAAGTGT GAGGGACTTT 540
 AACAAAATAA GAAGTATGAC TCTGTGGATT ACTGTTATnA CTATTATGAT CATAAACCTG 600
 CTCTGATAAG CGCTTnCAT ATATCACTTC TATCTTTA 638

(2) INFORMATION FOR SEQ ID NO: 258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

AGTCTCTnTC TCTCTCACTG TCCACTCTGC CTGTCAAAAA ATAAAAATAA AAACAAAAAA 60
 TAAAAAAGT ATCTCTGTG ATTGAAATTT GTGTTTTTTT TTATTAACT CATTTGCATA 120
 TCTTTATCAA CATTTTGGCC ATCTGTTTTA TTCTCTGAAA TATCTTTTTG TGAAGTCTAT 180
 TTAATTTTTT TCTGAAGATT TACTTGTTTA TTTGAAAGGC AGAGTTACAG AGAGGGAGGG 240
 TGAGACAGAA AGAGCTGAGA GAGAGAGTGT GAGAGAGAGA TGGATCTTCC ATCTACTAGC 300
 TCCTTCCCTA AATGGCTATA ATGGCAAGGA CTGGGGCAAG TTTAAGCTAG GAGCCAGAAA 360
 CTCCATGCAA GTCTCCCATG TGGGTGGCnG GGnCCATGTA CTGGGG 406

(2) INFORMATION FOR SEQ ID NO: 259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

AGAGAGCTGG ATCAGAAGTG GTGCAGTTGG GACTTGAACC AGTGCTCATA TGGGATGCCT 60
 GTGTCTCAGG GTTAACCTGT ACCACAATGC CTACCCTCAT TATACCACTA ATAATCTGGA 120
 ATCAGATTCA TTATTGCTTC AACTCCTGGT AAGGAGTATA GATCAGTAAA GGTTCTTAGA 180
 GTAGATTAAG ACAAGCTGCC TAAAAAAGCA AAGGTTTGAA GTAATAAGCT CTTGGAGAAA 240
 ATAGATGTTG TCGAAGGGAA TGCTCGAGTG ATTCTAATAA ACCGTCATTC CCTGTGATTG 300
 CTTTACATGG CGTGCAGTGC ATTTGGAACA AGACAGACGC CAAGTCAAAT CCTATTCCTG 360
 GCTATATGAT GTTGACTGGA GATAGTTCCC ATCTCTGAGA CCCAGTTCTT ACTGGGTAGA 420

CTGTGACACT GGCTGTCTCC AAG

443

(2) INFORMATION FOR SEQ ID NO: 260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 656 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

AGGTCTTTAA TCCATGCTGA GTGGATTTTT GTGTAAGGTG CAAGGTAGGG GTCTTGCTTC	60
ATGCTTCTGC ACGTGGAAAT CCAGTTTTC CAGCACATGG AACCCCAAAC CCCCTTAAGA	120
TGGTATTTTT ACCACCCAGC CTAAGTGTTA AAGTGATCAT ATGGATAGGA TTGAGTGTCT	180
GGTAATAATA ATAGATAGAA TTTAAAAGGA GTGAATGCCT CAACATGGGA AGCAGTCCAC	240
ACAGCAGACT CATAATTGCT TTAAAAAGCA CTCTGACCTC AGAATCAGCC CTTAAGGCAT	300
TCTGGTCTGG CTGAAAAGTC CACGAGAGCA TTCAGACATG GAAAGCCAAG ATATTGTGAC	360
AAAAATGTCC TACACGAAGG ACTTAGATGG TGGAAAGAAG TGTCCATTAA AGAAGGAGGC	420
ATTTTCTCTA AAGAGAGGAG AGAACTTCAA CTTTGCTTAT GACCTTGTCT AACTACGGAA	480
TGAGTTTGTG GATTCAGAAG GCTTCCATAA CCTTGGTACC TCATGTCAAG AGCCTCAGAT	540
GATCACTGAC ATCATACTTA AGAATGTTAA TTGTTGGGGC TGGTGCTGTG GGCACAGCAG	600
GTTAAAGCCC TGGCCTGAAG AACTGGGCAT CCCCATATTG GGCACCAGTT CTAGTT	656

(2) INFORMATION FOR SEQ ID NO: 261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

ATCAGTGCCT TGTAATTAGG TGCATATACA TCTATAATAG TTACATCTTC CTGTTGACTT	60
GATCCCTTAG TCATTATATA GTATTCCTCT CTGTCTCCCT TAACTGTTTT TGTGTTAAAG	120
TTTATTTTAT CTGATATTAA ATGGCTATGC CTGCTCTTTT TTCATTTCTG TTTGCATGTA	180
ATATCTTTTT CCAAACCTTC ACTTTCAGTC TGCATGCATC TTTGTTGGAA AGATGCATTT	240
CTTGTAAGCA GCAAATAGAT GGGTTTTGTT CCTTAATCTA CTCAGCCATT CTGTGTCTTT	300

889

TAAGTGGACA GTTGAGGCCA TTAACATTCG ATATGACTGT TGATAAGTAG TGACTTGCCC	360
TGCCCTTTCC CAAAGATATT CTAATATATG CTTGAAGTCC GTGATCTTTA CGTGAGGTTT	420
TCTCCTTACC TCTTCATATG AGGCCAGTTT CGTGTGTAAC ACATATTATG CATTTTGTGA	480

(2) INFORMATION FOR SEQ ID NO: 262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

CnAAATTCAA AAACCTGGA GGATGACATA TATTAACCAC TTATTCCAGT AGTAGCACAT	60
GTACGGCTAT TATAAATATA GATGTATTGG GGTAGCTATT GCTTACTTAA CTATTTAAAT	120
AGTCATTGGC TTAGCTTGTA TAGGTCAGGC TCAGCCGAGT AGTCCTGGCT TTCACTGGGC	180
TACCTGGTGA ATCTTGAACC CGTGATATAC CAGGGAGGTG TCTCTGCTTC AGAGTATGGC	240
TGGTTGTTGC CTGGGACAGT GGAACCAATG GCCCAAATGT CTCCTCATCTC CAAAAATAGC	300
CCAAGCTTTT TCACATAGTG TTTCCAACGA TCCAACAGGA AGAAAAGCAG GCAAGGCCTG	360
GAGACTTAGG CTCAGAACCA GCTTACCTTC ATTTCTGCTG TGTTCATTTC ACAAAGCAA	420
ATCACAAAGC CAGCCACAT TGAAGGGGTG AGAAATAATT TTTTTTTTGA CAGGCAGAGT	480
TAGATAGTGA GAGAAAGAGA CAGAGAGAAA GGTCTTCCTT TTCCAATGTT TCACCCCC	538

(2) INFORMATION FOR SEQ ID NO: 263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

GCnCTTCCAG AAAAATCTTA TTTACTACTT TGGCCCTAGA AATCATAAAT GACTATGATA	60
GAATGTAACT TTTAACAGAG GTGAGGAAGG CATGGTTTAA TATCCAGTTT TGAGAATACA	120
ATTTTCATTT GTATTTTATT GATGTTTATA GTTCTTTTAA GATTATTGA TTTATTTGGA	180
AGTCAGAGTT ACAGAGAAGG AGAGGCACAC ACACAGAGAG AGAGAGGTGT TTTCCATCTG	240
CTGGTTCACT CCCCAATTGG CAGCAGCACC ACAGACCGA CCCCTTATAG TTCTTTTCAA	300

890

ATCATTTTAC ACTGTCTTTT TATTCATCTA GTACAGAGAC AGAAGAATGG ACACAGAGCT 360
AACATAGCTG AGTATTCAAG GAGACAGGTT AAGGGGTAA ATGCCTCATA TCATATTATT 420
TATACCTTAG ATTAATTCTG GGGACAGTAT TATCTGGAGT TTACAAAGTA GAAACTGAAT 480
GGAAAGAGCT TAGAAAAATA CCGTGTTTTT TAATATCATT AAAAAGGCCA ATCAAGGGGC 540
CAGCACTGTG AAATAGCAGG TAAAGCTACT GCCAGCATGG ACATTCCATA TGGGTGGAGG 600
TTGAGCCCGG CTAGTCTGCT TTCAATCCAA CTCTCTGCTA TGGCCAGGGA AAGCAGTGGA 660
AGATGGCCCA AGTCCTGGGC A 681

(2) INFORMATION FOR SEQ ID NO: 264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 653 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

TGGCTTCTAG CTTGGGATTG GCTCAGCTCC AACTGTGGCA GCCATCTGGG GAGTGAACCA 60
GTGGATGGAA GACCTCTCTT TCTCTCTGCC TTTGCCTTTC TGTAACTTT GCCTTCAAAA 120
AATAAATAAA TAAAAAGAAT TGAATTAGAG AACATCTAGC TAGTGTCCAC TATAGAACTG 180
AATATTCATT TAAAAAATGG TTAGAGAGTG TATAGGGCAA AAGAAAGGGC TGCTTCTCTCA 240
AGTACATCGT CAATTCCCAG GGAGGCTGGG ATCAGCTTGC CTTGGGGTTG GTCAGGAGAA 300
TGTCAGGAT TACAGCAGCT CTTAGAGCCT GGTGTGAAG GGAAGTAATG GTGATCAAAT 360
GAGAATTGTA CCAGTGAAGG TCAGCAGAAA GGACCAGCTC TGCTGCTGAT GGTGGGGATG 420
TAAGAGGAGC TTGGAAGCTA CTGCAGTGAA TGTGAGCTTT GGAGATTTAT GTATTTGAGC 480
TGTACAATA TGGGGAAGAC TTTTTTTTTT TATCnTGTA GCTTCAATTT TTCAAACGT 540
GAAATGGGGC GAATAATTAT AGACATAAAT ACAGAGCAAC AGTTTGAAG TACCATAAAC 600
CTCATGTCCT TCAACAGTG nTATTCATAC CnTATAGGGG TATTGTGAGT TCC 653

(2) INFORMATION FOR SEQ ID NO: 265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

TGGTGTTCAA AAGAGGAAAT CCAAATGGCC AACAGGCACA TGAAAAAATG TTCAGGATCA	60
CTAGCAATCA GGGAAATGCA AATCAAAATC ACAATGAGCT TTTACCTCAC CCCGGTTAGA	120
ATGGCTCACA TTCAGAAATC TACCAGCAAT AGATGCTGGC GAGGATGTGG GGGAAAAGAG	180
ACACTAACCC ACTGTTGGTG GGAATGCAAA CTCGTCAAGC CACTGTGGAA GTCAGTCTGG	240
AGATTCCCTCA GAAACCTGAA GATAACCCCTA CCATTCAACC CAGCCATCCC ACTCCTTGGA	300
ATTTACCCAA AGGAAATGAA ATTGGCAAAC AAACAAGCTA TCTGCACATT AATGTTTATT	360
GCAGCTCAAT TCACAATAGC TAAGACCTGG AACCAACCCA AATGGCCCAT CAACAGTAGA	420
CTGGGATAAA AGAAATTATG GGACATGTAC TCTATAAAA	459

(2) INFORMATION FOR SEQ ID NO: 266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 707 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

GGAGTCTAAA AATATTATTT CATAGAAGTT AACAATATAA TGATGGAGAC CAGAGTTGTG	60
GCACAGTGGG CAAAGCTGCC ACCTGTGACA CCAGCACCCC ATGTGGGCGC CAGTTCATGT	120
CCCAGCTGCT GCACTTGACAG TCCAGCTCCC TGCCAATGGT TTGGGAAAGC AACAGAAGAT	180
GGCCCAAGTG TTTGGGTCCC TGCCACCCAC GTGGGAGACC TGGGTCAAGC TCCTGGTTCC	240
TGACTTTGGC CTGGCTCAGC ATTGGCCATT GCAGGTGTCT AGGAAGTGAA TCAGCAGATA	300
GAAGATCTCT CTCTCTCTCT CTCTAACTCT TTCAAATAA GTAAATAAAT ATTTTAAAA	360
TATATATGGT GGATATCAGA CGCTGGGGAG GGAAGTAGAG AGGGAGAGAT AGTGAAAGGT	420
CTATGGTGGG TACAGCTGAA GAAAAGTGAG AAATCTGAG GTTGTATTGC ACCATGTGAC	480
AACAGATAAT GTGTGCCAAC AGATAATGTA CCATACAGTT CTACATTTAA GAAAAGAAAA	540
CTAGAAGATA CAATTTTGGA TATTTTCACT ACAAAGAAA ATGTTAACAA TTAAAGGAGA	600
TAGATATATG TACCCCACTA GACATTTAAC AAGATAGACA TGTATCAAAA TGTCAAATGC	660
TACCCAATAA ATATTTATAA ATTGTAAATG TCTGTAAAT TTTAAAA	707

(2) INFORMATION FOR SEQ ID NO: 267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

TGAGAGGCAA AATGTAGAAA GAGAACAGAG AGAGAGAGAG AGAGAGAGAG AGAGCGAGCT	60
TTCATCTGCT GGTTCACTCC CAATTGCAGA ACCAGCCAGA GACAGTATAG GCAGAATCCA	120
GGAGCTGGGA ACTCTGTCAG GGTCTCTCAT GTGGGTGGTA AGGGCCCAGA TACTTGGGCC	180
ATCTTCAGTT GCCTTCCCAC ACGCATTAGC AAGGAGCTGG ATCAGGACTT GAACCAGCAT	240
TCTGATATGG GATTCTGACA TTACACACAG CAGCTTAACC CACTATGCCA CAGTGGCGGC	300
CCTTGCCCTC ATCCTTAATA ACCTATATAC TACATCTGCC TGACTIONAT CAAAGTGGCA	360
GAACCTGGGA GCATCTCAAG ACATAGGAAT GGTGTAAGAA TTTTACTAGT GGGGCTGGTG	420
TTGTTGCACA GTGAGTTAAG CCGCTGCCTG CAATGCCGGA CTTCCCATAC GGGTGCCAGT	480
TCAAGTCCTG GCTGGCTCCA CTTCTGATCC AGCTCCCTAC TAATGCACCT GGGAAAGCAG	540
CAAAGACAG TGCAAGTGCT TGGGCCGCTG TCACTCATGT AGGAGACCTG GGTGAAGCTn	600
CCTGGGCTCC TGGGGCnTTC AGCCTGGCCC AGTTCCTGG	639

(2) INFORMATION FOR SEQ ID NO: 268:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 550 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

TGCCTTTCAA ATAAATAAAA TAAACCTTGA AAAGAAAAAC TAATAGATTA TTAAAGGACG	60
AAAGAAGCTT GAATACAATT GCTTTTTAGC AAGTGTTAGT TATTTTGTG AGGACACGAT	120
CCACCTCGGT GTCCTTGAGT GCAGCCTCTC AGGGCAGTCA CAAGTCTTCA GAATTGGTCT	180
TAAAAGTCCT TTAGGAAGCT GCAGCGTTGG AGGGGGTCCA AAATCTGACA CCTCCAGGTT	240
CTCCTCACTG ATGGGGAGAT CATGGCTTCT CAGCACAGCA CCAACTGGGG TTAGTGTTTT	300
ATTTTGTGTT TAGATTTATG TACTTGACAG GCAGAGGGAG AGAGAGAGAG GAGAGAGAGA	360
GAGAAAGAGA GGAAACCTTC ATCTGTTGAT TCACTCCCTA AATGTCCATA ACAACTGGGG	420
CTGGACCAGT CCCAACCCAG GAGCCAGAAA CTCTCTCTGG ATCTCCCATG TGGACTGTAG	480

893

GGACCCAAGC ACTTGGGCCA TCAACTCCTG CCTTCCAGAT ACATCAGCAG GAAGCTGAAT 540
CAAAAGTGCA 550

(2) INFORMATION FOR SEQ ID NO: 269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

GTGGGGGAT CTGGGATGGA GCTCAAGAGT TCCTGGCTTC TGCTTGATTG AGCTCTGGCC 60
ATTTTGGGAA CGAATCAGCA GATGGAAGAT CTCTTGCTCA CTC'TTTTATT TTTTCAAAGC 120
TTTATTTTAT TTATTTAAAT GGAAGAGTTA GAACGCTCTT CCATCCACTG GATTCACTCC 180
CCAAATGGCA GCAATGGCCA GCGCTGGGTC AGGCTGAAGC CAGGAATTTC TTCTGGATTT 240
CCCACATGGC TGCAGAGGTC CAAGGACTTG GGCCATTCTC CACTGCTTTC TTGGGCACAT 300
TAGCAGGGAG CTGGATCAGA ACTGGAGCAG CTGGGACTTG AACCAGTGCC ATATGGGATG 360
CGGGCACTGT AGGCAGCAGC TTTACCTGCT ATGCCACTGC GCTGGCCCCA TTCTCTCTTT 420
CTCTGTCTCT TTCATCTCTCT CTCCCCATCC ACCATCTCTC TGTCAC'TTG CCTTTGAATA 480
TATGAAAGTG ATTTT'TAAAA ATnAAAGTAA TTCTTAATAA TATCAGGAAA TGAATTCTAT 540
A 541

(2) INFORMATION FOR SEQ ID NO: 270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

CGGTTTATTT AAAAGATATG TTAAGGGACT TAAAGGGAGA CTTAGACTCC AATACAATAG 60
TACTGGGGGA CTTCAATACT CCACTCTCAG AAATAGACAG ATCAACTGGA CAGAAGATCA 120
ACAAGGAGAC AGTAGATTTA AATGACACTA TAGCCCAAAT GGACCTAACA GATATCTACA 180
GAAC'TTTTCA TCTGACATTT AAAGATTTTA CATTC'TTCTC AGCAGTGCAT GGAACCTTCT 240
CTAGGATTGA CCACATCCTA GGCCATAAAG CAAGTCTCAG CAAATTCAA AGAATTAGAA 300

894

TCATACGATG CAGCTGCTCA GACCATAGCG GAATTAAGTT GGAAATTATC AACTCAGGGA	360
ATCCCTAAAG TACACAGAAA CACATGGAGA CTGGAACAAC ATGGCTCCTG GAATGAACAG	420
TGGGTCATAG GAAGAAATCA AAAGAGAAAT CAAAACTTT CTGGAAGTAA AGGAGGGT	478

(2) INFORMATION FOR SEQ ID NO: 271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

GAATTGAGCn CGAAACAGGT GTAnCCATAA GTTTTGATAT GTTGTCATGT CACATCATTA	60
GTTTCCAGAA AATTTTGTAT TTCTATTTTG ATTTCTTCTA TTACCCAGTG TTCATTCAGG	120
AACTTGTTAT TCATGTGTTT GCATATGCTC TAGATATTCC CGAGTTGCTG ATTTCCAGCT	180
TTTTTCCACC ATGGTATGAG AAGCTGCATG GTATGATTCC AATTCTTTTG ACATTGTGA	240
GACTTGCTTT ATGGCCTAGT ATGTGGTCAA TCCTAGAAAA AGTTCCATGT ACTGCTGAGA	300
AGAATCTGTA TTCTTCAAGT GTAGGAATAA AAGTTCTGTA GATATTAGAT CCATTGGGCT	360
ACAGTGnTGA TTAAATCCCT GnTTCCTGnT GGATTTGTC GGGGACCGTC CATGCT	416

(2) INFORMATION FOR SEQ ID NO: 272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

TTGTTCTTAC TGAAGTGCAT CAGTGGCCTC TACCCTGCTT CTGCTGCCTT CCGCCCTCCC	60
TGGCCAACAA GCACTTGGA GAGGAGCCCT GGATGAACGT TGTAACAGA CCTCAAGACT	120
CCCTTGGGAT GCTGGCATCC CAGTTCCTAG CGCTGGGTT CCAGTCCTCT GCTTTCCTGT	180
CCCTGCCGGC TAAGTGGGAG AACTGGATTG GGAGCAGGTG CAAGCATCTG GGGAGTGAAC	240
CAGCAGAGAG GGGACCACGT TTAATCCTTT TCTCTCTGCC TCTCAGATAC ATGCAGATAT	300
ATACAAGTTT AAAAGGAATG CTCGGTTTT TGGCAAATTA TTTGTTAATA AAAATTTAAA	360
TATTTCTGTC ACTTTTTAAA CATTTATTTA TTATTTGAGA GAGTTACGAG AGGGAGAGAC	420

895

AGAGAGAGGT CTCTATCTGC GGTTCACCTCC CCAGGTGGGC TGCAAGGGCC AGGG

474

(2) INFORMATION FOR SEQ ID NO: 273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

CGGACTGTGC CTGCATGGCC TGCATGTGAA CAGACTTGCC ATTGGCTGGG AGCGTCCTGC	60
TAGGGGAACC TAGGGTATAT AATGGGGATA GGATTGTGTA GGGGGATGAG GGCTTGGCTT	120
CTTTTCTTTC GCCTTGCATC TGGATGAATA AAGTTCCATG AGAACCGAGT AAGCAGCGAT	180
CGTGTCTGTTA CTATGCTGGA CTCTCGCGGG CAAGCGTCCG GCAGCCCCTA GACTCAAATG	240
TTGTCAGAAG TTTGAGAACT GCCATCCTAA AGAATTTCTG ATGGGGCCAG TACGGTGGCA	300
TAGCAGGTTA ACACAGTGTC TGCAGTGCTG GCATTCCATA TAGGCGCTGG TTCGAGTCCT	360
GGCTGCTCCA CTCCAATCC AGCTCTCTGG CTAATGGCCT GGGAAAGCAG CAGAGGGATG	420
GCCCAGG	427

(2) INFORMATION FOR SEQ ID NO: 274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

CATCAACCACC ACAAATGAAA ACTTAAGCAT GCACTGGTGA TCCACAGGAG AATGGAATTC	60
CTCTCTCCTA TAGGCCTGAG CACCACCCTG CAGGAGGGGC TTAAAAAGGC AGATGCAGCA	120
CATCTTTGAA TACCTTGTTT CTACTTGTGG TTGTGTGATT TTCTTTTTTT TTAAGATTTT	180
CTTTATTTTA CTTGGGAGGT AGAGTTTGAG ACAGTAAGAG GGAGAGACGG AGAGAAATGT	240
CTTCCCTATG TTGGTTCATT CCACAAATGG CTGCAATAGC TAGAGCTGCA CCAATCTGAA	300
GCCAGGAGAC AGGCACCTCT TTCTGGTCTT CCAAATGAGG GCAGAGGCCC AAGGATCCAG	360
GCCATCCTCC ACTGCTTTCC CAGGCCATAG CAGAGAGCTG GATTGGAAGT GGAGCAGCCG	420
GGGCTAGAAT CAGCACCCAT ATGTGAACCT GTGCTGCAGG CAGAGGATTA ACCTACTGCA	480

896

CCACTGTGCT GGGCCTGGCT GTGTGATTTT CAGCATTTAG CATTGGAGCA TGGGTGTGTC	540
ATGGTTGGCC ATTCCCTAAC ACCATGGCTG ATCTCTACTC AGGTTTGCAG TTTTAGGCAA	600
CATTTTGAGC TGCACA	616

(2) INFORMATION FOR SEQ ID NO: 275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

TGTGATAnTC TGnACTTTCA AATAAATAAA TAAATGAATC TTTTTTTTTTA AAAAAGTGGA	60
TTAGGGTACC TTTTCCCCAC AGCCTTGCCA TCATTTATTG TTTTTTTGAT TTATATATGA	120
TAGCCATTCT AACTAGGGGG AGGTGAAACC TCATTGTGGA TTTTATTGTC ATTTATTGAT	180
GGCTAGTGAT CCTGAGCAGA TTTTAAATTT CACCCTTTGA AAAATGCCTG CTCATGTCCT	240
TTTTCCTTTG CCTATTTCTT AACTGGATCG TTTGTTGCTG CTGAGTTTCT TGACTCTTTA	300
TAGATTCTTG ACATCAATCC TTTATCAGTT GCATAGTTTG AAAACATTTT CTTTGTAT	360
GTCAGTTGCC TCTTCAGTTT GTTGGGTGAT CCTTTACAGT GCAGAATCTT CTTAACTTGA	420
TGTAATTCCA TGGTCTATTT TTGCCTTTAn TGCCAGTGTT ATGGGGTnTT TCCAAGAAGT	480
CTTT	484

(2) INFORMATION FOR SEQ ID NO: 276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

CAGTGTGCC TTTCAACTTT CCATCTTGTC CGTGTGAGGG GGTCCCTCAC AGGGGACGGT	60
GGGCCCAGCC TGTCGTGTGC TCACTTGCTGTGACATCAC GGATGGGAAC TGnGTGAAAT	120
TTCAGCTCCC CAGATCTGAA ATTTACAGA GCAGCCTTTG TCACCTTGTT AGAGAATGTT	180
TTTCCATCTC AACTCAGCGG TAAACGGATC ATTTATACGC ACCTGTTTTT ATCTGGATGG	240
TGAATTTACC TGGTGGGTGG AAATTGGATG TGAGATTCAC ACAGCCTCAG AGCGTCTGGT	300

897

CAGAGGTACT TACTGAGGCT GCGCCATGG TGCAGTGGGC TAAGGCACCG CCTGTGACAC	360
CGGCATGGCT GCTCCATTG CAGTCCAGCT CCCTGCATAA AGCTCCTGGC TCCTGGCTTC	420
AGCCTGGCCC AGCCTTGGTC ACTGTGGCTA TTTGGGAAT GAACCAGCAA ATGGAAGAG	480
TCAGTCTCTC TCTCTCTCTC TCTCTCTCTC TCTCTCTCTC TCTCTCTGTA ATTCTGCCTT	540
TCAAAAAAAAA TTTAGGATGT ATGTATGTAT GTATTTATnT ATnTAT	586

(2) INFORMATION FOR SEQ ID NO: 277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

TCACTTTAAC ACTTAAAATG CTATTTTCCC TCTTAGCACA AGAGGACTTG GGGTGTCTATG	60
TCAAATTTT AAACATAACC CTTAGAAATA AATCTGTGGT AATGTATACA GAATTATGCA	120
GCTTTGCAGT TACAACTTC ATACACTTCA TAATTATGAC TTTAGGAACA TGGTGATTCT	180
TTCCACTCTG CCTGTCTGC CACCCACATC CCCACCCCTC TTCCTCCTCC CTCTCTTATT	240
CCCTCTTTTA TTTTGGACTA GGATATATTT TAATTTAACT TTATACATAT ATGATTAAC	300
CTATGTTAAG AGAAGAGTTC AGCAAAT	327

(2) INFORMATION FOR SEQ ID NO: 278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

TTCTAAAAAG ATTTTCTACT TCTACTTATA TACAAAAAAA TAAAATATTT CTTTATCTAA	60
TTGACACAAC CCTCTGTCCT GCTTTTTTGT TTAAAAGATT TATTTATTTA TTTGAAAGAG	120
AGTTAGAGAA AGGTAGACAG AGAGAGAGAG AGAATCACCA GGAACCTTTT CCAGGTCTCC	180
TGCTAGAGAG TAGGGGTCCA AGGACTTGGG CCATCTTACA CTGCTTTCCC AGACCAAAG	240
GAGACAGATG GGCTGGAAGT AGAGCAGCCA GATCTTGAAC TGGCACCCAT ATGAGATGCT	300
GGCACTGCAG GCTGTGGCTT TGCCCGCTAA GCCACAGTTC AAGCCCAAT ATGTCCGGCT	360

898

TTTTCGGATC ATATCAGTCT ATGACGTGCC ACTTATATTA CTATTAATCA ATGGCACCTC 420
TTACTCTGAA ATGTGATTAT CTTGTATGAT AAATTATACA TAAGTTCTTA AAATAAGTGT 480
C 481

(2) INFORMATION FOR SEQ ID NO: 279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

GCGTGAGGAG CAAGATCAGC CTGGAAAACG TGTGACAGCG TACCACTTTG AAACAGCTGA 60
GTATAAAGCA ATAGAATTTC CTTGGAGCTA CACATGCCAA AACTAAAAA AGCAAGTTCC 120
CCAGGCCAAC TGTTCCTTC TTCTTCTTCA TTTT TTTT TAAAGATTTA TTTATTGGA 180
AGGCAGAGTT ACGAGAGAGA CGGAAAATA GAAAGAGATC TTCCATCTGC TGGTCACTC 240
CTCAAATGGC CATTAACAGC CAGAGCTGGG CCAGGTTGAA GCTGGGAGCC AAGAGGTCCA 300
TCCCAGTCTC CCCCATGGGT GCAGGGGCCA AACACTTGGG CTATCCTCCT CTGCTTTTCC 360
CAGGCCCTTT AGCAGGGAGC TGGATCAGAA TTGGGGCAnC CGGGAnTTAA ACCCAGGCCC 420
ATGTGGGATG CCGGTGCTGT AGGTGGATGG CTAAC TCACT GCACCACAAT GCCAGCCCCA 480
A 481

(2) INFORMATION FOR SEQ ID NO: 280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

AACAGACATT CTTGCAGAT CTAGAAAAA TGATGCTGAA ATTCATATGG AGGCACAAGA 60
GACCTCGAAT AGCTAAAGCA ATCTTG TACA AAAAAACAA AGCCGGAGnA TCACAATACC 120
AGACTTCAGG ACGTACTACA GGCAGTTGT AATCAAAACA GCATGGTACT GGTACAGAAA 180
CAGATGGATA GACCAATGGA ACAGAATTGA AACACCAGAA ATCAACCCAA ACATCTACAG 240
CCAACTTATA TTTGATCAAG GATCTAAAAC TAATTCCTGG AGCAAGGACA GTCTATTCAA 300

899

TAAATGGTGC TGGGAAACT GGATTTCAC GTGCAGAATC ATGAAGCAAG ACCCCTACCT 360
TACACCTTAC AAAAAATCC ACTCAACGTG GATTAAAGAC CTAAATCTTC GTCCTGACAC 420
CATTAAAGTT ATTAGAGGAA CATTGGGnGA AAnCC 455

(2) INFORMATION FOR SEQ ID NO: 281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

GGCACTGGGG AGTGAAATAG CACGTGGGCA CTGTCTTTCT GTCTCTCAAA CATGTGAACA 60
CATTTTTTTA AAGAAGATGA CAAAAATAG GTAAAGTCCT CTGTCCGACG TGTTCACACC 120
ATTTAATTCA GTCTCTCGAT TGTTTTTACA AAAATAAAAG CCTTTTTTGT TTTACAACAG 180
TTTTTTTTTT TAAGGATGTA TTTATTTGAA AGACAATTAG AGGGAGGTCT TCCATCTGCT 240
GGTTCAGTCC CTAGATGGCC ACAGCGGCCA GGGCTGGGCC AGGCCAAAGC CAGGAACCGG 300
GAGCTTCTTT TGGGTCTCTC AAATGTGTGG CAGGGCCAAG CAGTTGGGCC GTCTCCACTG 360
CTCTCCCAGG CCGCTAGCAG GGAGCTGGGT CGGAAGCGGA CTGACGTTGC TGGCCTCGGC 420
CTACCTGCTG GCACCGTAAG CTGGCTCCAG GACAGTTTGA TGGAGGTGCA GTCCAGCACA 480
CTGTGTGTGT GTAAAAGTCA CACTTCCAGC ATACA 515

(2) INFORMATION FOR SEQ ID NO: 282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 585 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

GGAATGCCAG CCCGCCACTG CCGTCCGTCC TGGGTTGTTT CATACCCTAG CTCTTCTCCA 60
CGTCGTGAAA GCCCAGGCGA GGAGACCTGG TGA CTGTCCC GGGCACAGCA CTCGGTGAGG 120
CGTTCCAAGG GCATCCCAGG GTGCAGGCGT GGGCTGCCAC GTTCTCGCCC CACTCCACGT 180
GACCCTTTT GGCCCTCAGG GACAGGGCGA GGATGTTGGC TGGCCCTGGC CGCCCTTCAT 240
AGGGGTGCTC CTCAGAACCT GAGGGAGAAA TTCTTTTTCT CTGAGATTTA TTTATTTATT 300

900

TGAAAGAGAC AGAGATCTTT CATCTACTGG TTTACTCCCC AAATGGCCTC AACAGTCAGG 360
 GCTGGGCCAG GCCAAAGTCA GGAGCCAGGA ACTCCATCCA GGTCTCCAC ACAGATGGCA 420
 GGGACCAAAG TACTTGGGCC ATCTCTGCT GCCTTCCCAG GCGCATTAGC GTGGAGCTGG 480
 ATCAGAAGCA GGAAAGCCGG GATTCAGCTG GCCTCCAACG TGGGATGTGG GACAGAGCCC 540
 ACCCCTGGCA GGTTTTTTTT TTTnnGnnTT TTTTTATAT TnnAT 585

(2) INFORMATION FOR SEQ ID NO: 283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

ACTCTGCCTG TCAAAAAAAA AAAAAATCT TAAGGGGGCT CAGCTCAGCT GTGACTCCGT 60
 GATCCGCTAA TATGAGGTCT ATTTCCAGTC CCTCCTCCTC CATTTCCAAT CCAGTCCTT 120
 GCTAATTCAC CTGGAAAGCC ACGGGAAGAT TGACCCACTA CTTGGACCAG CTGGGAGATG 180
 TGGAACAGAT GAAGCTCCCG GCACCTGCCT CCTGGATTG CCCTGGCCAC CCAGAGCCCA 240
 TCCAGCAGAT GGAAGATCTC TCTCCTCTC CCAACTCTCA GCCAGTCACC CCACAACTCT 300
 TTCACATAAA TAAGAGTACA TTAAATTTAA AAGAGAATTG GCCAACTAAG TCTCTGAAGG 360
 TGGGGGGGTT GGGCTGACCC TGGGGCATAG TAGGTTAAGC ATCTATCTGT GGCTCCAGTT 420
 TGAGATGGAA GGACTCTCTG TAACTCTGAC TCTCCAGAAA AAAAAAAAAA GATAAAAATC 480
 TTAAAAAGAA TTATTATTAT TATTATTATT ATTATTATTA TGGGGCCTGT GCTGTGGTGT 540
 AGCAGGTAAA ACTGCCACAA GCAGTGCCGG CATCCCATAT GGGCTCCCAT TCGGAATCCC 600
 ATCCCCAGCT GGGCTGCTCT CTGCTAnGGT CTGGCA 636

(2) INFORMATION FOR SEQ ID NO: 284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 656 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

TAGAGATTTA GTAATCTTCT GAACTCTTTG CTTTCAACCA TTTTCAGTTG CCAAAGATCT 60